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(54) Title: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME

(57) Abstract:

HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME

Cross Reference to Related Applications

This application claims priority to the following provisional applications: U.S. Ser. No. 60/188,914, filed March 13, 2000, entitled, "NOVEL OLFACTORY RECEPTORS AND GENES ENCODING SAME," to Zozulya; U.S. Ser. No. 60/192,033, filed March 24, 2000, entitled, "NOVEL OLFACTORY RECEPTORS AND GENES ENCODING SAME," to Zozulya; U.S. Ser. No. 60/198,474, filed April 12, 2000, entitled, "NOVEL OLFACTORY RECEPTORS AND GENE ENCODING THE SAME" to Zozulya; U.S. Ser. No. 60/199,335, filed April 24, 2000, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/207,702, filed May 26, 2000, entitled, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/213,849, filed June 23, 2000, entitled, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/226,534, filed August 16, 2000, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/230,732, filed September 7, 2000, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; and U.S. Ser. No. 60/266,862, filed February 7, 2001, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya. All of these applications are herein incorporated by reference in their entireties.

Field of the Invention

The invention relates to newly identified mammalian chemosensory G protein-coupled receptors, particularly olfactory receptors, fragments thereof, classes of such receptors, genes and cDNAs encoding said receptors, vectors including said receptors, and cells that express said receptors. The invention also relates to methods of using such receptors, fragments, genes, cDNAs, vectors, and cells to identify molecules involved in olfactory perception. The invention therefore has application in the selection and design of odorant compositions, as well as malodor blockers (olfactory receptor antagonists), particularly perfumes and fragrance compositions and components of deodorants and other malodor blocking compositions.

Description of the Related Art

The olfactory system provides sensory information about the chemical composition of the external world. Olfactory sensation is thought to involve distinct
5 signaling pathways. These pathways are believed to be mediated by olfactory receptors (ORs). Cells which express olfactory receptors, when exposed to certain chemical stimuli, elicit olfactory sensation by depolarizing to generate an action potential, which is believed to trigger the sensation.

As such, olfactory receptors specifically recognize molecules that elicit
10 specific olfactory sensation. These molecules are also referred to herein as "odorants." Olfactory receptors belong to the 7-transmembrane receptor superfamily (Buck *et al.*, *Cell* 65:175-87 (1991)), which are also known as G protein-coupled receptors (GPCRs). G protein-coupled receptors control many physiological functions, such as endocrine function, exocrine function, heart rate, lipolysis,
15 carbohydrate metabolism, and transmembrane signaling. The biochemical analysis and molecular cloning of a number of such receptors has revealed many basic principles regarding the function of these receptors.

For example, U. S. Patent No. 5,691,188 describes how upon a ligand binding to a GPCR, the receptor presumably undergoes a conformational change leading to
20 activation of the G protein. G proteins are comprised of three subunits: a guanyl nucleotide binding α subunit, a β subunit, and a γ subunit. G proteins cycle between two forms, depending on whether GDP or GTP is bound to the α subunit. When GDP is bound, the G protein exists as a heterotrimer: the $G\alpha\beta\gamma$ complex. When GTP is bound, the α subunit dissociates from the heterotrimer, leaving a $G\beta\gamma$ complex. When
25 a $G\alpha\beta\gamma$ complex operatively associates with an activated G protein-coupled receptor in a cell membrane, the rate of exchange of GTP for bound GDP is increased and the rate of dissociation of the bound $G\alpha$ subunit from the $G\alpha\beta\gamma$ complex increases. The free $G\alpha$ subunit and $G\beta\gamma$ complex are thus capable of transmitting a signal to downstream elements of a variety of signal transduction pathways. These events form
30 the basis for a multiplicity of different cell signaling phenomena, including for example the signaling phenomena that are identified as neurological sensory perceptions such as taste and/or smell.

Genes encoding the olfactory receptors are active primarily in olfactory neurons (Axel, *Sci. Amer.*, 273:154-59 (1995)). Individual olfactory receptor types are expressed in subsets of cells distributed in distinct zones of the olfactory epithelium (Breer, *Semin. Cell Biol.*, 5:25-32 (1994)). The human genome contains approximately one thousand genes that encode a diverse repertoire of olfactory receptors (Rouquier, *Nat. Genet.*, 18:243-50 (1998); Trask, *Hum. Mol. Genet.*, 7:2007-20 (1998)). It has been demonstrated that members of the OR gene family are distributed on all but a few human chromosomes. Through fluorescence *in situ* hybridization analysis, Rouquier showed that OR sequences reside at more than 25 locations in the human genome. Rouquier also determined that the human genome has accumulated a striking number of dysfunctional OR copies: 72% of the analyzed sequences were found to be pseudogenes. An understanding of an animal's ability to detect and discriminate among the thousands of distinct odorants or tastants, and more particularly to distinguish, for example beneficial tastants or odorants from toxic tastants or odorants, is complicated by the fact that chemosensory receptors belong to a multigene family with over a thousand members. For instance, there are up to 1,000 odorant receptors in mammals.

Moreover, each chemosensory receptor neuron may express only one or a few of these receptors. With respect to odorant receptors, any given olfactory neuron can respond to a small set of odorant ligands. In addition, odorant discrimination for a given neuron may depend on the ligand specificity of the one or few receptors it expresses. To analyze odorant-receptor interactions and their effects on olfactory cells, specific ligands and the olfactory receptors to which they bind are identified. This analysis requires isolation and expression of olfactory polypeptides, followed by binding assays.

Some studies suggest that OR genes can be expressed in tissues other than the olfactory epithelium, indicating potential alternative biological roles for this class of chemosensory receptors. Expression of various ORs has been reported in human and murine erythroid cells (Feingold 1999), developing rat heart (Drutel, *Receptor Channels*, 3(1):33-40 (1995)), avian notochord (Nef, *PNAS*, 94(9):4766-71 (1997)) and lingual epithelium (Abe, *FES Lett.*, 316(3):253-56 (1993)). One experimentally documented case also established the existence of a large subset of mammalian ORs transcribed in testes and expressed on the surface of mature spermatozoa, thereby

suggesting a possible role of ORs in sperm chemotaxis (Parmenthler, *Nature*, 355:453-55 (1992); Walensky, *Mol. Med.*, 1(2):130-41 (1998); Branscomb, *Genetics*, 156(2):785-97 (2000)). It was also hypothesized that olfactory receptors might provide molecular codes for highly specific cell-cell recognition functions in development and embryogenesis (Dreyer, *PNAS*, 95(11):9072-77 (1998)).

Complete or partial sequences of numerous human and other eukaryotic chemosensory receptors are currently known. See, e.g., Pilpel, Y. and Lancet, D., *Protein Science*, 8:969-77 (1999); Mombaerts, P., *Annu. Rev. Neurosci.*, 22:487-50 (1999); see also, EP0867508A2, US 5874243, WO 92/17585, WO 95/18140, WO 97/17444, WO 99/67282. Due to the complexity of ligand-receptor interactions, and more particularly odorant-receptor interactions, information about ligand-receptor recognition is lacking. In part, the present invention addresses the need for better understanding of these interactions. The present invention also provides, among other things, novel chemosensory receptors, and methods for utilizing such novel chemosensory receptors and the genes and cDNAs encoding such receptors, especially for identifying compounds that can be used to module chemosensory transduction, such as olfaction.

Summary of the Invention

Toward that end, it is an object of the invention to provide a new family of G protein-coupled receptors comprising over two hundred fifty olfactory G protein-coupled receptors (OR) active in olfactory perception. It is another object of the invention to provide fragments and variants of such ORs which retain odorant-binding activity.

It is yet another object of the invention to provide nucleic acid sequences or molecules that encode such ORs, fragments, or allelic variants.

It is still another object of the invention to provide expression vectors which include nucleic acid sequences that encode such ORs, or fragments, or variants thereof, which are operably linked to at least one regulatory sequence such as a promoter, enhancer, or other sequences involved in positive or negative gene transcription and/or translation.

It is still another object of the invention to provide human or non-human cells that functionally express at least one of such ORs, or fragments, or variants thereof.

It is still another object of the invention to provide OR fusion proteins or polypeptides which include at least a fragment of at least one of such ORs.

It is another object of the invention to provide an isolated nucleic acid molecule encoding an OR comprising a nucleic acid sequence that is at least 30%,
5 more preferably at least 50%, still more preferably at least 60-70%, and still more preferably 75%, preferably 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to a nucleic acid sequence selected from the group consisting of: SEQ. ID. NO. 2, SEQ. ID. NO. 4, SEQ. ID. NO. 6, SEQ. ID. NO. 8, SEQ. ID. NO. 10, SEQ. ID. NO. 12, SEQ. ID. NO. 14, SEQ. ID. NO. 16, SEQ. ID. NO. 18, SEQ. ID. NO. 20, SEQ. ID. NO. 22, SEQ. ID. NO. 24, SEQ. ID. NO. 26, SEQ. ID. NO. 28, SEQ. ID. NO. 30, SEQ. ID. NO. 32, SEQ. ID. NO. 34, SEQ. ID. NO. 36, SEQ. ID. NO. 38, SEQ. ID. NO. 40, SEQ. ID. NO. 42, SEQ. ID. NO. 44, SEQ. ID. NO. 46, SEQ. ID. NO. 48, SEQ. ID. NO. 50, SEQ. ID. NO. 52, SEQ. ID. NO. 54, SEQ. ID. NO. 56, SEQ. ID. NO. 58, SEQ. ID. NO. 60, SEQ. ID. NO. 62, SEQ. ID. NO. 64, SEQ. ID. NO. 66, SEQ. ID. NO. 68, SEQ. ID. NO. 70, SEQ. ID. NO. 72, SEQ. ID. NO. 74, SEQ. ID. NO. 76, SEQ. ID. NO. 78, SEQ. ID. NO. 80, SEQ. ID. NO. 82, SEQ. ID. NO. 84, SEQ. ID. NO. 86, SEQ. ID. NO. 88, SEQ. ID. NO. 90, SEQ. ID. NO. 92, SEQ. ID. NO. 94, SEQ. ID. NO. 96, SEQ. ID. NO. 98, SEQ. ID. NO. 100, SEQ. ID. NO. 102, SEQ. ID. NO. 104, SEQ. ID. NO. 106, SEQ. ID. NO. 108, SEQ. ID. NO. 110, SEQ. ID. NO. 112, SEQ. ID. NO. 114, SEQ. ID. NO. 116, SEQ. ID. NO. 118, SEQ. ID. NO. 120, SEQ. ID. NO. 122, SEQ. ID. NO. 124, SEQ. ID. NO. 126, SEQ. ID. NO. 128, SEQ. ID. NO. 130, SEQ. ID. NO. 132, SEQ. ID. NO. 134, SEQ. ID. NO. 136, SEQ. ID. NO. 138, SEQ. ID. NO. 140, SEQ. ID. NO. 142, SEQ. ID. NO. 144, SEQ. ID. NO. 146, SEQ. ID. NO. 148, SEQ. ID. NO. 150, SEQ. ID. NO. 152, SEQ. ID. NO. 154, SEQ. ID. NO. 156, SEQ. ID. NO. 158, SEQ. ID. NO. 160, SEQ. ID. NO. 162, SEQ. ID. NO. 164, SEQ. ID. NO. 166, SEQ. ID. NO. 168, SEQ. ID. NO. 170, SEQ. ID. NO. 172, SEQ. ID. NO. 174, SEQ. ID. NO. 176, SEQ. ID. NO. 178, SEQ. ID. NO. 180, SEQ. ID. NO. 182, SEQ. ID. NO. 184, SEQ. ID. NO. 186, SEQ. ID. NO. 188, SEQ. ID. NO. 190, SEQ. ID. NO. 192, SEQ. ID. NO. 194, SEQ. ID. NO. 196, SEQ. ID. NO. 198, SEQ. ID. NO. 200, SEQ. ID. NO. 202, SEQ. ID. NO. 204, SEQ. ID. NO. 206, SEQ. ID. NO. 208, SEQ. ID. NO. 210, SEQ. ID. NO. 212, SEQ. ID. NO. 214, SEQ. ID. NO. 216, SEQ. ID. NO. 218, SEQ. ID. NO. 220, SEQ. ID. NO. 222, SEQ. ID.

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SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID
NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512.

It is a further object of the invention to provide an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a polypeptide having an amino acid sequence which is at least 40%, more preferably at least 50%, still more preferably at least 60-70%, and still more preferably 75%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID.

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It is still a further object of the invention to provide an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a fragment of a polypeptide having an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID. NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO. 241, SEQ. ID. NO. 243, SEQ. ID. NO. 245, SEQ. ID. NO. 247, SEQ. ID. NO. 249, SEQ. ID. NO. 251, SEQ. ID. NO. 253,

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ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO:
30 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and
SEQ ID NO: 511, wherein the fragment is at least 10, preferably 20, 30, 50, 70, 100,
or 150 amino acids in length.

It is still a further object of the invention to provide an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a variant of said fragment, wherein there is a variation in at most 10, preferably 5, 4, 3, 2, or 1 amino acid residues.

5 It is still another object of the invention to provide an isolated polypeptide comprising an amino acid sequence that is at least 40%, 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, or 99% identical to an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID.

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ID. NO. 491, SEQ. ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO:

499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

It is still a further object of the invention to provide an isolated polypeptide comprising a fragment of a polypeptide having an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID. NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO. 241, SEQ. ID. NO.

243, SEQ. ID. NO. 245, SEQ. ID. NO. 247, SEQ. ID. NO. 249, SEQ. ID. NO. 251,
SEQ. ID. NO. 253, SEQ. ID. NO. 255, SEQ. ID. NO. 257, SEQ. ID. NO. 259, SEQ.
ID. NO. 261, SEQ. ID. NO., 263, SEQ. ID. NO., 265, SEQ. ID. NO. 267, SEQ. ID.
NO. 269, SEQ. ID. NO. 271, SEQ. ID. NO. 273, SEQ. ID. NO. 275, SEQ. ID. NO.
5 277, SEQ. ID. NO. 279, SEQ. ID. NO. 281, SEQ. ID. NO. 283, SEQ. ID. NO. 285,
SEQ. ID. NO. 287, SEQ. ID. NO. 289, SEQ. ID. NO. 291, SEQ. ID. NO. 293, SEQ.
ID. NO. 295, SEQ. ID. NO. 297, SEQ. ID. NO. 299, SEQ. ID. NO. 301, SEQ. ID.
NO. 303, SEQ. ID. NO. 305, SEQ. ID. NO. 307, SEQ. ID. NO. 309, SEQ. ID. NO.
311, SEQ. ID. NO. 313, SEQ. ID. NO. 315, SEQ. ID. NO. 317, SEQ. ID. NO. 319,
10 SEQ. ID. NO. 321, SEQ. ID. NO. 323, SEQ. ID. NO. 325, SEQ. ID. NO. 327, SEQ.
ID. NO. 329, SEQ. ID. NO. 331, SEQ. ID. NO. 333, SEQ. ID. NO. 335, SEQ. ID.
NO. 337, SEQ. ID. NO. 339, SEQ. ID. NO. 341, SEQ. ID. NO. 343, SEQ. ID. NO.
345, SEQ. ID. NO. 347, SEQ. ID. NO. 349, SEQ. ID. NO. 351, SEQ. ID. NO. 353,
SEQ. ID. NO. 355, SEQ. ID. NO. 357, SEQ. ID. NO. 359, SEQ. ID. NO. 361, SEQ.
15 ID. NO. 363, SEQ. ID. NO. 365, SEQ. ID. NO. 367, SEQ. ID. NO. 369, SEQ ID NO:
371, SEQ. ID. NO. 373, SEQ. ID. NO. 375, SEQ. ID. NO. 377, SEQ. ID. NO. 379,
SEQ. ID. NO. 381, SEQ. ID. NO. 383, SEQ. ID. NO. 385, SEQ. ID. NO. 387, SEQ.
ID. NO. 389, SEQ. ID. NO. 391, SEQ. ID. NO. 393, SEQ. ID. NO. 395, SEQ. ID.
NO. 397, SEQ. ID. NO. 399, SEQ. ID. NO. 401, SEQ. ID. NO. 403, SEQ. ID. NO.
20 405, SEQ. ID. NO. 407, SEQ. ID. NO. 409, SEQ. ID. NO. 411, SEQ. ID. NO. 413,
SEQ. ID. NO. 415, SEQ. ID. NO. 417, SEQ. ID. NO. 419, SEQ. ID. NO. 421, SEQ.
ID. NO. 423, SEQ. ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID.
NO. 431, SEQ. ID. NO. 433, SEQ. ID. NO. 435, SEQ. ID. NO. 437, SEQ. ID. NO.
439, SEQ. ID. NO. 441, SEQ. ID. NO. 443, SEQ. ID. NO. 445, SEQ. ID. NO. 447,
25 SEQ. ID. NO. 449, SEQ. ID. NO. 451, SEQ. ID. NO. 453, SEQ. ID. NO. 455, SEQ.
ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID.
NO. 465, SEQ. ID. NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO.
473, SEQ. ID. NO. 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481,
SEQ. ID. NO. 483, SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ.
30 ID. NO. 491, SEQ. ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO:
499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ
ID NO: 509 and SEQ ID NO: 511, wherein the fragment is at least 40, preferably 60,
80, 100, 150, 200, or 250 amino acids in length.

It is still a further object of the invention to provide an isolated polypeptide comprising a variant of said fragment, especially naturally occurring allelic variants, the expression of which may be significant in the manner by which different persons in the human population perceive odors differently, both on a qualitative and
5 quantitative level, wherein there is a variation in at most 10, preferably 5, 4, 3, 2, or 1 amino acid residues.

It is still another object of the invention to provide agonists, including inverse agonists, or antagonists of such ORs, or fragments or variants thereof.

It is yet another object of the invention to provide methods for representing the
10 perception of odor and/or for predicting the perception of odor in a mammal, including in a human. Preferably, such methods may be performed by using the ORs, or fragments or variants thereof, and genes encoding such ORs, or fragments or variants thereof, disclosed herein.

It is yet another object of the invention to provide novel molecules or combinations of
15 molecules which elicit a predetermined olfactory perception in a mammal. Such molecules or compositions can be generated by determining a value of olfactory perception in a mammal for a known molecule or combinations of molecules; determining a value of olfactory perception in a mammal for one or more unknown molecules or combinations of molecules; comparing the value of olfactory perception
20 in a mammal for one or more unknown compositions to the value of olfactory perception in a mammal for one or more known compositions; selecting a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal; and combining two or more unknown molecules or combinations of molecules to form a molecule or combination of molecules that elicits a
25 predetermined olfactory perception in a mammal. The combining step yields a single molecule or a combination of molecules that elicits a predetermined olfactory perception in a mammal.

It is still a further object of the invention to provide a method of screening one or more compounds for the presence of an odor detectable by a mammal, comprising:
30 a step of contacting said one or more compounds with the disclosed ORs, fragments or variants thereof, preferably wherein the mammal is a human.

It is another object of the invention to provided a method for simulating a fragrance, comprising: for each of a plurality of ORs, or fragments of variants thereof

disclosed herein, preferably human ORs, ascertaining the extent to which the OR interacts with the fragrance; and combining a plurality of compounds, each having a previously ascertained interaction with one or more of the ORs, in amounts that together provide a receptor-stimulation profile that mimics the profile for the fragrance. Interaction of a fragrance with an OR can be determined using any of the binding or reporter assays described herein. The plurality of compounds may then be combined to form a mixture. If desired, one or more of the plurality of the compounds can be combined covalently. The combined compounds substantially stimulate at least 50%, 60%, 70%, 75%, 80% or 90% or all of the receptors that are substantially stimulated by the fragrance.

In yet another aspect of the invention, a method is provided wherein a plurality of standard compounds are tested against a plurality of ORs, or fragments or variants thereof, to ascertain the extent to which the ORs each interact with each standard compound, thereby generating a receptor stimulation profile for each standard compound. These receptor stimulation profiles may then be stored in a relational database on a data storage medium. The method may further comprise providing a desired receptor-stimulation profile for a scent; comparing the desired receptor stimulation profile to the relational database; and ascertaining one or more combinations of standard compounds that most closely match the desired receptor-stimulation profile. The method may further comprise combining standard compounds in one or more of the ascertained combinations to simulate the scent.

It is a further object of the invention to provide a method for representing olfactory perception of a particular smell in a mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n ORs of said vertebrate, where n is greater than or equal to 4, n is greater than or equal to 12; n is greater than or equal to 24, n is greater than or equal to 48; n is greater than or equal to 72; n is greater than or equal to 96; n is greater than or equal to 120; n is greater than or equal to 144; n is greater than or equal to 168; n is greater than or equal to 192; n is greater than or equal to 216, or n is greater than or equal to 256; and generating from said values a quantitative representation of olfactory perception. The ORs may be an olfactory receptor disclosed herein, or fragments or variants thereof, the representation may constitute a point or a volume in n -dimensional space, may constitute a graph or a spectrum, and may constitute a matrix of quantitative representations. Also, the

providing step may comprise contacting a plurality of recombinantly produced ORs, or fragments or variants thereof, with a test composition and quantitatively measuring the interaction of said composition with said receptors.

It is yet another object of the invention to provide a method for predicting the
5 olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n ORs of said vertebrate, where n is greater than or equal to 4 n is greater than or equal to 12; n is greater than or equal to 24, n is greater than or equal to 48; n is greater than or equal to 72; n is greater than or equal to 96; n is greater than or equal to 120; n is greater than or equal to 144; n is greater than or equal to 168; n is greater than or equal to 192; n is greater than or equal to 216, or n is greater than or equal to 256; for one or more molecules or combinations of molecules yielding known olfactory perception in a mammal; and generating from said values a quantitative
10 representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known olfactory perception in a mammal, providing values X_1 to X_n representative of the quantitative stimulation of each of n ORs of said vertebrate, where n is greater than or equal to 4, n is greater than or equal to 12; n is greater than or equal to 24, n is greater than or equal to 48; n is greater than or equal to 72; n is greater than or equal to 96; n is greater than or equal to 120; n is greater than or equal to 144; n is greater than or equal to 168; n is greater than or equal to 192; n is greater than or equal to 216, or n is greater than or equal to 273; for one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal; and generating from said values a quantitative representation of
20 olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal, and predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal by comparing the quantitative representation of olfactory perception in a mammal for the
25 one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal to the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known

olfactory perception in a mammal. The ORs used in this method may include an olfactory receptor, or fragment or variant thereof, disclosed herein.

Brief Description of the Drawings

5 Figure 1 illustrates the multiple sequence alignment derived for fifty novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty novel human olfactory receptors (hOR) proteins described herein are designated AOLFR1 through AOLFR52. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences
10 AOLFR2 through AOLFR52 were analyzed for alignment with the AOLFR1 amino acid sequence.

 Figure 2 illustrates the multiple sequence alignment derived for fifty novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty novel human olfactory receptors (hOR) proteins
15 described herein are designated AOLFR54 through AOLFR109. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR55 through AOLFR109 were analyzed for alignment with the AOLFR54 amino acid sequence.

 Figure 3 illustrates the multiple sequence alignment derived for fifty novel
20 ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty novel human olfactory receptors (hOR) proteins described herein are designated AOLFR110 through AOLFR163. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR111 through AOLFR163 were analyzed for alignment with the
25 AOLFR110 amino acid sequence.

 Figure 4 illustrates the multiple sequence alignment derived for fifty-four novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty-four novel human olfactory receptors (hOR) proteins described herein are designated AOLFR165 through AOLFR217. The
30 alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR166 through AOLFR217 were analyzed for alignment with the AOLFR165 amino acid sequence.

Figure 5 illustrates the multiple sequence alignment derived for fifty-two novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty-two novel human olfactory receptors (hOR) proteins described herein, which are designated AOLFR218 through AOLFR328. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR219 through AOLFR328 were analyzed for alignment with the AOLFR218 amino acid sequence.

Detailed Description of the Invention

The invention thus provides isolated nucleic acid molecules encoding olfactory-cell-specific G protein-coupled receptors ("GPCRs"), and the polypeptides they encode. These nucleic acid molecules and the polypeptides that they encode are members of the olfactory receptor family. Other members of the olfactory receptor family are disclosed in Krautwurst, *et al.*, *Cell*, 95:917-26 (1998), and WO 0035274, the contents of which are herein incorporated by reference in their entireties.

According to one aspect of the invention, genes encoding over two hundred fifty distinct, novel human olfactory (odorant) receptors (also herein referred to ORs) have been identified in genome sequence databases. All of these receptor genes have been initially detected by computer DNA sequence analysis of genomic clones (unfinished High Throughput Genomic Sequence database accession numbers AB045359, AP002532, AP002533, AL365440, AC073487, AL359636, AL359955, AP002535, AB045365, AL359218, AC002555, AB045361, AL359512, AC023255, AL358773, AL357767, AL358874, AC068380, AC025283, AP002407, AC018700, AC022289, AC006313, AC002556, AC011571, AL121944, AC007194, AP001112, AC021660, AP000723, AC016856, AC018700, AP000818, AC00596, AP000916, AC011517, AP001112, AP000916, AC021427, AC021427, AC020884, AC019108, AL135841, AL133410, AF186996, AL138834, AC009237, AC025249, AC010930, AC009758, AC009642, AC009758, AC025249, AF101706, AC009642, AC025249, AC021660, AC011647, AC011711, AC09642, AC020597, AC011711, AC019088, AC022882, AC011571, AL121944, AP000435, AC012616, AC010332, AC010766, AP000743, AC021809, AC011879, AC021304, AC023226, AL160314, AC021304, AC020380, AC011904, AC004977, AC021304, AP000868, AP000825, AC023080, AC022207, AC121986, AC010814, AC018700, AC021304, AC008620, AC011537,

AC010760, AC027641, AC017103, AC024729, AC024257, AC025115, AP001524, AP000916, AC010814, AL162254, AC025234, AP001521, AC026090, AC019088, AC016856, AC016787, AC009594, AC026038, AQ628489, AC025942, AL163152, AC026975, AC024654, AP001803, AP001804, AL353767, AP001884, AC026083, 5 AC018793, AP000818, AL353894, AL049734, AL355366, AC011464, AC037472, AC036111, AC019093, AC027239, AC027522, AC009545, AC021333, AC036216, AC021935, AC022762, AL356019, AC055861, AC018375, AC072059, AC068339, AC022891, AL357039, AP002345, AC044810, AC073113, AC024399, AC023564, AL390860, AC074365, AP002826, AL359636, AL391534, AC055731, AC076959, 10 AP002826, AC019088, AC009779, AL445307, AP002512, AP000818, AC079190) by virtue of their sequence homology to some of the known human and other mammalian olfactory receptor genes.

Alternatively, nucleic acids encoding the olfactory receptors (ORs) and polypeptides of the invention can be isolated from a variety of sources, genetically 15 engineered, amplified, synthesized, and/or expressed recombinantly according to the methods disclosed in WO 0035374, which is herein incorporated by reference in its entirety.

These nucleic acids provide valuable probes for the identification of olfactory cells, as the nucleic acids are specifically expressed in olfactory cells. They can also 20 serve as tools for the generation of sensory topographical maps that elucidate the relationship between olfactory cells and olfactory sensory neurons leading to olfactory centers in the brain. Furthermore, the nucleic acids and the polypeptides they encode can be used as probes to elucidate olfactory-induced behaviors.

The invention also provides methods of screening for modulators, *e.g.*, 25 activators, inhibitors, stimulators, enhancers, agonists, inverse agonists and antagonists, of the ORs, or fragments or variants thereof, of the invention. Such modulators of olfactory transduction are useful for pharmacological and genetic modulation of olfactory signaling pathways. These methods of screening can be used to identify high affinity agonists and antagonists of olfactory cell activity. These 30 modulator compounds can then be used in the food, pharmaceutical, and cosmetic industries to customize odors and fragrances.

Thus, the invention provides assays for olfactory modulation, where the ORs, or fragments or variants thereof, of the invention act as direct or indirect reporter

molecules for the effect of modulators on olfactory transduction. The ORs, or fragments or variants thereof, can be used in assays, *e.g.*, to measure changes in ion concentration, membrane potential, current flow, ion flux, transcription, signal transduction, receptor-ligand interaction, second messenger concentrations, *in vitro*, *in vivo* and *ex vivo*. In one embodiment, the ORs, or fragments or variants thereof, can be used as an indirect reporters via attachment to second reporter molecules, such as green fluorescent protein (*see, e.g., Mistili et al., Nature Biotech., 15:961-64 (1997)*). In another embodiment, the ORs, or fragments or variants thereof, can be expressed in host cells, and modulation of olfactory transduction via OR activity can be assayed by measuring changes in Ca^{2+} levels.

Methods of assaying for modulators of olfactory transduction include *in vitro* ligand binding assays using the ORs of the invention, or fragments or variants thereof. More particularly, such assays can use the ORs; portions thereof such as the extracellular or transmembrane domains; chimeric proteins comprising one or more of such domains; oocyte receptor expression; tissue culture cell receptor expression; transcriptional activation of the receptor; G protein binding to the receptor; ligand binding assays; voltage, membrane potential and conductance changes; ion flux assays; changes in intracellular second messengers such as cAMP and inositol triphosphate; changes in intracellular Ca^{2+} levels; and neurotransmitter release.

The invention also provides for methods of detecting olfactory nucleic acid and protein expression, allowing for the investigation of olfactory transduction regulation and specific identification of olfactory receptor cells. The ORs, fragments, and variants of the invention can also be used to generate monoclonal and polyclonal antibodies useful for identifying olfactory receptor cells. Olfactory receptor cells can be identified using techniques such as reverse transcription and amplification of mRNA, isolation of total RNA or poly A⁺ RNA, northern blotting, dot blotting, *in situ* hybridization, RNase protection, S1 digestion, probing DNA microchip arrays, western blots, and the like.

A. Identification and Characterization of Olfactory Receptors

The amino acid sequences of the ORs and polypeptides of the invention can be identified by putative translation of the coding nucleic acid sequences. These various

amino acid sequences and the coding nucleic acid sequences may be compared to one another or to other sequences according to a number of methods.

For example, in sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence
5 comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program parameters can be used, as described below for the BLASTN and BLASTP programs, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent
10 sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window," as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of: from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in
15 which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well known in the art. Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment
20 algorithm of Needleman & Wunsch, *J Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *PNAS*, 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (*see, e.g., Current*
25 *Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 supplement)).

A preferred example of an algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, *Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al.*, *J Mol. Biol.* 215:403-410 (1990), respectively. Software for
30 performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued

threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, Altschul *et al.*, *Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al.*, *J Mol. Biol.* 215:403-410 (1990)). These initial neighborhood word hits act as seeds for initiating
5 searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a
10 scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and
15 X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, *PNAS*, 89:10915 (1989))
20 alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

Another example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments to show relationship and percent sequence identity. It also plots a so-called "tree" or "dendrogram" showing the clustering relationships used to create the
25 alignment (*see, e.g.*, Figure 2). PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, *J Mol. Evol.* 35:351-60 (1987). The method used is similar to the method described by Higgins & Sharp, *CABIOS* 5:151-153 (1989). The program can align up to 300 sequences, each of a maximum length of
30 5,000 nucleotides or amino acids. The multiple alignment procedure begins with the pairwise alignment of the two most similar sequences, producing a cluster of two aligned sequences. This cluster is then aligned to the next most related sequence or cluster of aligned sequences. Two clusters of sequences are aligned by a simple

extension of the pairwise alignment of two individual sequences. The final alignment is achieved by a series of progressive, pairwise alignments. The program is run by designating specific sequences and their amino acid or nucleotide coordinates for regions of sequence comparison and by designating the program parameters. Using
5 PILEUP, a reference sequence is compared to other test sequences to determine the percent sequence identity relationship using the following parameters: default gap weight (3.00), default gap length weight (0.10), and weighted end gaps. PILEUP can be obtained from the GCG sequence analysis software package, *e.g.*, version 7. 0 (Devereaux *et al.*, *Nuc. Acids Res.* 12:387-395 (1984) encoded by the genes were
10 derived by conceptual translation of the corresponding open reading frames. Comparison of these protein sequences to all known proteins in the public sequence databases using BLASTP algorithm revealed their strong homology to the members of the mammalian olfactory receptor family, each of the odorant receptor sequences having at least 50%, and preferably at least 55%, at least 60%, at least 65%, and most
15 preferably at least 70%, amino acid identity to at least one known member of the family.

The nucleic acid molecules of the present invention are typically intronless and encode putative OR proteins generally having lengths of approximately 290 to approximately 400 amino acid residues that contain seven transmembrane domains, as
20 predicted by hydrophobicity plotting analysis, indicating that they belong to the G protein-coupled receptor 7-transmembrane (7TM) superfamily, which includes the subset of taste and olfactory receptors. In addition to the overall structural similarity, each of the ORs identified herein has a characteristic sequence signature of an olfactory receptor. In particular, all the identified sequences contain very close
25 matches to the following consensus amino acid motifs (Mombaerts, 1999, Pilpel 1999): EFILL (SEQ ID NO: 513) before transmembrane domain 1, LHTPMY (SEQ ID No: 514) in intracellular loop 1, MAYDRYVAIC (SEQ ID NO: 510) at the end of transmembrane domain 3 and the beginning of intracellular loop 2, SY at the end of transmembrane domain 5, FSTCSSH (SEQ ID NO: 516) in the beginning of
30 transmembrane domain 6, and PMLNPF (SEQ ID NO: 517) in transmembrane domain 7. Combination of all the above-mentioned structural features of the identified genes and encoded proteins strongly suggests that they represent novel members of the human olfactory receptor family.

As noted above, complete or partial sequences of numerous human and other eukaryotic olfactory receptors are currently known. The novel human receptors have amino acid sequences distinctly different from the previously known human olfactory receptors, which suggests their different specificity in odorant recognition. Therefore, these novel receptors and their genes can be used, alone or in combination with known olfactory receptors, in developing detection systems and assays for chemically distinct types of odorants not recognized by the known receptors, as well as for diagnostic and research purposes.

B. Definitions

As used herein, the following terms have the meanings ascribed to them unless specified otherwise.

“OR” refers to one or more members of a family of G protein-coupled receptors that are expressed in olfactory cells. Olfactory receptor cells can also be identified on the basis of morphology (*see, e.g., Roper, supra*), or by the expression of proteins specifically expressed in olfactory cells. OR family members may have the ability to act as receptors for olfactory transduction.

“OR” nucleic acids encode a family of GPCRs with seven transmembrane regions that have “G protein-coupled receptor activity,” *e.g.*, they may bind to G proteins in response to extracellular stimuli and promote production of second messengers such as IP₃, cAMP, cGMP, and Ca²⁺ via stimulation of enzymes such as phospholipase C and adenylate cyclase (for a description of the structure and function of GPCRs, *see, e.g., Fong, supra*, and Baldwin, *supra*). A single olfactory cell may contain many distinct OR polypeptides.

Topologically, certain chemosensory GPCRs have an “N-terminal domain,” “extracellular domains;” “transmembrane domains” comprising seven transmembrane regions, and corresponding cytoplasmic, and extracellular loops; “cytoplasmic domains,” and a “C-terminal domain” (*see, e.g., Hoon et al., Cell*, 96:541-51 (1999); Buck & Axel, *Cell*, 65:175-87 (1991)). These domains can be structurally identified using methods known to those of skill in the art, such as sequence analysis programs that identify hydrophobic and hydrophilic domains (*see, e.g., Stryer, Biochemistry*, (3rd ed. 1988); *see also* any of a number of Internet based sequence analysis programs, such as those found at dot.imgen.bcm.tmc.edu). Such domains are useful

for making chimeric proteins and for *in vitro* assays of the invention, *e.g.*, ligand binding assays.

"Extracellular domains" therefore refers to the domains of OR polypeptides that protrude from the cellular membrane and are exposed to the extracellular face of the cell. Such domains generally include the "N terminal domain" that is exposed to the extracellular face of the cell, and optionally can include portions of the extracellular loops of the transmembrane domain that are exposed to the extracellular face of the cell, *i.e.*, the loops between transmembrane regions 2 and 3, between transmembrane regions 4 and 5, and between transmembrane regions 6 and 7.

The "N terminal domain" region starts at the N-terminus and extends to a region close to the start of the transmembrane domain. "Transmembrane domain," which comprises the seven "transmembrane regions," refers to the domain of OR polypeptides that lies within the plasma membrane, and may also include the corresponding cytoplasmic (intracellular) and extracellular loops. The seven transmembrane regions and extracellular and cytoplasmic loops can be identified using standard methods, as described in Kyte & Doolittle, *J. Mol. Biol.*, 157:105-32 (1982)), or in Stryer, *supra*. The general secondary and tertiary structure of transmembrane domains, in particular the seven transmembrane domains of 7-transmembrane receptors such as olfactory receptors, are well known in the art. Thus, primary structure sequence can be designed or predicted based on known transmembrane domain sequences, as described in detail below. These transmembrane domains are useful for *in vitro* ligand-binding assays, both soluble and solid phase.

"Cytoplasmic domains" refers to the domains of OR polypeptides that face the inside of the cell, *e.g.*, the "C terminal domain" and the intracellular loops of the transmembrane domain, *e.g.*, the intracellular loop between transmembrane regions 1 and 2, the intracellular loop between transmembrane regions 3 and 4, and the intracellular loop between transmembrane regions 5 and 6. "C terminal domain" refers to the region that spans the end of the last transmembrane domain and the C-terminus of the protein, and which is normally located within the cytoplasm.

The term "ligand-binding region" or "ligand-binding domain" refers to sequences derived from a chemosensory receptor, particularly an olfactory receptor,

that substantially incorporates at least transmembrane domains II to VII. The ligand-binding region may be capable of binding a ligand, and more particularly, an odorant.

The phrase "functional effects" in the context of assays for testing compounds that modulate OR family member mediated olfactory transduction includes the
5 determination of any parameter that is indirectly or directly under the influence of the receptor, *e.g.*, functional, physical and chemical effects. It includes ligand binding, changes in ion flux, membrane potential, current flow, transcription, G protein binding, GPCR phosphorylation or dephosphorylation, signal transduction, receptor-ligand interactions, second messenger concentrations (*e.g.*, cAMP, cGMP,
10 IP₃, or intracellular Ca²⁺), *in vitro*, *in vivo*, and *ex vivo* and also includes other physiologic effects such increases or decreases of neurotransmitter or hormone release.

By "determining the functional effect" in the context of assays is meant assays for a compound that increases or decreases a parameter that is indirectly or directly
15 under the influence of an OR family member, *e.g.*, functional, physical and chemical effects. Such functional effects can be measured by any means known to those skilled in the art, *e.g.*, changes in spectroscopic characteristics (*e.g.*, fluorescence, absorbance, refractive index), hydrodynamic (*e.g.*, shape), chromatographic, or solubility properties, patch clamping, voltage-sensitive dyes, whole cell currents,
20 radioisotope efflux, inducible markers, oocyte OR gene expression; tissue culture cell OR expression; transcriptional activation of OR genes; ligand-binding assays; voltage, membrane potential and conductance changes; ion flux assays; changes in intracellular second messengers such as cAMP, cGMP, and inositol triphosphate (IP₃); changes in intracellular calcium levels; neurotransmitter release, and the like.

25 "Inhibitors," "activators," and "modulators" of OR genes or proteins are used interchangeably to refer to inhibitory, activating, or modulating molecules identified using *in vitro* and *in vivo* assays for olfactory transduction, *e.g.*, ligands, agonists, antagonists, and their homologs and mimetics. Inhibitors are compounds that, *e.g.*, bind to, partially or totally block stimulation, decrease, prevent, delay activation,
30 inactivate, desensitize, or down regulate olfactory transduction, *e.g.*, antagonists. Activators are compounds that, *e.g.*, bind to, stimulate, increase, open, activate, facilitate, enhance activation, sensitize, or up regulate olfactory transduction, *e.g.*, agonists. Modulators include compounds that, *e.g.*, alter the interaction of a receptor

with: extracellular proteins that bind activators or inhibitor (*e.g.*, ebnerin and other members of the hydrophobic carrier family); G proteins; kinases (*e.g.*, homologs of rhodopsin kinase and beta adrenergic receptor kinases that are involved in deactivation and desensitization of a receptor); and arrestins, which also deactivate
5 and desensitize receptors. Modulators can include genetically modified versions of OR family members, *e.g.*, with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, small chemical molecules and the like. Such assays for inhibitors and activators include, *e.g.*, expressing OR family members in cells or cell membranes, applying putative modulator compounds, in the presence or
10 absence of tastants, *e.g.*, sweet tastants, and then determining the functional effects on olfactory transduction, as described above. Samples or assays comprising OR family members that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of modulation. Control samples (untreated with modulators) are assigned a
15 relative OR activity value of 100%. Inhibition of a OR is achieved when the OR activity value relative to the control is about 80%, optionally 50% or 25-0%. Activation of an OR is achieved when the OR activity value relative to the control is 110%, optionally 150%, optionally 200-500%, or 1000-3000% higher.

The terms "purified," "substantially purified," and "isolated" as used herein
20 refer to the state of being free of other, dissimilar compounds with which the compound of the invention is normally associated in its natural state, so that the "purified," "substantially purified," and "isolated" subject comprises at least 0.5%, 1%, 5%, 10%, or 20%, and most preferably at least 50% or 75% of the mass, by weight, of a given sample. In one preferred embodiment, these terms refer to the
25 compound of the invention comprising at least 95% of the mass, by weight, of a given sample. As used herein, the terms "purified," "substantially purified," and "isolated" "isolated," when referring to a nucleic acid or protein, of nucleic acids or proteins, also refers to a state of purification or concentration different than that which occurs naturally in the mammalian, especially human, body. Any degree of purification or
30 concentration greater than that which occurs naturally in the mammalian, especially human, body, including (1) the purification from other associated structures or compounds or (2) the association with structures or compounds to which it is not normally associated in the mammalian, especially human, body, are within the

meaning of "isolated." The nucleic acid or protein or classes of nucleic acids or proteins, described herein, may be isolated, or otherwise associated with structures or compounds to which they are not normally associated in nature, according to a variety of methods and processes known to those of skill in the art.

5 As used herein, the term "isolated," when referring to a nucleic acid or polypeptide refers to a state of purification or concentration different than that which occurs naturally in the mammalian, especially human, body. Any degree of purification or concentration greater than that which occurs naturally in the body, including (1) the purification from other naturally-occurring associated structures or
10 compounds, or (2) the association with structures or compounds to which it is not normally associated in the body are within the meaning of "isolated" as used herein. The nucleic acids or polypeptides described herein may be isolated or otherwise associated with structures or compounds to which they are not normally associated in nature, according to a variety of methods and processed known to those of skill in the
15 art.

 As used herein, the terms "amplifying" and "amplification" refer to the use of any suitable amplification methodology for generating or detecting recombinant or naturally expressed nucleic acid, as described in detail, below. For example, the invention provides methods and reagents (*e.g.*, specific degenerate oligonucleotide
20 primer pairs) for amplifying (*e.g.*, by polymerase chain reaction, PCR) naturally expressed (*e.g.*, genomic or mRNA) or recombinant (*e.g.*, cDNA) nucleic acids of the invention (*e.g.*, tastant-binding sequences of the invention) *in vivo* or *in vitro*.

 The term "7- transmembrane receptor" means a polypeptide belonging to a superfamily of transmembrane proteins that have seven domains that span the plasma
25 membrane seven times (thus, the seven domains are called "transmembrane" or "TM" domains TM I to TM VII). The families of olfactory and certain taste receptors each belong to this super-family. 7-transmembrane receptor polypeptides have similar and characteristic primary, secondary and tertiary structures, as discussed in further detail below.

30 The term "library" means a preparation that is a mixture of different nucleic acid or polypeptide molecules, such as the library of recombinantly generated chemosensory, particularly olfactory receptor ligand-binding domains generated by amplification of nucleic acid with degenerate primer pairs, or an isolated collection of

vectors that incorporate the amplified ligand-binding domains, or a mixture of cells each randomly transfected with at least one vector encoding an olfactory receptor.

The term "nucleic acid" or "nucleic acid sequence" refers to a deoxy-ribonucleotide or ribonucleotide oligonucleotide in either single- or double-stranded
5 form. The term encompasses nucleic acids, i.e., oligonucleotides, containing known analogs of natural nucleotides. The term also encompasses nucleic-acid-like structures with synthetic backbones (*see e.g., Oligonucleotides and Analogues, a Practical Approach*, ed. F. Eckstein, Oxford Univ. Press (1991); *Antisense Strategies, Annals of the N.Y. Acad. of Sci.*, Vol. 600, Eds. Baserga *et al.* (NYAS 1992); Milligan
10 *J. Med. Chem.* 36:1923-1937 (1993); *Antisense Research and Applications* (1993, CRC Press), WO 97/03211; WO 96/39154; Mata, *Toxicol. Appl. Pharmacol.* 144:189-197 (1997); Strauss-Soukup, *Biochemistry* 36:8692-8698 (1997); Samstag, *Antisense Nucleic Acid Drug Dev.* 6:153-156 (1996)).

Unless otherwise indicated, a particular nucleic acid sequence also implicitly
15 encompasses conservatively modified variants thereof (*e.g.*, degenerate codon substitutions) and complementary sequences, as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating, *e.g.*, sequences in which the third position of one or more selected codons is substituted with mixed-base and/or deoxyinosine residues (Batzer *et al.*, *Nucleic
20 Acid Res.*, 19:5081 (1991); Ohtsuka *et al.*, *J. Biol. Chem.*, 260:2605-08 (1985); Rossolini *et al.*, *Mol. Cell. Probes*, 8:91-98 (1994)). The term nucleic acid is used interchangeably with gene, cDNA, mRNA, oligonucleotide, and polynucleotide.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid
25 polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers and non-naturally occurring amino acid polymer.

The term "plasma membrane translocation domain" or simply "translocation domain" means a polypeptide domain that, when incorporated into the amino terminus
30 of a polypeptide coding sequence, can with great efficiency "chaperone" or "translocate" the hybrid ("fusion") protein to the cell plasma membrane. For instance, a "translocation domain" may be derived from the amino terminus of the bovine rhodopsin receptor polypeptide. In one embodiment, the translocation domain may be

functionally equivalent to an exemplary translocation domain (5'-MNGTEGPNFYVPFSNKTGVV; SEQ ID NO: 518). However, rhodopsin from any mammal may be used, as can other translocation facilitating sequences. Thus, the translocation domain is particularly efficient in translocating 7-transmembrane fusion
5 proteins to the plasma membrane, and a protein (*e.g.*, an olfactory receptor polypeptide) comprising an amino terminal translocating domain will be transported to the plasma membrane more efficiently than without the domain. However, if the N-terminal domain of the polypeptide is active in binding, the use of other translocation domains may be preferred.

10 "Functional equivalency" means the domain's ability and efficiency in translocating newly translated proteins to the plasma membrane as efficiently as exemplary SEQ ID NO: 518 under similar conditions; relative efficiencies can be measured (in quantitative terms) and compared, as described herein. Domains falling within the scope of the invention can be determined by routine screening for their
15 efficiency in translocating newly synthesized polypeptides to the plasma membrane in a cell (mammalian, *Xenopus*, and the like) with the same efficiency as the twenty amino acid long translocation domain SEQ ID NO: 518, as described in detail below.

The "translocation domain," "ligand-binding domain", and chimeric receptors compositions described herein also include "analogs," or "conservative variants" and
20 "mimetics" ("peptidomimetics") with structures and activity that substantially correspond to the exemplary sequences. Thus, the terms "conservative variant" or "analog" or "mimetic" refer to a polypeptide which has a modified amino acid sequence, such that the change(s) do not substantially alter the polypeptide's (the conservative variant's) structure and/or activity, as defined herein. These include
25 conservatively modified variations of an amino acid sequence, *i.e.*, amino acid substitutions, additions or deletions of those residues that are not critical for protein activity, or substitution of amino acids with residues having similar properties (*e.g.*, acidic, basic, positively or negatively charged, polar or non-polar, *etc.*) such that the substitutions of even critical amino acids does not substantially alter structure and/or
30 activity. Conservative substitution tables providing functionally similar amino acids are well known in the art.

More particularly, "conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences,

conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids
5 encode any given protein.

For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded polypeptide.

10 Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes every possible silent variation of the nucleic acid. One of skill will recognize that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only
15 codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, each silent variation of a nucleic acid which encodes a polypeptide is implicit in each described sequence.

Conservative substitution tables providing functionally similar amino acids are well known in the art. For example, one exemplary guideline to select conservative
20 substitutions includes (original residue followed by exemplary substitution): ala/gly or ser; arg/lys; asn/gln or his; asp/glu; cys/ser; gln/asn; gly/asp; gly/ala or pro; his/asn or gln; ile/leu or val; leu/ile or val; lys/arg or gln or glu; met/leu or tyr or ile; phe/met or leu or tyr; ser/thr; thr/ser; trp/tyr; tyr/trp or phe; val/ile or leu. An alternative exemplary guideline uses the following six groups, each containing amino acids that
25 are conservative substitutions for one another: 1) Alanine (A), Serine (S), Threonine (T); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (I); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); and 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); (*see also, e.g., Creighton, Proteins*, W.H. Freeman and Company (1984); Schultz and Schimer, *Principles of*
30 *Protein Structure*, Springer-Verlag (1979)). One of skill in the art will appreciate that the above-identified substitutions are not the only possible conservative substitutions. For example, for some purposes, one may regard all charged amino acids as conservative substitutions for each other whether they are positive or negative. In

addition, individual substitutions, deletions or additions that alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence can also be considered "conservatively modified variations."

The terms "mimetic" and "peptidomimetic" refer to a synthetic chemical
5 compound that has substantially the same structural and/or functional characteristics of the polypeptides, e.g., translocation domains, ligand-binding domains, or chimeric receptors of the invention. The mimetic can be either entirely composed of synthetic, non-natural analogs of amino acids, or may be a chimeric molecule of partly natural peptide amino acids and partly non-natural analogs of amino acids. The mimetic can
10 also incorporate any amount of natural amino acid conservative substitutions as long as such substitutions also do not substantially alter the mimetic's structure and/or activity.

As with polypeptides of the invention which are conservative variants, routine experimentation will determine whether a mimetic is within the scope of the
15 invention, i.e., that its structure and/or function is not substantially altered. Polypeptide mimetic compositions can contain any combination of non-natural structural components, which are typically from three structural groups: a) residue linkage groups other than the natural amide bond ("peptide bond") linkages; b) non-natural residues in place of naturally occurring amino acid residues; or c) residues
20 which induce secondary structural mimicry, i.e., to induce or stabilize a secondary structure, e.g., a beta turn, gamma turn, beta sheet, alpha helix conformation, and the like. A polypeptide can be characterized as a mimetic when all or some of its residues are joined by chemical means other than natural peptide bonds. Individual peptidomimetic residues can be joined by peptide bonds, other chemical bonds or
25 coupling means, such as, e.g., glutaraldehyde, N-hydroxysuccinimide esters, bifunctional maleimides, N,N'-dicyclohexylcarbodiimide (DCC) or N,N'-diisopropylcarbodiimide (DIC). Linking groups that can be an alternative to the traditional amide bond ("peptide bond") linkages include, e.g., ketomethylene (e.g., -C(=O)-CH₂- for -C(=O)-NH-), aminomethylene (CH₂-NH), ethylene, olefin
30 (CH=CH), ether (CH₂-O), thioether (CH₂-S), tetrazole (CN₄), thiazole, retroamide, thioamide, or ester (see, e.g., Spatola, *Chemistry and Biochemistry of Amino Acids, Peptides and Proteins*, 7:267-357, "Peptide Backbone Modifications," Marcell Dekker, NY (1983)). A polypeptide can also be characterized as a mimetic by

containing all or some non-natural residues in place of naturally occurring amino acid residues; non-natural residues are well described in the scientific and patent literature.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, or chemical means. For example, useful labels include ^{32}P , fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe.

As used herein a "nucleic acid probe or oligonucleotide" is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, for example, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. It will be understood by one of skill in the art that probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are optionally directly labeled as with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one

source and a coding region from another source. Similarly, a heterologous protein indicates that the protein comprises two or more subsequences that are not found in the same relationship to each other in nature (*e.g.*, a fusion protein).

5 A "promoter" is defined as an array of nucleic acid sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter
10 that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, wherein the
15 expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

As used herein, "recombinant" refers to a polynucleotide synthesized or otherwise manipulated *in vitro* (*e.g.*, "recombinant polynucleotide"), to methods of using recombinant polynucleotides to produce gene products in cells or other
20 biological systems, or to a polypeptide ("recombinant protein") encoded by a recombinant polynucleotide. "Recombinant means" also encompass the ligation of nucleic acids having various coding regions or domains or promoter sequences from different sources into an expression cassette or vector for expression of, *e.g.*, inducible or constitutive expression of a fusion protein comprising a translocation domain of the
25 invention and a nucleic acid sequence amplified using a primer of the invention.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (*e.g.*, total cellular or library DNA or RNA).

30 The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acid, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer

sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Techniques in Biochemistry and Molecular Biology - Hybridisation with Nucleic Probes*, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent

5 conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at

10 equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the

15 addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least two times background, optionally 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42°C, or, 5x SSC, 1% SDS, incubating at 65°C, with wash in 0.2x SSC, and 0.1 % SDS at 65°C. Such

20 hybridizations and wash steps can be carried out for, e.g., 1, 2, 5, 10, 15, 30, 60; or more minutes.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially related if the polypeptides that they encode are substantially related. This occurs, for example, when a copy of a nucleic acid is created using the maximum

25 codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 1x SSC at 45°C. Such hybridizations and wash steps can be carried out for, e.g., 1, 2, 5, 10, 15, 30, 60, or

30 more minutes. A positive hybridization is at least twice background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency.

“Antibody” refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad
5 immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair
10 having one “light” (about 25 kDa) and one “heavy” chain (about 50-70 kDa). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (VL) and variable heavy chain (VH) refer to these light and heavy chains respectively.

A “chimeric antibody” is an antibody molecule in which (a) the constant
15 region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, *e.g.*, an enzyme, toxin, hormone, growth factor, drug, *etc.*; or (b) the variable region, or a portion thereof, is altered, replaced or
20 exchanged with a variable region having a different or altered antigen specificity.

An “anti-OR” antibody is an antibody or antibody fragment that specifically binds a polypeptide encoded by a OR gene, cDNA, or a subsequence thereof.

The term “immunoassay” is an assay that uses an antibody to specifically bind
25 an antigen. The immunoassay is characterized by the use of specific binding properties of a particular antibody to isolate, target, and/or quantify the antigen.

The phrase “specifically (or selectively) binds” to an antibody or, “specifically (or selectively) immunoreactive with,” when referring to a protein or peptide, refers to a binding reaction that is determinative of the presence of the protein in a heterogeneous population of proteins and other biologics. Thus, under designated
30 immunoassay conditions, the specified antibodies bind to a particular protein at least two times the background and do not substantially bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions may require an antibody that is selected for its specificity for a particular

protein. For example, polyclonal antibodies raised to an OR family member from specific species such as rat, mouse, or human can be selected to obtain only those polyclonal antibodies that are specifically immunoreactive with the OR polypeptide or an immunogenic portion thereof and not with other proteins, except for orthologs or polymorphic variants and alleles of the OR polypeptide. This selection may be achieved by subtracting out antibodies that cross-react with OR molecules from other species or other OR molecules. Antibodies can also be selected that recognize only OR GPCR family members but not GPCRs from other families. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select antibodies specifically immunoreactive with a protein (*see, e.g., Harlow & Lane, Antibodies, A Laboratory Manual, (1988), for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity*). Typically a specific or selective reaction will be at least twice background signal or noise and more typically more than 10 to 100 times background.

The phrase "selectively associates with" refers to the ability of a nucleic acid to "selectively hybridize" with another as defined above, or the ability of an antibody to "selectively (or specifically) bind to a protein, as defined above.

The term "expression vector" refers to any recombinant expression system for the purpose of expressing a nucleic acid sequence of the invention *in vitro* or *in vivo*, constitutively or inducibly, in any cell, including prokaryotic, yeast, fungal, plant, insect or mammalian cell. The term includes linear or circular expression systems. The term includes expression systems that remain episomal or integrate into the host cell genome. The expression systems can have the ability to self-replicate or not, i.e., drive only transient expression in a cell. The term includes recombinant expression "cassettes which contain only the minimum elements needed for transcription of the recombinant nucleic acid.

By "host cell" is meant a cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, HEK-293, and the like, *e.g.,* cultured cells, explants, and cells *in vivo*.

C. Isolation and Expression of Olfactory Receptors

Isolation and expression of the ORs, or fragments or variants thereof, of the invention can be performed as described below. PCR primers can be used for the amplification of nucleic acids encoding olfactory receptor ligand-binding regions and libraries of these nucleic acids can thereby be generated. Libraries of expression vectors can then be used to infect or transfect host cells for the functional expression of these libraries. These genes and vectors can be made and expressed *in vitro* or *in vivo*. One of skill will recognize that desired phenotypes for altering and controlling nucleic acid expression can be obtained by modulating the expression or activity of the genes and nucleic acids (*e.g.*, promoters, enhancers and the like) within the vectors of the invention. Any of the known methods described for increasing or decreasing expression or activity can be used. The invention can be practiced in conjunction with any method or protocol known in the art, which are well described in the scientific and patent literature.

The nucleic acid sequences of the invention and other nucleic acids used to practice this invention, whether RNA, cDNA, genomic DNA, vectors, viruses or hybrids thereof, may be isolated from a variety of sources, genetically engineered, amplified, and/or expressed recombinantly. Any recombinant expression system can be used, including, in addition to mammalian cells, *e.g.*, bacterial, yeast, insect or plant systems.

Alternatively, these nucleic acids can be synthesized *in vitro* by well-known chemical synthesis techniques, as described in, *e.g.*, Carruthers, *Cold Spring Harbor Symp. Quant. Biol.* 47:411-418 (1982); Adams, *Am. Chem. Soc.* 105:661 (1983); Belousov, *Nucleic Acids Res.* 25:3440-3444 (1997); Frenkel, *Free Radic. Biol. Med.* 19:373-380 (1995); Blommers, *Biochemistry* 33:7886-7896 (1994); Narang, *Meth. Enzymol.* 68:90 (1979); Brown, *Meth. Enzymol.* 68:109 (1979); Beaucage, *Tetra. Lett.* 22:1859 (1981); U.S. Patent No. 4,458,066. Double-stranded DNA fragments may then be obtained either by synthesizing the complementary strand and annealing the strands together under appropriate conditions, or by adding the complementary strand using DNA polymerase with an appropriate primer sequence..

Techniques for the manipulation of nucleic acids, such as, for example, for generating mutations in sequences, subcloning, labeling probes, sequencing, hybridization and the like are well described in the scientific and patent literature.

See, e.g., Sambrook, ed., *Molecular Cloning: a Laboratory manual* (2nd ed.), Vols. 1-3, Cold Spring Harbor Laboratory (1989); *Current Protocols in Molecular Biology*, Ausubel, ed. John Wiley & Sons, Inc., New York (1997); *Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I*,
5 Theory and Nucleic Acid Preparation, Tijssen, ed. Elsevier, N.Y. (1993).

Nucleic acids, vectors, capsids, polypeptides, and the like can be analyzed and quantified by any of a number of general means well known to those of skill in the art. These include, e.g., analytical biochemical methods such as NMR, spectrophotometry, radiography, electrophoresis, capillary electrophoresis, high performance liquid
10 chromatography (HPLC), thin layer chromatography (TLC), and hyperdiffusion chromatography, various immunological methods, e.g., fluid or gel precipitin reactions, immunodiffusion, immunoelectrophoresis, radioimmunoassays (RIAs), enzyme-linked immunosorbent assays (ELISAs), immuno-fluorescent assays, Southern analysis, Northern analysis, dot-blot analysis, gel electrophoresis (e.g., SDS-
15 PAGE), RT-PCR, quantitative PCR, other nucleic acid or target or signal amplification methods, radiolabeling, scintillation counting, and affinity chromatography.

Oligonucleotide primers are used to amplify nucleic acid encoding an olfactory receptor ligand-binding region. The nucleic acids described herein can also be cloned
20 or measured quantitatively using amplification techniques. Using exemplary degenerate primer pair sequences, (see below), the skilled artisan can select and design suitable oligonucleotide amplification primers. Amplification methods are also well known in the art, and include, e.g., polymerase chain reaction, PCR (PCR Protocols, a Guide to Methods and Applications, ed. Innis. Academic Press, N.Y.
25 (1990) and PCR Strategies, ed. Innis, Academic Press, Inc., N.Y. (1995), ligase chain reaction (LCR) (see, e.g., Wu, *Genomics* 4:560 (1989); Landegren, *Science* 241:1077,(1988); Barringer, *Gene* 89:117 (1990)); transcription amplification (see, e.g., Kwok, *PNAS*, 86:1173 (1989)); and, self-sustained sequence replication (see, e.g., Guatelli, *PNAS*, 87:1874 (1990)); Q Beta replicase amplification (see, e.g.,
30 Smith, *J. Clin. Microbiol.* 35:1477-1491 (1997)); automated Q-beta replicase amplification assay (see, e.g., Burg, *Mol. Cell. Probes* 10:257-271 (1996)) and other RNA polymerase mediated techniques (e.g., NASBA, Cangene, Mississauga, Ontario); see also Berger, *Methods Enzymol.* 152:307-316 (1987); Sambrook;

Ausubel; U.S. Patent Nos. 4,683,195 and 4,683,202; Sooknanan, *Biotechnology* 13:563-564 (1995).

Once amplified, the nucleic acids, either individually or as libraries, may be cloned according to methods known in the art, if desired, into any of a variety of vectors using routine molecular biological methods; methods for cloning *in vitro* amplified nucleic acids are described, *e.g.*, U.S. Pat. No. 5,426,039. To facilitate cloning of amplified sequences, restriction enzyme sites can be "built into" the PCR primer pair. For example, Pst I and Bsp E1 sites were designed into the exemplary primer pairs of the invention. These particular restriction sites have a sequence that, when ligated, are "in-frame" with respect to the 7-membrane receptor "donor" coding sequence into which they are spliced (the ligand-binding region coding sequence is internal to the 7-membrane polypeptide, thus, if it is desired that the construct be translated downstream of a restriction enzyme splice site, out of frame results should be avoided; this may not be necessary if the inserted ligand-binding domain comprises substantially most of the transmembrane VII region). The primers can be designed to retain the original sequence of the "donor" 7-membrane receptor (the Pst I and Bsp E1 sequence in the primers of the invention generate an insert that, when ligated into the Pst I/Bsp E1 cut vector, encode residues found in the "donor" mouse olfactory receptor M4 sequence). Alternatively, the primers can encode amino acid residues that are conservative substitutions (*e.g.*, hydrophobic for hydrophobic residue, see above discussion) or functionally benign substitutions (*e.g.*, do not prevent plasma membrane insertion, cause cleavage by peptidase, cause abnormal folding of receptor, and the like).

The primer pairs are designed to selectively amplify ligand-binding regions of olfactory receptor proteins. These domain regions may vary for different ligands, and more particularly odorants; thus, what may be a minimal binding region for one ligand, and more particularly odorants, may be too limiting for a second potential ligand. Thus, domain regions of different sizes comprising different domain structures may be amplified; for example, transmembrane (TM) domains II through VII, III through VII, III through VI or II through VI, or variations thereof (*e.g.*, only a subsequence of a particular domain, mixing the order of the domains, and the like), of a 7-transmembrane OR.

As domain structures and sequence of many 7-membrane proteins, particularly olfactory receptors, are known, the skilled artisan can readily select domain-flanking and internal domain sequences as model sequences to design degenerate amplification primer pairs. For example, a nucleic acid sequence encoding domain regions II through VII can be generated by PCR amplification using a primer pair. To amplify a nucleic acid comprising transmembrane domain I (TM I) sequence, a degenerate primer can be designed from a nucleic acid that encodes the amino acid sequence LFLLYL3' (SEQ ID NO: 519). Such a degenerate primer can be used to generate a binding domain incorporating TM I through TM III, TM I through TM IV, TM I through TM V, TM I through TM VI or TM I through TM VII).

To amplify a nucleic acid comprising a transmembrane domain III (TM III) sequence, a degenerate primer (of at least about 17 residues) can be designed from a nucleic acid that encodes the amino acid sequence M(A/G)(Y/F)DRYVAI 3' (SEQ ID NO: 520) (encoded by a nucleic acid sequence such as 5'-ATGG(G/C)CT(A/T)TGACCG(C/A/T)T(AT)(C/T)GT-3' (SEQ ID NO: 521)). Such a degenerate primer can be used to generate a binding domain incorporating TM III through TM IV, TM III through TM V, TM III through TM VI or TM III through TM VII.

To amplify transmembrane domain VI (TM VI) sequence, a degenerate primer (of at least about 17 residues) can be designed from nucleic acid encoding an amino acid sequence TC(G/A)SHL (SEQ ID NO: 522), encoded by a sequence such as 5'-AG(G/A)TGN(G/C)(T/A)N(G/C)C(G/A)CANGT-3' (SEQ ID NO: 522). Such a degenerate primer can be used to generate a binding domain incorporating TM I through TM VI, TM II through TM VI, TM III through TM VI or TM IV through TM VI).

Paradigms to design degenerate primer pairs are well known in the art. For example, a COnsensus-DEgenerate Hybrid Oligonucleotide Primer (CODEHOP) (SEQ ID NO: 523) strategy computer program is accessible as <http://blocks.fhcrc.org/codehop.html>, and is directly linked from the BlockMaker multiple sequence alignment site for hybrid primer prediction beginning with a set of related protein sequences, as known olfactory receptor ligand-binding regions (*see, e.g., Rose, Nucleic Acids Res.* 26:1628-1635 (1998); *Singh, Biotechniques*, 24:318-19 (1998)).

Means to synthesize oligonucleotide primer pairs are well known in the art. "Natural" base pairs or synthetic base pairs can be used. For example, use of artificial nucleobases offers a versatile approach to manipulate primer sequence and generate a more complex mixture of amplification products. Various families of artificial nucleobases are capable of assuming multiple hydrogen bonding orientations through internal bond rotations to provide a means for degenerate molecular recognition. Incorporation of these analogs into a single position of a PCR primer allows for generation of a complex library of amplification products. *See, e.g., Hoops, Nucleic Acids Res.* 25:4866-4871 (1997). Nonpolar molecules can also be used to mimic the shape of natural DNA bases. A non-hydrogen-bonding shape mimic for adenine can replicate efficiently and selectively against a nonpolar shape mimic for thymine (*see, e.g., Morales, Nat. Struct. Biol.* 5:950-954 (1998)). For example, two degenerate bases can be the pyrimidine base 6H, 8H-3,4-dihydropyrimido[4,5-c][1,2]oxazin-7-one or the purine base N6-methoxy-2,6-diaminopurine (*see, e.g., Hill, PNAS*, 95:4258-63 (1998)). Exemplary degenerate primers of the invention incorporate the nucleobase analog 5'-Dimethoxytrityl-N-benzoyl-2'-deoxy-Cytidine, 3'-[(2-cyanoethyl)-(N,N-diisopropyl)]-phosphoramidite (the term "P" in the sequences, *see above*). This pyrimidine analog hydrogen bonds with purines, including A and G residues.

Exemplary primer pairs for amplification of olfactory receptor transmembrane domains II through VII include:

- (a) 5'-GGGGTCCGGAG(A/G)(C/G)(A/G)TA(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-3' (SEQ ID NO: 524) and
5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3' (SEQ ID NO: 525).
- (b) 5'-GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-3' (SEQ ID NO: 526); and
5'-GGGGCTGCAGACACC(AC/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3' (SEQ ID NO: 527)
- (c) 5'-GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/C/T)A(A/G/C/T)(A/G/C/T)GG-3' (SEQ ID NO: 528) and
5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3' (SEQ ID NO: 558)

Nucleic acids that encode ligand-binding regions of olfactory receptors may be generated by amplification (*e.g., PCR*) of appropriate nucleic acid sequences using

degenerate primer pairs. The amplified nucleic acid can be genomic DNA from any cell or tissue or mRNA or cDNA derived from olfactory receptor-expressing cells, *e.g.*, olfactory neurons or olfactory epithelium.

Isolation from olfactory receptor-expressing cells is well known in the art
5 (cells expressing naturally or inducibly expressing olfactory receptors can be used to express the hybrid olfactory receptors of the invention to screen for potential odorants and odorant effect on cell physiology, as described below). For example, cells can be identified by olfactory marker protein (OMP), an abundant cytoplasmic protein expressed almost exclusively in mature olfactory sensory neurons (*see, e.g.*, Buiakova,
10 *PNAS*, 93:9858-63 (1996)). Shirley, *Eur. J. Biochem.* 32:485-494 (1983), describes a rat olfactory preparation suitable for biochemical studies *in vitro* on olfactory mechanisms. Cultures of adult rat olfactory receptor neurons are described by Vargas, *Chem. Senses* 24:211-216 (1999). Because these cultured neurons exhibit typical voltage-gated currents and are responsive to application of odorants, they can also be
15 used to express the hybrid olfactory receptors of the invention for odorant screening (endogenous olfactory receptor can be initially blocked, if desired, by, *e.g.*, antisense, knockout, and the like). U.S. Patent No. 5,869,266 describes culturing human olfactory neurons for neurotoxicity tests and screening. Murrell, *J. Neurosci.* 19:8260-8270 (1999), describes differentiated olfactory receptor-expressing cells in
20 culture that respond to odorants, as measured by an influx of calcium.

In one embodiment, hybrid protein-coding sequences comprising nucleic acids ORs fused to the translocation sequences described herein may be constructed. Also provided are hybrid ORs comprising the translocation motifs and ligand-binding domains of olfactory receptors. These nucleic acid sequences can be operably linked
25 to transcriptional or translational control elements, *e.g.*, transcription and translation initiation sequences, promoters and enhancers, transcription and translation terminators, polyadenylation sequences, and other sequences useful for transcribing DNA into RNA. In construction of recombinant expression cassettes, vectors, transgenics, and a promoter fragment can be employed to direct expression of the
30 desired nucleic acid in all tissues. Olfactory cell-specific transcriptional elements can also be used to express the fusion polypeptide receptor, including, *e.g.*, a 6.7 kb region upstream of the M4 olfactory receptor coding region. This region was sufficient to direct expression in olfactory epithelium with wild type zonal restriction and

distributed neuronal expression for endogenous olfactory receptors (Qasba, *J. Neurosci.* 18:227-236 (1998)). Receptor genes are normally expressed in a small subset of neurons throughout a zonally restricted region of the sensory epithelium. The transcriptional or translational control elements can be isolated from natural
5 sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

In another embodiment, fusion proteins, either having C-terminal or, more preferably, N-terminal translocation sequences, may also comprise the translocation motif described herein. However, these fusion proteins can also comprise additional
10 elements for, *e.g.*, protein detection, purification, or other applications. Detection and purification facilitating domains include, *e.g.*, metal chelating peptides such as polyhistidine tracts or histidine-tryptophan modules or other domains that allow purification on immobilized metals; maltose binding protein; protein A domains that allow purification on immobilized immunoglobulin; or the domain utilized in the
15 FLAGS extension/affinity purification system (Immunex Corp, Seattle WA).

The inclusion of a cleavable linker sequences such as Factor Xa (*see, e.g.*, Ottavi, *Biochimie* 80:289-293 (1998)), subtilisin protease recognition motif (*see, e.g.*, Polyak, *Protein Eng.* 10:615-619 (1997)); enterokinase (Invitrogen, San Diego, CA), and the like, between the translocation domain (for efficient plasma membrane
20 expression) and the rest of the newly translated polypeptide may be useful to facilitate purification. For example, one construct can include a polypeptide-encoding nucleic acid sequence linked to six histidine residues followed by a thioredoxin, an enterokinase cleavage site (*see, e.g.*, Williams, *Biochemistry* 34:1787-1797 (1995)), and an amino terminal translocation domain. The histidine residues facilitate
25 detection and purification while the enterokinase cleavage site provides a means for purifying the desired protein(s) from the remainder of the fusion protein. Technology pertaining to vectors encoding fusion proteins and application of fusion proteins are well described in the scientific and patent literature (*see, e.g.*, Kroll, *DNA Cell. Biol.* 12:441-53 (1993)).

30 Expression vectors, either as individual expression vectors or as libraries of expression vectors, comprising the olfactory binding domain-encoding sequences may be introduced into a genome or into the cytoplasm or a nucleus of a cell and expressed by a variety of conventional techniques, well described in the scientific and patent

literature (*see, e.g.*, Roberts, *Nature* 328:731 (1987); Berger *supra*; Schneider, *Protein Expr. Purif.* 6435:10 (1995); Sambrook; Tijssen; Ausubel). Product information from manufacturers of biological reagents and experimental equipment also provide information regarding known biological methods. The vectors can be isolated from
5 natural sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

The nucleic acids can be expressed in expression cassettes, vectors or viruses which are stably or transiently expressed in cells (*e.g.*, episomal expression systems). Selection markers can be incorporated into expression cassettes and vectors to confer
10 a selectable phenotype on transformed cells and sequences. For example, selection markers can code for episomal maintenance and replication such that integration into the host genome is not required. For example, the marker may encode antibiotic resistance (*e.g.*, chloramphenicol, kanamycin, G418, bleomycin, hygromycin) or herbicide resistance (*e.g.*, chlorosulfuron or Basta) to permit selection of those cells
15 transformed with the desired DNA sequences (*see, e.g.*, Blondelet-Rouault, *Gene* 190:315-17 (1997); Aubrecht, *J. Pharmacol. Exp. Ther.*, 281:992-97 (1997)). Because selectable marker genes conferring resistance to substrates like neomycin or hygromycin can only be utilized in tissue culture, chemoresistance genes are also used as selectable markers *in vitro* and *in vivo*.

20 A chimeric nucleic acid sequence may encode a ligand-binding domain within any 7-transmembrane polypeptide. 7-transmembrane receptors belong to a superfamily of transmembrane (TM) proteins having seven domains that traverse a plasma membrane seven times. Each of the seven domains spans the plasma membrane (TM I to TM VII). Because 7-transmembrane receptor polypeptides have
25 similar primary sequences and secondary and tertiary structures, structural domains (*e.g.*, TM domains) can be readily identified by sequence analysis. For example, homology modeling, Fourier analysis and helical periodicity detection can identify and characterize the seven domains with a 7-transmembrane receptor sequence. Fast Fourier Transform (FFT) algorithms can be used to assess the dominant periods that
30 characterize profiles of the hydrophobicity and variability of analyzed sequences. To predict TM domains and their boundaries and topology, a "neural network algorithm" by "PHD server" can be used, as done by Pilpel, *Protein Science* 8:969-977 (1999); Rost, *Protein Sci.* 4:521-533 (1995). Periodicity detection enhancement and alpha

helical periodicity index can be done as by, *e.g.*, Donnelly, *Protein Sci.* 2:55-70 (1993). Other alignment and modeling algorithms are well known in the art, *see, e.g.*, Peitsch, *Receptors Channels* 4:161-164 (1996); Cronet, *Protein Eng.* 6:59-64 (1993) (homology and "discover modeling"); <http://bioinfo.weizmann.ac.il/>.

5 The library sequences include receptor sequences that correspond to TM ligand-binding domains, including, *e.g.*, TM II to VII, TM II to VI, TM III to VII, and TM III to VII, that have been amplified (*e.g.*, PCR) from mRNA of or cDNA derived from, *e.g.*, olfactory receptor-expressing neurons or genomic DNA.

10 Libraries of olfactory receptor ligand-binding TM domain sequences can include a various TM domains or variations thereof, as described above. These sequences can be derived from any 7-transmembrane receptor. Because these polypeptides have similar primary sequences and secondary and tertiary structures, the seven domains can be identified by various analyses well known in the art, including, *e.g.*, homology modeling, Fourier analysis and helical periodicity (*see, e.g.*, Pilpel
15 *supra*), as described above. Using this information sequences flanking the seven domains can be identified and used to design degenerate primers for amplification of various combinations of TM regions and subsequences.

20 The present invention also includes not only the DNA and proteins having the specified amino acid sequences, but also DNA fragments, particularly fragments of, for example, 40, 60, 80, 100, 150, 200, or 250 nucleotides, or more, as well as protein fragments of, for example, 10, 20, 30, 50, 70, 100, or 150 amino acids, or more.

25 Also contemplated are chimeric proteins, comprising at least 10, 20, 30, 50, 70, 100, or 150 amino acids, or more, of one of at least one of the olfactory receptors described herein, coupled to additional amino acids representing all or part of another G protein receptor, preferably a member of the 7TM superfamily. These chimeras can be made from the instant receptors and a G protein receptor described herein, or they can be made by combining two or more of the present proteins. In one preferred embodiment, one portion of the chimera corresponds to and is derived from one or more of the domains of the seven transmembrane protein described herein, and the
30 remaining portion or portions come from another G protein-coupled receptor. Chimeric receptors are well known in the art, and the techniques for creating them and the selection and boundaries of domains or fragments of G protein-coupled receptors for incorporation therein are also well known. Thus, this knowledge of those skilled

in the art can readily be used to create such chimeric receptors. The use of such chimeric receptors can provide, for example, an olfactory selectivity characteristic of one of the receptors specifically disclosed herein, coupled with the signal transduction characteristics of another receptor, such as a well known receptor used in prior art assay systems.

For example, a domain such as a ligand-binding domain, an extracellular domain, a transmembrane domain (*e.g.*, one comprising seven transmembrane regions and corresponding extracellular and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, etc., can be covalently linked to a heterologous protein. For instance, an extracellular domain can be linked to a heterologous GPCR transmembrane domain, or a heterologous GPCR extracellular domain can be linked to a transmembrane domain. Other heterologous proteins of choice can include, *e.g.*, green fluorescent protein, β -gal, glutamate receptor, and the rhodopsin presequence.

Polymorphic variants, alleles, and interspecies homologs that are substantially identical to an olfactory receptor disclosed herein can be isolated using the nucleic acid probes described above. It is hypothesized that allelic differences in receptors may explain why there is a difference in olfactory sensation in different human subjects. Accordingly, the identification of such alleles may be significant, especially with respect to producing receptor libraries that adequately represent the olfactory capability of the human population, *i.e.*, which take into account allelic differences in different individuals. Alternatively, expression libraries can be used to clone olfactory receptors and polymorphic variants, alleles, and interspecies homologs thereof, by detecting expressed homologs immunologically with antisera or purified antibodies made against an olfactory polypeptide, which also recognize and selectively bind to the olfactory receptor homolog.

Also within the scope of the invention are host cells for expressing the ORs, fragments, or variants of the invention. To obtain high levels of expression of a cloned gene or nucleic acid, such as cDNAs encoding the olfactory receptors, fragments, or variants of the invention, one of skill typically subclones the nucleic acid sequence of interest into an expression vector that contains a strong promoter to direct transcription, a transcription/translation terminator, and if for a nucleic acid encoding a protein, a ribosome binding site for translational initiation. Suitable

bacterial promoters are well known in the art and described, *e.g.*, in Sambrook *et al.* However, bacterial or eukaryotic expression systems can be used.

Any of the well-known procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate
5 transfection, polybrene, protoplast fusion, electroporation, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (*see, e.g.*, Sambrook *et al.*) It is only necessary that the particular genetic
10 engineering procedure used be capable of successfully introducing at least one gene into the host cell capable of expressing the olfactory receptor, fragment, or variant of interest.

After the expression vector is introduced into the cells, the transfected cells are cultured under conditions favoring expression of the receptor, fragment, or variant of interest, which is then recovered from the culture using standard techniques.
15 Examples of such techniques are well known in the art. *See, e.g.*, WO 00/06593, which is incorporated by reference in a manner consistent with this disclosure.

D. Immunological Detection of OR Polypeptides

In addition to the detection of OR genes and gene expression using nucleic acid hybridization technology, one can also use immunoassays to detect ORs, *e.g.*, to
20 identify olfactory receptor cells, and variants of OR family members. Immunoassays can be used to qualitatively or quantitatively analyze the ORs. A general overview of the applicable technology can be found in Harlow & Lane, *Antibodies: A Laboratory Manual* (1988).

1. Antibodies to OR family members

25 Methods of producing polyclonal and monoclonal antibodies that react specifically with a OR family member are known to those of skill in the art (*see, e.g.*, Coligan, *Current Protocols in Immunology* (1991); Harlow & Lane, *supra*; Goding, *Monoclonal Antibodies: Principles and Practice* (2d ed. 1986); and Kohler & Milstein, *Nature*, 256:495-97 (1975)). Such techniques include antibody preparation
30 by selection of antibodies from libraries of recombinant antibodies in phage or similar vectors, as well as preparation of polyclonal and monoclonal antibodies by

immunizing rabbits or mice (*see, e.g., Huse et al., Science, 246:1275-81 (1989); Ward et al., Nature, 341:544-46 (1989)*).

A number of OR-comprising immunogens may be used to produce antibodies specifically reactive with a OR family member. For example, a recombinant OR protein, or an antigenic fragment thereof, can be isolated as described herein. Suitable antigenic regions include, *e.g.*, the conserved motifs that are used to identify members of the OR family. Recombinant proteins can be expressed in eukaryotic or prokaryotic cells as described above, and purified as generally described above. Recombinant protein is the preferred immunogen for the production of monoclonal or polyclonal antibodies. Alternatively, a synthetic peptide derived from the sequences disclosed herein and conjugated to a carrier protein can be used as an immunogen. Naturally occurring protein may also be used either in pure or impure form. The product is then injected into an animal capable of producing antibodies. Either monoclonal or polyclonal antibodies may be generated, for subsequent use in immunoassays to measure the protein.

Methods of production of polyclonal antibodies are known to those of skill in the art. For example, an inbred strain of mice (*e.g.*, BALB/C mice) or rabbits may be immunized with the protein using a standard adjuvant, such as Freund's adjuvant, and a standard immunization protocol. The animal's immune response to the immunogen preparation is monitored by taking test bleeds and determining the titer of reactivity to the OR. When appropriately high titers of antibody to the immunogen are obtained, blood is collected from the animal and antisera are prepared. Further fractionation of the antisera to enrich for antibodies reactive to the protein can be done if desired (*see Harlow & Lane, supra*).

Monoclonal antibodies may be obtained by various techniques familiar to those skilled in the art. Briefly, spleen cells from an animal immunized with a desired antigen may be immortalized, commonly by fusion with a myeloma cell (*see Kohler & Milstein, Eur. J. Immunol., 6:511-19 (1976)*). Alternative methods of immortalization include transformation with Epstein Barr Virus, oncogenes, or retroviruses, or other methods well known in the art. Colonies arising from single immortalized cells are screened for production of antibodies of the desired specificity and affinity for the antigen, and yield of the monoclonal antibodies produced by such cells may be enhanced by various techniques, including injection into the peritoneal cavity of a

vertebrate host. Alternatively, one may isolate DNA sequences which encode a monoclonal antibody or a binding fragment thereof by screening a DNA library from human B cells according to the general protocol outlined by Huse *et al.*, *Science*, 246:1275-1281 (1989).

5 Monoclonal antibodies and polyclonal sera are collected and titered against the immunogen protein in an immunoassay, for example, a solid phase immunoassay with the immunogen immobilized on a solid support. Typically, polyclonal antisera with a titer of 10⁹ or greater are selected and tested for their cross reactivity against non-OR proteins, or even other OR family members or other related proteins from other
10 organisms, using a competitive binding immunoassay. Specific polyclonal antisera and monoclonal antibodies will usually bind with a K_d of at least about 0.1 mM, more usually at least about 1 pM, optionally at least about 0.1 pM or better, and optionally 0.01 pM or better.

Once OR family member specific antibodies are available, individual OR
15 proteins can be detected by a variety of immunoassay methods. For a review of immunological and immunoassay procedures, *see Basic and Clinical Immunology* (Stites & Terr eds., 7th ed. 1991). Moreover, the immunoassays of the present invention can be performed in any of several configurations, which are reviewed extensively in *Enzyme Immunoassay* (Maggio, ed., 1980); and Harlow & Lane, *supra*.

20 2. Immunological binding assays

OR proteins can be detected and/or quantified using any of a number of well recognized immunological binding assays (*see, e.g.*, U.S. Patents 4,366,241; 4,376,110; 4,517,288; and 4,837,168). For a review of the general immunoassays, *see also Methods in Cell Biology: Antibodies in Cell Biology*, volume 37 (Asai, ed. 1993);
25 *Basic and Clinical Immunology* (Stites & Terr, eds., 7th ed. 1991). Immunological binding assays (or immunoassays) typically use an antibody that specifically binds to a protein or antigen of choice (in this case an OR family member or an antigenic subsequence thereof). The antibody (*e.g.*, anti-OR) may be produced by any of a number of means well known to those of skill in the art and as described above.

30 Immunoassays also often use a labeling agent to specifically bind to and label the complex formed by the antibody and antigen. The labeling agent may itself be one of the moieties comprising the antibody/antigen complex. Thus, the labeling agent may be a labeled OR polypeptide or a labeled anti-OR antibody. Alternatively, the

labeling agent may be a third moiety, such a secondary antibody that specifically binds to the antibody/OR complex (a secondary antibody is typically specific to antibodies of the species from which the first antibody is derived). Other proteins capable of specifically binding immunoglobulin constant regions, such as protein A or protein G may also be used as the label agent. These proteins exhibit a strong non-immunogenic reactivity with immunoglobulin constant regions from a variety of species (*see, e.g., Kronval et al., J. Immunol., 111:1401-1406 (1973); Akerstrom et al., J. Immunol., 135:2589-2542 (1985)*). The labeling agent can be modified with a detectable moiety, such as biotin, to which another molecule can specifically bind, such as streptavidin. A variety of detectable moieties are well known to those skilled in the art.

Throughout the assays, incubation and/or washing steps may be required after each combination of reagents. Incubation steps can vary from about 5 seconds to several hours, optionally from about 5 minutes to about 24 hours. However, the incubation time will depend upon the assay format, antigen, volume of solution, concentrations, and the like. Usually, the assays will be carried out at ambient temperature, although they can be conducted over a range of temperatures, such as 10°C to 40°C.

a. Non-competitive assay formats

Immunoassays for detecting an OR protein in a sample may be either competitive or noncompetitive. Noncompetitive immunoassays are assays in which the amount of antigen is directly measured. In one preferred "sandwich" assay, for example, the anti-OR antibodies can be bound directly to a solid substrate on which they are immobilized. These immobilized antibodies then capture the OR protein present in the test sample. The OR protein is thus immobilized is then bound by a labeling agent, such as a second OR antibody bearing a label. Alternatively, the second antibody may lack a label, but it may, in turn, be bound by a labeled third antibody specific to antibodies of the species from which the second antibody is derived. The second or third antibody is typically modified with a detectable moiety, such as biotin, to which another molecule specifically binds, *e.g., streptavidin*, to provide a detectable moiety.

b. Competitive assay formats

In competitive assays, the amount of OR protein present in the sample is measured indirectly by measuring the amount of a known, added (exogenous) OR

protein displaced (competed away) from an anti-OR antibody by the unknown OR protein present in a sample. In one competitive assay, a known amount of OR protein is added to a sample and the sample is then contacted with an antibody that specifically binds to the OR. The amount of exogenous OR protein bound to the antibody is inversely proportional to the concentration of OR protein present in the sample. In a particularly preferred embodiment, the antibody is immobilized on a solid substrate. The amount of OR protein bound to the antibody may be determined either by measuring the amount of OR protein present in a OR/antibody complex, or alternatively by measuring the amount of remaining uncomplexed protein. The amount of OR protein may be detected by providing a labeled OR molecule.

A hapten inhibition assay is another preferred competitive assay. In this assay the known OR protein is immobilized on a solid substrate. A known amount of anti-OR antibody is added to the sample, and the sample is then contacted with the immobilized OR. The amount of anti-OR antibody bound to the known immobilized OR protein is inversely proportional to the amount of OR protein present in the sample. Again, the amount of immobilized antibody may be detected by detecting either the immobilized fraction of antibody or the fraction of the antibody that remains in solution. Detection may be direct where the antibody is labeled or indirect by the subsequent addition of a labeled moiety that specifically binds to the antibody as described above.

c. Cross-reactivity determinations

Immunoassays in the competitive binding format can also be used for cross-reactivity determinations. For example, a protein at least partially encoded by the nucleic acid sequences disclosed herein can be immobilized to a solid support. Proteins (*e.g.*, OR proteins and homologs) are added to the assay that compete for binding of the antisera to the immobilized antigen. The ability of the added proteins to compete for binding of the antisera to the immobilized protein is compared to the ability of the OR polypeptide encoded by the nucleic acid sequences disclosed herein to compete with itself. The percent cross-reactivity for the above proteins is calculated, using standard calculations. Those antisera with less than 10% cross-reactivity with each of the added proteins listed above are selected and pooled. The cross-reacting antibodies are optionally removed from the pooled antisera by immunoabsorption with the added considered proteins, *e.g.*, distantly related

homologs. In addition, peptides comprising amino acid sequences representing conserved motifs that are used to identify members of the OR family can be used in cross-reactivity determinations.

5 The immunoabsorbed and pooled antisera are then used in a competitive binding immunoassay as described above to compare a second protein, thought to be perhaps an allele or polymorphic variant of a OR family member, to the immunogen protein (*i.e.*, OR protein encoded by the nucleic acid sequences disclosed herein). In order to make this comparison, the two proteins are each assayed at a wide range of concentrations and the amount of each protein required to inhibit 50% of the binding
10 of the antisera to the immobilized protein is determined. If the amount of the second protein required to inhibit 50% of binding is less than 10 times the amount of the protein encoded by nucleic acid sequences disclosed herein required to inhibit 50% of binding, then the second protein is said to specifically bind to the polyclonal antibodies generated to a OR immunogen.

15 Antibodies raised against OR conserved motifs can also be used to prepare antibodies that specifically bind only to GPCRs of the OR family, but not to GPCRs from other families.

Polyclonal antibodies that specifically bind to a particular member of the OR family, *e.g.*, AOLFR1, can be make by subtracting out cross-reactive antibodies using
20 other OR family members. Species-specific polyclonal antibodies can be made in a similar way. For example, antibodies specific to human AOLFR1 can be made by, subtracting out antibodies that are cross-reactive with orthologous sequences, *e.g.*, rat OR1 or mouse OR1.

d. Other assay formats

25 Western blot (immunoblot) analysis is used to detect and quantify the presence of OR protein in the sample. The technique generally comprises separating sample proteins by gel electrophoresis on the basis of molecular weight, transferring the separated proteins to a suitable solid support, (such as a nitrocellulose filter, a nylon filter, or derivatized nylon filter), and incubating the sample with the antibodies that
30 specifically bind the OR protein. The anti-OR polypeptide antibodies specifically bind to the OR polypeptide on the solid support. These antibodies may be directly labeled or alternatively may be subsequently detected using labeled antibodies (*e.g.*, labeled sheep anti-mouse antibodies) that specifically bind to the anti-OR antibodies.

Other, assay formats include liposome immunoassays (LIA), which use liposomes designed to bind specific molecules (e.g., antibodies) and release encapsulated reagents or markers. The released chemicals are then detected according to standard techniques (see Monroe *et al.*, *Amer. Clin. Prod. Rev.*, 5:34-41 (1986)).

5 e. Reduction of non-specific binding

One of skill in the art will appreciate that it is often desirable to minimize non-specific binding in immunoassays. Particularly, where the assay involves an antigen or antibody immobilized on a solid substrate it is desirable to minimize the amount of non-specific binding to the substrate. Means of reducing such non-specific
10 binding are well known to those of skill in the art. Typically, this technique involves coating the substrate with a proteinaceous composition. In particular, protein compositions such as bovine serum albumin (BSA), nonfat powdered milk, and gelatin are widely used with powdered milk being most preferred.

 f. Labels

15 The particular label or detectable group used in the assay is not a critical aspect of the invention, as long as it does not significantly interfere with the specific binding of the antibody used in the assay. The detectable group can be any material having a detectable physical or chemical property. Such detectable labels have been well-developed in the field of immunoassays and, in general, most any label useful in such
20 methods can be applied to the present invention. Thus, a label is any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include magnetic beads (e.g., DYNABEADS™) (SEQ ID NO: 529), fluorescent dyes (e.g., fluorescein isothiocyanate, Texas red, rhodamine, and the like), radiolabels (e.g., ³H, ¹²⁵I, ³⁵S, ¹⁴C,
25 or ³²P), enzymes (e.g., horseradish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and colorimetric labels such as colloidal gold or colored glass or plastic beads (e.g., polystyrene, polypropylene, latex, *etc.*).

The label may be coupled directly or indirectly to the desired component of the assay according to methods well known in the art. As indicated above, a wide variety
30 of labels may be used, with the choice of label depending on sensitivity required, ease of conjugation with the compound, stability requirements, available instrumentation, and disposal provisions.

Non-radioactive labels are often attached by indirect means. Generally, a ligand molecule (*e.g.*, biotin) is covalently bound to the molecule. The ligand then binds to another molecule (*e.g.*, streptavidin) molecule, which is either inherently detectable or covalently bound to a signal system, such as a detectable enzyme, a fluorescent compound, or a chemiluminescent compound. The ligands and their targets can be used in any suitable combination with antibodies that recognize a OR protein, or secondary antibodies that recognize anti-OR.

The molecules can also be conjugated directly to signal generating compounds, *e.g.*, by conjugation with an enzyme or fluorophore. Enzymes of interest as labels will primarily be hydrolases, particularly phosphatases, esterases and glycosidases, or oxidotases, particularly peroxidases. Fluorescent compounds include fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone, *etc.* Chemiluminescent compounds include luciferin, and 2,3-dihydrophthalazinediones, *e.g.*, luminol. For a review of various labeling or signal producing systems that may be used, *see* U.S. Patent No. 4,391,904.

Means of detecting labels are well known to those of skill in the art. Thus, for example, where the label is a radioactive label, means for detection include a scintillation counter or photographic film as in autoradiography. Where the label is a fluorescent label, it may be detected by exciting the fluorochrome with the appropriate wavelength of light and detecting the resulting fluorescence. The fluorescence may be detected visually, by means of photographic film, by the use of electronic detectors such as charge coupled devices (CCDs) or photomultipliers and the like. Similarly, enzymatic labels may be detected by providing the appropriate substrates for the enzyme and detecting the resulting reaction product. Finally simple colorimetric labels may be detected simply by observing the color associated with the label. Thus, in various dipstick assays, conjugated gold often appears pink, while various conjugated beads appear the color of the bead.

Some assay formats do not require the use of labeled components. For instance, agglutination assays can be used to detect the presence of the target antibodies. In this case, antigen-coated particles are agglutinated by samples comprising the target antibodies. In this format, none of the components need be labeled and the presence of the target antibody is detected by simple visual inspection.

E. Detection of Olfactory Modulators

Methods and compositions for determining whether a test compound specifically binds to a mammalian chemosensory, and more particularly, an olfactory receptor of the invention, both *in vitro* and *in vivo* are described below. Many aspects of cell physiology can be monitored to assess the effect of ligand-binding to a naturally-occurring or chimeric olfactory receptor. These assays may be performed on intact cells expressing an olfactory receptor, on permeabilized cells or on membrane fractions produced by standard methods.

Olfactory receptors are normally located on the specialized cilia of olfactory neurons. These receptors bind odorants and initiate the transduction of chemical stimuli into electrical signals. An activated or inhibited G protein will in turn alter the properties of target enzymes, channels, and other effector proteins. Some examples include the activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G protein, phospholipase C by Gq and other cognate G proteins, and modulation of diverse channels by Gi and other G proteins. Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

The OR protein of the assay will typically be selected from a polypeptide having a sequence selected from SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID.

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Alternatively, the OR protein of the assay can be derived from a eukaryote host cell and can include an amino acid subsequence having at least about 30-40% amino acid sequence identity to SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID.

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Preferably, the amino acid sequence identity will be at least 50-75% preferably 85%, 90%, 95%, 96%, 97%, 98%, or 99%. Optionally, the polypeptide of the assays can comprise a domain of an OR protein, such as an extracellular domain, transmembrane region, transmembrane domain, cytoplasmic domain, ligand-binding domain, subunit association domain, active site, and the like. Either the OR protein or a domain thereof can be covalently linked to a heterologous protein to create a chimeric protein used in the assays described herein. As discussed *infra*, the family of ORs provided herein exhibits substantial sequence similarity at both the DNA and protein level, but also significant dissimilarity. In particular, the members possess an average percentage sequence identity to other members of the family when determined over the full length of the gene by about 30%. Moreover, different members of the genes at the protein level exhibit an average on the order of about 40% sequence identity to other members of the family when the full length protein sequences are compared. However, while there exist differences, there are characteristic similarities, e.g. the consensus sequence already mentioned, which further define members of this novel genus of receptors.

Modulators of OR activity can be tested using OR polypeptides as described above, either recombinant or naturally occurring. The protein can be isolated, expressed in a cell, expressed in a membrane derived from a cell, expressed in tissue or in an animal, either recombinant or naturally occurring. Modulation can be tested using one of the *in vitro* or *in vivo* assays described herein.

1. In vitro binding assays

Olfactory transduction can also be examined *in vitro* with soluble or solid state reactions, using a full-length OR or a chimeric molecule such as an extracellular domain or transmembrane region, or combination thereof, of a OR covalently linked
5 to a heterologous signal transduction domain, or a heterologous extracellular domain and/or transmembrane region covalently linked to the transmembrane and/or cytoplasmic domain of an OR. Furthermore, ligand-binding domains of the protein of interest can be used *in vitro* in soluble or solid state reactions to assay for ligand binding. In numerous embodiments, a chimeric receptor will be made that comprises
10 all or part of a OR polypeptide, as well an additional sequence that facilitates the localization of the OR to the membrane, such as a rhodopsin, *e.g.*, an N-terminal fragment of a rhodopsin protein, *e.g.* bovine or another mammalian rhodopsin.

Ligand binding to a OR protein, a domain, or chimeric protein can be tested in solution, in a bilayer membrane, attached to a solid phase, in a lipid monolayer, or in
15 vesicles. Binding of a modulator can be tested using, *e.g.*, changes in spectroscopic characteristics (*e.g.*, fluorescence, absorbance, refractive index) hydrodynamic (*e.g.*, shape), chromatographic, or solubility properties.

Receptor-G protein interactions can also be examined. For example, binding of the G protein to the receptor or its release from the receptor can be examined. For
20 example, in the absence of GTP, an activator will lead to the formation of a tight complex of a G protein (all three subunits) with the receptor. This complex can be detected in a variety of ways, as noted above. Such an assay can be modified to search for inhibitors, *e.g.*, by adding an activator to the receptor and G protein in the absence of GTP, which form a tight complex, and then screen for inhibitors by
25 looking at dissociation of the receptor-G protein complex. In the presence of GTP, release of the alpha subunit of the G protein from the other two G protein subunits serves as a criterion of activation.

An activated or inhibited G protein will in turn alter the properties of target enzymes, channels, and other effector proteins. The classic examples are the
30 activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G protein, phospholipase C by Gq and other cognate G proteins, and modulation of diverse channels by Gi and other G proteins.

Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

In another embodiment of the invention, a GTP γ S assay may be used. As described above, upon activation of a GPCR, the G α subunit of the G protein complex is stimulated to exchange bound GDP for GTP. Ligand-mediated stimulation of G protein exchange activity can be measured in a biochemical assay measuring the binding of added radioactively-labeled GTP γ ³⁵S to the G protein in the presence of a putative ligand. Typically, membranes containing the chemosensory receptor of interest are mixed with a complex of G proteins. Potential inhibitors and/or activators and GTP γ S are added to the assay, and binding of GTP γ S to the G protein is measured. Binding can be measured by liquid scintillation counting or by any other means known in the art, including scintillation proximity assays (SPA). In other assays formats, fluorescently-labeled GTP γ S can be utilized.

2. Fluorescence Polarization Assays

In another embodiment, Fluorescence Polarization ("FP") based assays may be used to detect and monitor odorant binding. Fluorescence polarization is a versatile laboratory technique for measuring equilibrium binding, nucleic acid hybridization, and enzymatic activity. Fluorescence polarization assays are homogeneous in that they do not require a separation step such as centrifugation, filtration, chromatography, precipitation or electrophoresis. These assays are done in real time, directly in solution and do not require an immobilized phase. Polarization values can be measured repeatedly and after the addition of reagents since measuring the polarization is rapid and does not destroy the sample. Generally, this technique can be used to measure polarization values of fluorophores from low picomolar to micromolar levels. This section describes how fluorescence polarization can be used in a simple and quantitative way to measure the binding of odorants to the olfactory receptors of the invention.

When a fluorescently labeled molecule is excited with plane polarized light, it emits light that has a degree of polarization that is inversely proportional to its molecular rotation. Large fluorescently labeled molecules remain relatively stationary during the excited state (4 nanoseconds in the case of fluorescein) and the polarization of the light remains relatively constant between excitation and emission. Small fluorescently labeled molecules rotate rapidly during the excited state and the

polarization changes significantly between excitation and emission. Therefore, small molecules have low polarization values and large molecules have high polarization values. For example, a single-stranded fluorescein-labeled oligonucleotide has a relatively low polarization value but when it is hybridized to a complementary strand, it has a higher polarization value. When using FP to detect and monitor odorant-binding which may activate or inhibit the olfactory receptors of the invention, fluorescence-labeled odorants or auto-fluorescent odorants may be used.

Fluorescence polarization (P) is defined as:

$$P = \frac{Int_{\parallel} - Int_{\perp}}{Int_{\parallel} + Int_{\perp}}$$

Where \parallel is the intensity of the emission light parallel to the excitation light plane and \perp is the intensity of the emission light perpendicular to the excitation light plane. P, being a ratio of light intensities, is a dimensionless number. For example, the Beacon ® and Beacon 2000™ System may be used in connection with these assays. Such systems typically express polarization in millipolarization units (1 Polarization Unit = 1000 mP Units).

The relationship between molecular rotation and size is described by the Perrin equation and the reader is referred to Jolley, M. E. (1991) in Journal of Analytical Toxicology, pp. 236-240, which gives a thorough explanation of this equation. Summarily, the Perrin equation states that polarization is directly proportional to the rotational relaxation time, the time that it takes a molecule to rotate through an angle of approximately 68.5°. Rotational relaxation time is related to viscosity (η), absolute temperature (T), molecular volume (V), and the gas constant (R) by the following equation:

$$Rotational\ Relaxation\ Time = \frac{3\eta V}{RT}$$

The rotational relaxation time is small (≈ 1 nanosecond) for small molecules (e.g. fluorescein) and large (≈ 100 nanoseconds) for large molecules (e.g. immunoglobulins). If viscosity and temperature are held constant, rotational relaxation time, and therefore polarization, is directly related to the molecular volume. Changes in molecular volume may be due to interactions with other molecules, dissociation, polymerization, degradation, hybridization, or conformational changes of the fluorescently labeled molecule. For example, fluorescence polarization has been

used to measure enzymatic cleavage of large fluorescein labeled polymers by proteases, DNases, and RNases. It also has been used to measure equilibrium binding for protein/protein interactions, antibody/antigen binding, and protein/DNA binding.

3. Solid state and soluble high throughput assays

5 In yet another embodiment, the invention provides soluble assays using molecules such as a domain such as ligand-binding domain, an extracellular domain, a transmembrane domain (*e.g.*, one comprising seven transmembrane regions and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, etc.; a domain that is covalently linked to a heterologous
10 protein to create a chimeric molecule; an OR protein; or a cell or tissue expressing an OR protein, either naturally occurring or recombinant. In another embodiment, the invention provides solid phase based in vitro assays in a high throughput format, where the domain, chimeric molecule, OR protein, or cell or tissue expressing the OR is attached to a solid phase substrate.

15 In the high throughput assays of the invention, it is possible to screen up to several thousand different modulators or ligands in a single day. In particular, each well of a microtiter plate can be used to run a separate assay against a selected potential modulator, or, if concentration or incubation time effects are to be observed, every 5-10 wells can test a single modulator. Thus, a single standard microtiter plate
20 can assay about 100 (*e.g.*, 96) modulators. If 1536 well plates are used, then a single plate can easily assay from about 1000 to about 1500 different compounds. It is also possible to assay multiple compounds in each plate well. Further, it is possible to assay several different plates per day; assay screens for up to about 6,000-20,000 different compounds is possible using the integrated systems of the invention. More
25 recently, microfluidic approaches to reagent manipulation have been developed.

The molecule of interest can be bound to the solid state component, directly or indirectly, via covalent or non covalent linkage, *e.g.*, via a tag. The tag can be any of a variety of components. In general, a molecule which binds the tag (a tag binder) is fixed to a solid support, and the tagged molecule of interest (*e.g.*, the olfactory
30 transduction molecule of interest) is attached to the solid support by interaction of the tag and the tag binder.

A number of tags and tag binders can be used, based upon known molecular interactions well described in the literature. For example, where a tag has a natural

binder, for example, biotin, protein A, or protein G, it can be used in conjunction with appropriate tag binders (avidin, streptavidin, neutravidin, the Fc region of an immunoglobulin, *etc.*). Antibodies to molecules with natural binders such as biotin are also widely available and appropriate tag binders (*see*, SIGMA Immunochemicals
5 1998 catalogue SIGMA, St. Louis MO).

Similarly, any haptenic or antigenic compound can be used in combination with an appropriate antibody to form a tag/tag binder pair. Thousands of specific antibodies are commercially available and many additional antibodies are described in the literature. For example, in one common configuration, the tag is a first antibody
10 and the tag binder is a second antibody which recognizes the first antibody. In addition to antibody-antigen interactions, receptor-ligand interactions are also appropriate as tag and tag-binder pairs. For example, agonists and antagonists of cell membrane receptors (*e.g.*, cell receptor-ligand interactions such as transferrin, c-kit, viral receptor ligands, cytokine receptors, chemokine receptors, interleukin receptors,
15 immunoglobulin receptors and antibodies, the cadherein family, the integrin family, the selectin family, and the like; *see, e.g.*, Pigott & Power, The Adhesion Molecule Facts Book I (1993)). Similarly, toxins and venoms, viral epitopes, hormones (*e.g.*, opiates, steroids, *etc.*), intracellular receptors (*e.g.*, which mediate the effects of various small ligands, including steroids, thyroid hormone, retinoids and vitamin D;
20 peptides), drugs, lectins, sugars, nucleic acids (both linear and cyclic polymer configurations), oligosaccharides, proteins, phospholipids and antibodies can all interact with various cell receptors.

Synthetic polymers, such as polyurethanes, polyesters, polycarbonates, polyureas, polyamides, polyethyleneimines, polyarylene sulfides, polysiloxanes,
25 polyimides, and polyacetates can also form an appropriate tag or tag binder. Many other tag/tag binder pairs are also useful in assay systems described herein, as would be apparent to one of skill upon review of this disclosure.

Common linkers such as peptides, polyethers, and the like can also serve as tags, and include polypeptide sequences, such as poly gly sequences of between about
30 5 and 200 amino acids. Such flexible linkers are known to persons of skill in the art. For example, poly(ethylene glycol) linkers are available from Shearwater Polymers, Inc. Huntsville, Alabama. These linkers optionally have amide linkages, sulfhydryl linkages, or heterofunctional linkages.

Tag binders are fixed to solid substrates using any of a variety of methods currently available. Solid substrates are commonly derivatized or functionalized by exposing all or a portion of the substrate to a chemical reagent that fixes a chemical group to the surface which is reactive with a portion of the tag binder. For example, groups that are suitable for attachment to a longer chain portion would include amines, hydroxyl, thiol, and carboxyl groups. Aminoalkylsilanes and hydroxyalkylsilanes can be used to functionalize a variety of surfaces, such as glass surfaces. The construction of such solid phase biopolymer arrays is well described in the literature. See, e.g., Merrifield, *J. Am. Chem. Soc.*, 85:2149-54 (1963) (describing solid phase synthesis of, e.g., peptides); Geysen *et al.*, *J. Immun. Meth.*, 102:259-74 (1987) (describing synthesis of solid phase components on pins); Frank & Doring, *Tetrahedron*, 44:60316040 (1988) (describing synthesis of various peptide sequences on cellulose disks); Fodor *et al.*, *Science*, 251:767-77 (1991); Sheldon *et al.*, *Clinical Chemistry*, 39(4):718-19 (1993); and Kozal *et al.*, *Nature Medicine*, 2(7):753759 (1996) (all describing arrays of biopolymers fixed to solid substrates). Non-chemical approaches for fixing tag binders to substrates include other common methods, such as heat, cross-linking by UV radiation, and the like.

4. Computer-based assays

Yet another assay for compounds that modulate OR protein activity involves computer assisted compound design, in which a computer system is used to generate a three-dimensional structure of an OR protein based on the structural information encoded by its amino acid sequence. The input amino acid sequence interacts directly and actively with a preestablished algorithm in a computer program to yield secondary, tertiary, and quaternary structural models of the protein. The models of the protein structure are then examined to identify regions of the structure that have the ability to bind, e.g., ligands. These regions are then used to identify ligands that bind to the protein.

The three-dimensional structural model of the protein is generated by entering protein amino acid sequences of at least 10 amino acid residues or corresponding nucleic acid sequences encoding a OR polypeptide into the computer system. The nucleotide sequence encoding the polypeptide, or the amino acid sequence thereof, can be any of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID

NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID
NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID
NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID
NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID
5 NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID
NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID
NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID
NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID
NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107,
10 SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID
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NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143,
SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID
15 NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161,
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NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179,
SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID
NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197,
20 SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID
NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215,
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25 NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251,
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NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269,
SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID
NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,
30 SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID
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10 NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413,
SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID
NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431,
SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID
NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449,
15 SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID
NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467,
SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID
NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485,
SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID
20 NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503,
SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511, and
conservatively modified versions thereof.

The amino acid sequence represents the primary sequence or subsequence of
the protein, which encodes the structural information of the protein. At least 10
25 residues of the amino acid sequence (or a nucleotide sequence encoding 10 amino
acids) are entered into the computer system from computer keyboards, computer
readable substrates that include, but are not limited to, electronic storage media (*e.g.*,
magnetic diskettes, tapes, cartridges, and chips), optical media (*e.g.*, CD ROM),
information distributed by internet sites, and by RAM. The three-dimensional
30 structural model of the protein is then generated by the interaction of the amino acid
sequence and the computer system, using software known to those of skill in the art. .

The amino acid sequence represents a primary structure that encodes the
information necessary to form the secondary, tertiary and quaternary structure of the

protein of interest. The software looks at certain parameters encoded by the primary sequence to generate the structural model. These parameters are referred to as "energy terms," and primarily include electrostatic potentials, hydrophobic potentials, solvent accessible surfaces, and hydrogen bonding. Secondary energy terms include van der
5 Waals potentials. Biological molecules form the structures that minimize the energy terms in a cumulative fashion. The computer program is therefore using these terms encoded by the primary structure or amino acid sequence to create the secondary structural model.

The tertiary structure of the protein encoded by the secondary structure is then
10 formed on the basis of the energy terms of the secondary structure. The user at this point can enter additional variables such as whether the protein is membrane bound or soluble, its location in the body, and its cellular location, *e.g.*, cytoplasmic, surface, or nuclear. These variables along with the energy terms of the secondary structure are used to form the model of the tertiary structure. In modeling the tertiary structure, the
15 computer program matches hydrophobic faces of secondary structure with like, and hydrophilic faces of secondary structure with like.

Once the structure has been generated, potential ligand-binding regions are identified by the computer system. Three-dimensional structures for potential ligands are generated by entering amino acid or nucleotide sequences or chemical formulas of
20 compounds, as described above. The three-dimensional structure of the potential ligand is then compared to that of the OR protein to identify ligands that bind to the protein. Binding affinity between the protein and ligands is determined using energy terms to determine which ligands have an enhanced probability of binding to the protein.

25 Computer systems are also used to screen for mutations, polymorphic variants, alleles and interspecies homologs of OR genes. Such mutations can be associated with disease states or genetic traits. As described above, GeneChip™ and related technology can also be used to screen for mutations, polymorphic variants, alleles and interspecies homologs. Once the variants are identified, diagnostic assays can be used
30 to identify patients having such mutated genes. Identification of the mutated OR genes involves receiving input of a first nucleic acid or amino acid sequence of a OR gene, or conservatively modified versions thereof. The sequence is entered into the computer system as described above. The first nucleic acid or amino acid sequence is

- then compared to a second nucleic acid or amino acid sequence that has substantial identity to the first sequence. The second sequence is entered into the computer system in the manner described above. Once the first and second sequences are compared, nucleotide or amino acid differences between the sequences are identified.
- 5 Such sequences can represent allelic differences in various OR genes, and mutations associated with disease states and genetic traits.

5. Cell-based binding assays

In a preferred embodiment, an OR polypeptide is expressed in a eukaryotic cell as a chimeric receptor with a heterologous, chaperone sequence that facilitates its
10 maturation and targeting through the secretory pathway. In a preferred embodiment, the heterologous sequence is a rhodopsin sequence, such as an N-terminal fragment of a rhodopsin. Such chimeric OR receptors can be expressed in any eukaryotic cell, such as HEK-293 cells. Preferably, the cells comprise a functional G protein, *e.g.*, G α 15, that is capable of coupling the chimeric receptor to an intracellular signaling
15 pathway or to a signaling protein such as phospholipase C. Activation of such chimeric receptors in such cells can be detected using any standard method, such as by detecting changes in intracellular calcium by detecting FURA-2 dependent fluorescence in the cell.

Activated GPCR receptors become substrates for kinases that phosphorylate
20 the C-terminal tail of the receptor (and possibly other sites as well). Thus, activators will promote the transfer of ^{32}P from gamma-labeled GTP to the receptor, which can be assayed with a scintillation counter. The phosphorylation of the C-terminal tail will promote the binding of arrestin-like proteins and will interfere with the binding of G proteins. The kinase/arrestin pathway plays a key role in the desensitization of
25 many GPCR receptors. For example, compounds that modulate the duration an olfactory receptor stays active would be useful as a means of prolonging a desired odor or cutting off an unpleasant one. For a general review of GPCR signal transduction and methods of assaying signal transduction, *see, e.g., Methods in Enzymology*, vols. 237 and 238 (1994) and volume 96 (1983); Bourne *et al.*, *Nature*,
30 10:349:117-27 (1991); Bourne *et al.*, *Nature*, 348:125-32 (1990); Pitcher *et al.*, *Annu. Rev. Biochem.*, 67:653-92 (1998).

OR modulation may be assayed by comparing the response of an OR polypeptide treated with a putative OR modulator to the response of an untreated

control sample. Such putative OR modulators can include odorants that either inhibit or activate OR polypeptide activity. In one embodiment, control samples (untreated with activators or inhibitors) are assigned a relative OR activity value of 100. Inhibition of an OR polypeptide is achieved when the OR activity value relative to the control is about 90%, optionally 50%, optionally 25-0%. Activation of an OR polypeptide is achieved when the OR activity value relative to the control is 110%, optionally 150%, 200-500%, or 1000-2000%.

Changes in ion flux may be assessed by determining changes in polarization (*i.e.*, electrical potential) of the cell or membrane expressing a OR protein. One means to determine changes in cellular polarization is by measuring changes in current (thereby measuring changes in polarization) with voltage-clamp and patch-clamp techniques, *e.g.*, the "cell-attached" mode, the "inside-out" mode, and the "whole cell" mode (*see, e.g.*, Ackerman *et al.*, *New Engl. J Med.*, 336:1575-1595 (1997)). Whole cell currents are conveniently determined using the standard. Other known assays include: radiolabeled ion flux assays and fluorescence assays using voltage-sensitive dyes (*see, e.g.*, Vestergaard-Bogind *et al.*, *J. Membrane Biol.*, 88:67-75 (1988); Gonzales & Tsien, *Chem. Biol.*, 4:269277 (1997); Daniel *et al.*, *J. Pharmacol. Meth.*, 25:185-193 (1991); Holevinsky *et al.*, *J. Membrane Biology*, 137:59-70 (1994)). Generally, the compounds to be tested are present in the range from 1 pM to 100 mM.

The effects of the test compounds upon the function of the polypeptides can be measured by examining any of the parameters described above. Any suitable physiological change that affects GPCR activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as transmitter release, hormone release, transcriptional changes to both known and uncharacterized genetic markers (*e.g.*, northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as Ca^{2+} , IP3, cGMP, or cAMP.

Preferred assays for GPCRs include cells that are loaded with ion or voltage sensitive dyes to report receptor activity. Assays for determining activity of such receptors can also use known agonists and antagonists for other G protein coupled receptors as negative or positive controls to assess activity of tested compounds. In

assays for identifying modulatory compounds (*e.g.*, agonists, antagonists), changes in the level of ions in the cytoplasm or membrane voltage will be monitored using an ion sensitive or membrane voltage fluorescent indicator, respectively. Among the ion-sensitive indicators and voltage probes that may be employed are those disclosed
5 in the Molecular Probes 1997 Catalog. For G protein coupled receptors, promiscuous G proteins such as G α 15 and G α 16 can be used in the assay of choice (Wilkie *et al.*, *PNAS*, 88:10049-53 (1991)). Such promiscuous G proteins allow coupling of a wide range of receptors.

Receptor activation typically initiates subsequent intracellular events, *e.g.*,
10 increases in second messengers such as IP₃, which releases intracellular stores of calcium ions. Activation of some G protein coupled receptors stimulates the formation of inositol triphosphate (IP₃) through phospholipase C-mediated hydrolysis of phosphatidylinositol (Berridge & Irvine, *Nature*, 312:315-21 (1984)). IP₃ in turn stimulates the release of intracellular calcium ion stores. Thus, a change in
15 cytoplasmic calcium ion levels, or a change in second messenger levels such as IP₃ can be used to assess G protein coupled receptor function. Cells expressing such G protein coupled receptors may exhibit increased cytoplasmic calcium levels as a result of contribution from both intracellular stores and via activation of ion channels, in which case it may be desirable although not necessary to conduct such assays in
20 calcium-free buffer, optionally supplemented with a chelating agent such as EGTA, to distinguish fluorescence response resulting from calcium release from internal stores.

Other assays can involve determining the activity of receptors which, when activated, result in a change in the level of intracellular cyclic nucleotides, *e.g.*, cAMP or cGMP, by activating or inhibiting enzymes such as adenylate cyclase. There are
25 cyclic nucleotide-gated ion channels, *e.g.*, rod photoreceptor cell channels and olfactory neuron channels that are permeable to cations upon activation by binding of cAMP or cGMP (*see, e.g.*, Altenhofen *et al.*, *PNAS*, 88:9868-72 (1991) and Dhallan *et al.*, *Nature*, 347:184-187 (1990)). In cases where activation of the receptor results in a decrease in cyclic nucleotide levels, it may be preferable to expose the cells to agents
30 that increase intracellular cyclic nucleotide levels, *e.g.*, forskolin, prior to adding a receptor-activating compound to the cells in the assay. Cells for this type of assay can be made by co-transfection of a host cell with DNA encoding a cyclic nucleotide-gated ion channel, GPCR phosphatase and DNA encoding a receptor (*e.g.*,

certain glutamate receptors, muscarinic acetylcholine receptors, dopamine receptors, serotonin receptors, and the like), which, when activated, causes a change in cyclic nucleotide levels in the cytoplasm.

In a preferred embodiment, OR protein activity is measured by expressing a
5 OR gene in a heterologous cell with a promiscuous G protein that links the receptor to a phospholipase C signal transduction pathway (*see* Offermanns & Simon, *J. Biol. Chem.*, 270:15175-15180 (1995)). Optionally the cell line is HEK-293 (which does not naturally express OR genes) and the promiscuous G protein is G α 15/G α 16 (Offermanns & Simon, *supra*). Modulation of olfactory transduction is assayed by
10 measuring changes in intracellular Ca²⁺ levels, which change in response to modulation of the OR signal transduction pathway via administration of a molecule that associates with a OR protein. Changes in Ca²⁺ levels are optionally measured using fluorescent Ca²⁺ indicator dyes and fluorometric imaging.

In one embodiment, the changes in intracellular cAMP or cGMP can be
15 measured using immunoassays. The method described in Offermanns & Simon, *J. Bio. Chem.*, 270:15175-15180 (1995), may be used to determine the level of cAMP. Also, the method described in Felley-Bosco *et al.*, *Am. J. Resp. Cell and Mol. Biol.*, 11:159-164 (1994), may be used to determine the level of cGMP. Further, an assay kit for measuring cAMP and/or cGMP is described in U.S. Patent 4,115,538, herein
20 incorporated by reference.

In another embodiment, phosphatidyl inositol (PI) hydrolysis can be analyzed according to U.S. Patent 5,436,128, herein incorporated by reference. Briefly, the assay involves labeling of cells with 3H-myoinositol for 48 or more hrs. The labeled cells are treated with a test compound for one hour. The treated cells are lysed and
25 extracted in chloroform-methanol-water after which the inositol phosphates were separated by ion exchange chromatography and quantified by scintillation counting. Fold stimulation is determined by calculating the ratio of cpm in the presence of agonist, to cpm in the presence of buffer control. Likewise, fold inhibition is determined by calculating the ratio of cpm in the presence of antagonist, to cpm in the
30 presence of buffer control (which may or may not contain an agonist).

In another embodiment, transcription levels can be measured to assess the effects of a test compound on signal transduction. A host cell containing an OR protein of interest is contacted with a test compound for a sufficient time to effect any

interactions, and then the level of gene expression is measured. The amount of time to effect such interactions may be empirically determined, such as by running a time course and measuring the level of transcription as a function of time. The amount of transcription may be measured by using any method known to those of skill in the art to be suitable. For example, mRNA expression of the protein of interest may be detected using northern blots or their polypeptide products may be identified using immunoassays. Alternatively, transcription based assays using reporter gene may be used as described in U.S. Patent 5,436,128, herein incorporated by reference. The reporter genes can be, e.g., chloramphenicol acetyltransferase, luciferase, '3-galactosidase and alkaline phosphatase. Furthermore, the protein of interest can be used as an indirect reporter via attachment to a second reporter such as green fluorescent protein (*see, e.g.,* Mistili & Spector, *Nature Biotechnology*, 15:961-64 (1997)).

The amount of transcription is then compared to the amount of transcription in either the same cell in the absence of the test compound, or it may be compared with the amount of transcription in a substantially identical cell that lacks the OR protein of interest. A substantially identical cell may be derived from the same cells from which the recombinant cell was prepared but which had not been modified by introduction of heterologous DNA. Any difference in the amount of transcription indicates that the test compound has in some manner altered the activity of the OR protein of interest.

6. Transgenic non-human animals expressing olfactory receptors

Non-human animals expressing one or more olfactory receptor sequences of the invention, particularly human olfactory receptor sequences, can also be used for receptor assays. Such expression can be used to determine whether a test compound specifically binds to a mammalian olfactory transmembrane receptor polypeptide *in vivo* by contacting a non-human animal stably or transiently transfected with a nucleic acid encoding an olfactory receptor or ligand-binding region thereof with a test compound and determining whether the animal reacts to the test compound by specifically binding to the receptor polypeptide.

Use of the translocation domains of the invention in the fusion polypeptides generates a cell expressing high levels of olfactory receptor. Animals transfected or infected with the vectors of the invention are particularly useful for assays to identify and characterize odorants/ligands that can bind to a specific or sets of receptors. Such

vector-infected animals expressing libraries of human olfactory sequences can be used for *in vivo* screening of odorants and their effect on, *e.g.*, cell physiology (*e.g.*, on olfactory neurons), on the CNS (*e.g.*, olfactory bulb activity), or behavior.

Means to infect/express the nucleic acids and vectors, either individually or as
5 libraries, are well known in the art. A variety of individual cell, organ or whole animal parameters can be measured by a variety of means. For example, recording of stimulant-induced waves (bulbar responses) from the main olfactory bulb or accessory olfactory bulb is a useful tool for measuring quantitative stable olfactory responses. When electrodes are located on the olfactory bulb surface it is possible to record stable
10 responses over a period of several days (*see, e.g.*, Kashiwayanagi, *Brain Res. Protoc.* 1:287-291 (1997)). In this study, electroolfactogram recordings were made with a four-electrode assembly from the olfactory epithelium overlying the endoturbinates facing the nasal septum. Four electrodes were fixed along the dorsal-to-ventral axis of one turbinate bone or were placed in corresponding positions on four turbinate
15 bones and moved together up toward the top of the bone. *See also*, Scott, *J. Neurophysiol.* 77:1950-1962 (1997); Scott, *J. Neurophysiol.* 75:2036-2049 (1996); Ezech, *J. Neurophysiol.* 73:2207-2220 (1995). In other systems, fluorescence changes in nasal epithelium can be measured using the dye di-4-ANEPPS, which is applied on the rat's nasal septum and medial surface of the turbinates (*see, e.g.*, Youngentob, *J.*
20 *Neurophysiol.* 73:387-398 (1995)). Extracellular potassium activity (aK) measurements can also be carried out in *in vivo*. An increase in aK can be measured in the mucus and the proximal part of the nasal epithelium (*see, e.g.*, Khayari, *Brain Res.* 539:1-5 (1991)).

The OR sequences of the invention can be for example expressed in animal
25 nasal epithelium by delivery with an infecting agent, *e.g.*, adenovirus expression vector. Recombinant adenovirus-mediated expression of a recombinant gene in olfactory epithelium using green fluorescent protein as a marker is described by, *e.g.*, Touhara, *PNAS*, 96:4040-45 (1999).

The endogenous olfactory receptor genes can remain functional and wild-type
30 (native) activity can still be present. In other situations, where it is desirable that all olfactory receptor activity is by the introduced exogenous hybrid receptor, use of a knockout line is preferred. Methods for the construction of non-human transgenic

animals, particularly transgenic mice, and the selection and preparation of recombinant constructs for generating transformed cells are well known in the art.

Construction of a "knockout" cell and animal is based on the premise that the level of expression of a particular gene in a mammalian cell can be decreased or completely abrogated by introducing into the genome a new DNA sequence that serves to interrupt some portion of the DNA sequence of the gene to be suppressed. Also, "gene trap insertion" can be used to disrupt a host gene, and mouse embryonic stem (ES) cells can be used to produce knockout transgenic animals (*see, e.g.,* Holzschu, *Transgenic Res* 6:97-106 (1997)). The insertion of the exogenous is typically by homologous recombination between complementary nucleic acid sequences. The exogenous sequence is some portion of the target gene to be modified, such as exonic, intronic or transcriptional regulatory sequences, or any genomic sequence which is able to affect the level of the target gene's expression; or a combination thereof. Gene targeting via homologous recombination in pluripotent embryonic stem cells allows one to modify precisely the genomic sequence of interest. Any technique can be used to create, screen for, propagate, a knockout animal, *e.g., see* Bijvoet, *Hum. Mol. Genet.* 7:53-62 (1998); Moreadith, *J. Mol. Med.* 75:208-216 (1997); Tojo, *Cytotechnology* 19:161-165 (1995); Mudgett, *Methods Mol. Biol.* 48:167-184 (1995); Longo, *Transgenic Res.* 6:321-328 (1997); U.S. Patents Nos. 5,616,491; 5,464,764; 5,631,153; 5,487,992; 5,627,059; 5,272,071; WO 91/09955; WO 93/09222; WO 96/29411; WO 95/31560; WO 91/12650.

The nucleic acid libraries of the invention can also be used as reagents to produce "knockout" human cells and their progeny. Likewise, the nucleic acids of the invention can also be used as reagents to produce "knock-ins" in mice. The human or rat OR gene sequences can replace the orthologous ORs in the mouse genome. In this way, a mouse expressing a human or rat OR can be produced. This mouse can then be used to analyze the function of human or rat ORs, and to identify ligands for such ORs.

F. Modulators

The compounds tested as modulators of an OR family member can be any small chemical compound, or a biological entity, such as a protein, sugar, nucleic acid or lipid. Alternatively, modulators can be genetically altered versions of an OR gene.

Typically, test compounds will be small chemical molecules and peptides. Essentially any chemical compound can be used as a potential modulator or ligand in the assays of the invention, although most often compounds can be dissolved in aqueous or organic (especially DMSO-based) solutions are used. The assays are designed to
5 screen large chemical libraries by automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (e.g., in microtiter formats on microtiter plates in robotic assays). It will be appreciated that there are many suppliers of chemical compounds, including Sigma (St. Louis, MO), Aldrich (St. Louis, MO), Sigma-Aldrich (St. Louis, MO), Fluka
10 Chemika-Biochemica Analytika (Buchs, Switzerland) and the like.

The OR modulating compounds can be used in any number of consumer products, including, but not limited to, perfumes, fragrance compositions, deodorants, air fresheners, foods, drugs, *etc.*, or ingredients thereof, to thereby modulate the odor of the product, composition, or ingredient in a desired manner. As
15 one of skill in the art will recognize, OR modulating compounds can be used to enhance desirable odors, to block malodors, or a combination thereof.

In one preferred embodiment, high throughput screening methods involve providing a combinatorial chemical or peptide library containing a large number of potential therapeutic compounds (potential modulator or ligand compounds). Such
20 "combinatorial chemical libraries" or "ligand libraries" are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual odorant compositions.

25 A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis, by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (amino acids) in every possible way for a
30 given compound length (*i.e.*, the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks.

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (*see, e.g.,* U.S. Patent 5,010,175, Furka, *Int. J. Pept. Prot. Res.*, 37:487-93 (1991) and Houghton *et al.*, *Nature*, 354:84-88 (1991)). Other chemistries for generating chemical diversity libraries can also be used. Such chemistries include, but are not limited to: peptoids (*e.g.,* PCT Publication No. WO 91/19735), encoded peptides (*e.g.,* PCT Publication WO 93/20242), random bio-oligomers (*e.g.,* PCT Publication No. WO 92/00091), benzodiazepines (*e.g.,* U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs *et al.*, *PNAS*, 90:6909-13 (1993)), vinylogous polypeptides (Hagihara *et al.*, *J. Amer. Chem. Soc.*, 114:6568 (1992)), nonpeptidal peptidomimetics with glucose scaffolding (Hirschmann *et al.*, *J. Amer. Chem. Soc.*, 114:9217-18 (1992)), analogous organic syntheses of small compound libraries (Chen *et al.*, *J. Amer. Chem. Soc.*, 116:2661 (1994)), oligocarbamates (Cho *et al.*, *Science*, 261:1303 (1993)), peptidyl phosphonates (Campbell *et al.*, *J. Org. Chem.*, 59:658 (1994)), nucleic acid libraries (Ausubel, Berger and Sambrook, all *supra*), peptide nucleic acid libraries (U.S. Patent 5,539,083), antibody libraries (Vaughn *et al.*, *Nature Biotechnology*, 14(3):309-14 (1996) and PCT/US96/10287), carbohydrate libraries (Liang *et al.*, *Science*, 274:1520-22 (1996) and U.S. Patent 5,593,853), small organic molecule libraries (benzodiazepines, Baum, *C&EN*, Jan 18, page 33 (1993); thiazolidinones and metathiazanones, U.S. Patent 5,549,974; pynrolidines, U.S. Patents 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent 5,506,337; benzodiazepines, 5,288,514, and the like).

Devices for the preparation of combinatorial libraries are commercially available (*see, e.g.,* 357 MPS, 390 MPS (Advanced Chem Tech, Louisville KY), Symphony (Rainin, Woburn, MA), 433A (Applied Biosystems, Foster City, CA), 9050 Plus (Millipore, Bedford, MA)). In addition, numerous combinatorial libraries are themselves commercially available (*see, e.g.,* ComGenex, Princeton, NJ; Tripos, Inc., St. Louis, MO; 3D Pharmaceuticals, Exton, PA; Martek Biosciences; Columbia, MD; *etc.*).

G. Methods for Representing and Predicting the Perception of Odor

The invention also preferably provides methods for representing the perception of odor (or taste) and/or for predicting the perception of odor (or taste) in a mammal, including in a human. Preferably, such methods may be performed by using the
5 receptors and genes encoding said olfactory receptors disclosed herein.

Also contemplated as within the invention, is a method of screening one or more compounds for the presence of an odor detectable by a mammal, comprising: contacting said one or more compounds with the disclosed receptors, preferably wherein the mammal is a human. Also contemplated as within the invention is a
10 method for representing olfactory perception of a particular smell in a mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n olfactory receptors of said vertebrate, where n is greater than or equal to 4; and generating from said values a quantitative representation of olfactory perception. The olfactory receptors may be an olfactory receptor disclosed herein, the
15 representation may constitute a point or a volume in n -dimensional space, may constitute a graph or a spectrum, and may constitute a matrix of quantitative representations. Also, the providing step may comprise contacting a plurality of recombinantly-produced olfactory receptors with a test composition and quantitatively measuring the interaction of said composition with said receptors.

Also contemplated as within the invention, is a method for predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n olfactory receptors of said vertebrate, where n is greater than or equal to 4,
20 for one or more molecules or combinations of molecules yielding known olfactory perception in a mammal; and generating from said values a quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known olfactory perception in a mammal, providing values X_1 to X_n representative of the quantitative stimulation of each of n olfactory receptors of
25 said vertebrate, where n is greater than or equal to 4, for one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal; and generating from said values a quantitative representation of olfactory perception in a
30 mammal for the one or more molecules or combinations of molecules yielding

unknown olfactory perception in a mammal, and predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal by comparing the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal to the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known olfactory perception in a mammal. The olfactory receptors used in this method may include an olfactory receptor disclosed herein.

10 In another embodiment, novel molecules or combinations of molecules are generated which elicit a predetermined olfactory perception in a mammal by determining a value of olfactory perception in a mammal for a known molecule or combinations of molecules as described above; determining a value of olfactory perception in a mammal for one or more unknown molecules or combinations of molecules as described above; comparing the value of olfactory perception in a mammal for one or more unknown compositions to the value of olfactory perception in a mammal for one or more known compositions; selecting a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal; and combining two or more unknown molecules or combinations of molecules to form a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal. The combining step yields a single molecule or a combination of molecules that elicits a predetermined olfactory perception in a mammal.

25 In another embodiment of the invention, there is provided a method for simulating a fragrance, comprising: for each of a plurality of cloned olfactory receptors, preferably human receptors, ascertaining the extent to which the receptor interacts with the fragrance; and combining a plurality of compounds, each having a previously-ascertained interaction with one or more of the receptors, in amounts that together provide a receptor-stimulation profile that mimics the profile for the fragrance. Interaction of a fragrance with an olfactory receptor can be determined using any of the binding or reporter assays described herein. The plurality of compounds may then be combined to form a mixture. If desired, one or more of the plurality of the compounds can be combined covalently. The combined compounds

substantially stimulate at least 75%, 80% or 90% of the receptors that are substantially stimulated by the fragrance.

In another preferred embodiment of the invention, a plurality of standard compounds are tested against a plurality of olfactory receptors to ascertain the extent to which the receptors each interact with each standard compound, thereby generating a receptor stimulation profile for each standard compound. These receptor stimulation profiles may then be stored in a relational database on a data storage medium. The method may further comprise providing a desired receptor-stimulation profile for a scent; comparing the desired receptor stimulation profile to the relational database; and ascertaining one or more combinations of standard compounds that most closely match the desired receptor-stimulation profile. The method may further comprise combining standard compounds in one or more of the ascertained combinations to simulate the scent.

H. Kits

OR genes and their homologs are useful tools for identifying olfactory receptor cells, for forensics and paternity determinations, and for examining olfactory transduction. OR family member-specific reagents that specifically hybridize to OR nucleic acids, such as AOLFR1 probes and primers, and OR family member-specific reagents that specifically bind to an OR protein, *e.g.*, OR antibodies are used to examine olfactory cell expression and olfactory transduction regulation.

Nucleic acid assays for the presence of DNA and RNA for an OR family member in a sample include numerous techniques are known to those skilled in the art, such as southern analysis, northern analysis, dot blots, RNase protection, S1 analysis, amplification techniques such as PCR, and *in situ* hybridization. In *in situ* hybridization, for example, the target nucleic acid is liberated from its cellular surroundings in such a form so as to be available for hybridization within the cell, while preserving the cellular morphology for subsequent interpretation and analysis. The following articles provide an overview of the art of *in situ* hybridization: Singer *et al.*, *Biotechniques*, 4:230-50 (1986); Haase *et al.*, *Methods in Virology*, vol. VII, pp. 189-226 (1984); and *Nucleic Acid Hybridization: A Practical Approach* (Names *et al.*, eds. 1987). In addition, an OR protein can be detected with the various immunoassay

techniques described above. The test sample is typically compared to both a positive control (e.g., a sample expressing a recombinant OR protein) and a negative control.

The present invention also provides for kits for screening for modulators of OR family members. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise any one or more of the following materials: OR nucleic acids or proteins, reaction tubes, and instructions for testing OR activity. Optionally, the kit contains a biologically active OR receptor. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user.

EXAMPLES

Genomic, predicted amino acid sequence, and predicted coding sequences (cds), of novel G protein-coupled human odorant receptors, and classes of such receptors, are described. Each example describes a discrete protein and nucleic acid pair. Accordingly, Example 1 describes SEQ. ID. NOS. 1 and 2, for the human olfactory receptor protein designated AOLFR1, and the human DNA encoding AOLFR1, respectively; Example 2 describes SEQ. ID. NOS. 3 and 4, for the human olfactory receptor protein designated AOLFR2, and the human DNA encoding AOLFR2, respectively; and so on in the manner described, through the final Example sequence.

In the protein sequences presented herein, the one-letter code X or Xaa refers to any of the twenty common amino acid residues. In the DNA sequences presented herein, the one letter codes N or n refers to any of the of the four common nucleotide bases, A, T, C, or G.

EXAMPLES

AOLFR1 sequences:

MKTFSSFLQIGRNMHQGNQTTTTEFILLGFFKQDEHQNLLFVFLGMYLVTVIGNGLIIVAISLD
TYLHTPMYFLANLSFADISSISNSVPKMLVNIQTKSQSISYESCITQMYFSIVFVIDNLLLGTM
AYDHFVAICHPLNYTILMRPRFGILLTVISWFLSNIALHTLLLIQLLFCNHNTLPHFFCDLAPLL
KLSCSDTLINELVLFIVGLSVIIFPFTLSFFSYVCIRAVLRVSSTQGWKAFSTCGSHLTVLLFY
GTIVGVYFFPSSTHPEDTDKIGAVLFTVTPMINPFTYSLRNKDMKGALRKLINRKISSL (SEQ ID
NO: 1)

ATGAAGACTTTTAGTTCCTTTCTTCAGATCGGCAGAAATATGCATCAAGGAAACCAAACCA
CCATCACTGAATTCATTCTCCTGGGATTTTCAAGCAGGATGAGCATCAAAACCTCCTCTTT
GTGCTTTTCTGGGTATGTACCTGGTCACTGTGATTGGGAACGGGCTCATCATTGTGGCTA
TCAGCTTGGATACGTACCTTCATACCCCCATGTATCTCTTCCTTGCCAATCTATCCTTTGCT
GATATTTCTCCATTTCCAACCTCAGTCCCCAAAATGCTGGTGAATATTCAAACCAAGAGTC

AATCCATCTCTTATGAGAGCTGCATCACACAGATGTACTTTTCTATTGTGTTTGTGCGTCATT
 GACAATTTGCTCTTGGGGACCATGGCCTATGACCACCTTTGTGGCGATCTGCCACCCTCTGA
 ATTATACAATTCTCATGCGGCCAGGTTCCGCATTTTGTCTCACAGTCATCTCATGGTTCTCTC
 AGTAATATTATTGCTCTGACACACACCCTTCTGCTCATTCAATTGCTCTTCTGTAACCACAA
 5 CACTCTCCACACTTCTTCTGTGACTTGGCCCCCTCTGCTCAAACCTGTCCTGTTTACAGATACAT
 TGATCAATGAGCTTGTGTTGTTTATTGTGGGTTTATCAGTTATCATCTTCCCTTTTACACTC
 AGCTTCTTTTCCCTATGTCTGCATCATCAGAGCTGTCCTGAGAGTATCTTCCACACAGGGAA
 AGTGGAAGCCTTCTCCACTTGTGGCTCTCACCTGACAGTTGTATTACTGTTCTACGGAAC
 CATTGTAGGCGTGTACTTTTTCCCTCCTCCACTCACCTGAGGACACTGATAAGATTGGT
 10 GCTGTCTATTCACTGTGGTGACACCCATGATAAACCCTTCATCTACAGCTTGAGGAATA
 AGGATATGAAAGGTGCCCTGAGAAAGCTCATCAATAGAAAAATTTCTTCCCTTTGA (SEQ
 ID NO: 2)

AOLFR2 sequences:

15 MMMVLRNLSMEPTFALLGFTDYPKLQIPLFLVFLMYVITVVGNLGMIKKINPKFHTPMYFFL
 SHLSFVDFCYSSIVTPKLENLVMADKSIFYFSCMMQYFLSCTAVVTESFLLAVMAYDRFVAIC
 NPLLYTVAMSQLCALLVAGSYLWGMFGPLVLLCYALRLNFSGPNVINHFFCEYTA LISVSGS
 DILIPHLLLSFATFNEMCTLLILTSYVFIVTVLKIRSVSGRHKAFSTWASHLTAITIFHGTLFL
 YCVPNSKNSRQTVKVASVFYTVVNPMLNPPIYSLRNKDVKDAFWKLIHTQVPFH (SEQ ID NO:
 20 3)

ATGATGATGGTTTTAAGGAATCTGAGCATGGAGCCACCTTTGCCCTTTAGGTTTCACAG
 ATTACCCAAAGCTTCAGATTCTCTCTTCTTGTGTTTCTGCTCATGTATGTTATCACAGTG
 GTAGGAAACCTTGGGATGATCATAATAATCAAGATTAACCCCAAATTCACACTCCTATGT
 25 ACTTTTTCTTAGTCACCTCTCTTTTGTGATTTTGTACTCTTCCATTGTCACTCCCAAGC
 TGCTTGAGAACTTGGTAATGGCAGATAAAAGCATCTTCTACTTTAGCTGCATGATGCAGTA
 CTTCCTGTCCTGCACTGCTGTGGTGACAGAGTCTTCTTGCTGGCAGTGATGGCCTATGAC
 CGCTTTGTGGCCATCTGCAATCCTCTGCTTTATACAGTGGCCATGTACAGAGGCTCTGTG
 CCCTGCTGGTGGCTGGGTCATATCTCTGGGCGATGTTTGGCCCCCTTGGTACTCCTTTGTTAT
 30 GCTCTCCGGTTAAACTTCTCTGGACCTAATGTAATCAACCACTTCTTTTGTGAGTATACTGC
 TCTCATCTCTGTGTCTGGCTCTGATATACTCATCCCCACCTGCTGCTTTTACGCTTCGCCA
 CCTTCAATGAGATGTGTACACTACTGATCATCTCCTCACTTCTATGTTTTCAITTTTGTGACT
 TCTACTAAAAATCCGTTCTGTTAGTGGGCGCCACAAAGCCTTCTCCACCTGGGCTCCCAACC
 TGACTGCTATCACCATCTTCCATGGGACCATCCTTTTCTTTACTGTGTACCCAACTCCAAA
 35 AACTCTCGGCAAAACAGTCAAAGTGGCCTCTGTATTTTACACAGTTGTCAACCCCATGCTGA
 ACCCTCCGATCTACAGCCTAAGGAATAAAGACGTGAAGGATGCTTTCTGGAAGTTAATACA
 TACACAAGTTCCATTTCACTGA (SEQ ID NO: 4)

AOLFR3 sequences:

40 MLLTDRNTSGTTFILLGFSDDYPELQVPLFLVFLAIYNVTVLGNIGLIVIKINPKLHTPMYFFLSQ
 LSFVDFCYSSIIAPKMLVNLVVKDRITISFLGCVVQFFFFCTFVVTESFLLAVMAYDRFVAICNPL
 LYTVDMSQLCVLLVVGSYAWGVSCSLELTCSALKLCFHGFNTINHFFCEFSLLSLSCSDTYI
 NQWLLFFLATFNEISTLLIVLTSYAFIVVTILKMRSVSGRRKAFSTCASHLTAITIFHGTLFLYCV
 PNSKNSRHTVKVASVFYTVVIPMLNPLIYSLRNKDVKDTVTEILDTKVFSY (SEQ ID NO: 5)

45 ATGCTGCTGACAGATAGAAATACAAGTGGGACCACGTTACCCCTCTTGGGCTTCTCAGATT
 ACCCAGAACTGCAAGTCCCACTCTTCTGTTTCTTCTGGCCATCTACAATGTCACTGTGCTA
 GGAATATTGGGTGATTGTGATCATCAAAATCAACCCCAAACCTGCATACCCCATGTACT
 TTTTCTCAGCCAACTCTCCTTTGTGGATTTCTGCTATTCTCCATCATTGCTCCCAAGATG
 50 TTGGTGAACCTTGTGTCAAAGACAGAACCATTTCATTTTATAGCTGTGATGGCCTATGACCGC
 TTTCTTCTGTACCTTTGTGGTCACTGAATCCTTTTATTAGCTGTGATGGCCTATGACCGC
 TTCGTGGCCATTTGCAACCTCTGCTCTACACAGTTGACATGTCCAGAAACTCTGCGTGC
 TGCTGGTTGTGGGATCCTATGCCTGGGAGTCTCATGTTCTTGGAACTGACGTGCTCTGC
 TTTAAAGTTATGTTTTCATGGTTTCAACACAATCAATCACTTCTTCTGTGAGTTCTCCTCAC
 55 TACTCTCCCTTTCTGCTCTGATACTTACATCAACCACTGGCTGCTATTCTTTCTTGGCCACC
 TTTAATGAAATCAGCACACTACTCATCGTTCTCACATCTTATGCGTTCATTGTTGTAACCAT

5 CCTCAAGATGCGTTTCAGTCAGTGGGCGCCGCAAAGCCTTCTCCACCTGTGCCTCCCACCTG
ACTGCCATCACCATCTTCCATGGCACCATCCTCTTCTTTACTGTGTGCCCAACTCCAAAA
CTCCAGGCACACAGTCAAAGTGGCCTCTGTGTTTTACACCGTGGTGATCCCCATGTTGAAT
CCCCTGATCTACAGTCTGAGAAATAAAGATGTCAAGGATACAGTCACCGAGATACTGGAC
ACCAAAGTCTTCTCTTACTGA (SEQ ID NO: 6)

AOLFR4 sequences:

10 MENQNNVTEFILLGLTENLELWKIFSAVFLVMYVATVLENLLIVVTITTSQSLRSPMYFFLTFLS
LLDVMFSSVVPKVIVDTLSKSTTISLKGCLTQLFVEHFFGGVGILLTVMAYDRYVAICKPLHY
TIIMSPRVCCMLVGGAWVGGFMHAMIQLLFMYQIPFCGPNIIDHFICDLFQLLTLACTDTHILGL
LVTLSNGMMCVAFILILIASYTVILCSLKSYSKGRHKALSTCSSHLTVVVLFFVPCIFLYMRPV
VTHPIDKAMAVSDSIITPMLNPLIYTLRNAEVKSAMKKLWMKWEALAGK (SEQ ID NO: 7)

15 ATGGAAAAACAAAACAATGTGACTGAATTCATTCTTCTGGGTCTCACAGAGAACCTGGAGC
TGTGGAAAAATATTTTCTGCTGTGTTTCTTGTCTATGTATGTAGCCACAGTGTGGAAAAATCT
ACTTATTGTGGTAACTATTATCACAAGTCAGAGTCTGAGGTACCTATGTATTTTTTCTTA
CCTTCTTGTCCCTTTTGGATGTCTATGTTCTCATCTGTCTGTTGCCCCCAAGGTGATTGTAGAC
ACCCTCTCCAAGAGCACTACCATCTCTCTCAAAGGCTGCCTCACCCAGCTGTTTGTGGAGC
20 ATTTCTTTGGTGGTGTGGGGATCATCCTCCTCACTGTGATGGCCTATGACCGCTACGTGGC
CATCTGTAAGCCCTGCACTACACGATCATCATGAGTCCACGGGTGTGCTGCCTAATGGTA
GGAGGGGCTTGGGTGGGGGGATTATGCACGCAATGATACAACTTCTTTCATGTATCATCAAA
TACCCTTCTGTGGTCCCTAATATCATAGATCACCTTATATGTGATTGTGTTTCAGTTGTTGACA
CTTGCTGCACGGACACCCACATCCTGGGCTCTTAGTTACCCTCAACAGTGGGATGATGT
25 GTGTGGCCATCTTTCTTATCTTAATTGCGTCTACACGGTCATCCTATGCTCCTGAAGTCT
TACAGCTCTAAAGGGCGGCACAAAGCCCTCTCTACCTGCAGCTCCCACCTCACGGTGGTTG
TATTGTTCTTTGTCCCCTGTATTTTCTTGTACATGAGGCCTGTGGTCACTCACCCCATAGAC
AAGGCAATGGCTGTGTGCACTCAATCATCACCCCATGTAAATCCCTTGATCTATACAC
TGAGGAATGCAGAGGTGAAAAGTGCCATGAAGAACTCTGGATGAAATGGGAGGCTTTGG
CTGGGAAATAA (SEQ ID NO: 8)

30

AOLFR5 sequences:

35 MGKENCCTVAEFILLGLSDVPELRVCLFLLFLLIYGVTLNLANLGMIALIQVSSRLHTPMYFFLSH
LSSVDFCYSHIIVPKMLANIFNKDKAISFLGCMVQFYLFCTCVVTEVFLAVMAYDRFVAICNPL
LYTVMWSWKVRVELASCCYFCGTVCSLHLCLALRIPFYRSNVINHFFCDLPPVLSLACSDITVN
ETLLFLVATLNE SVTIMILTSYLLLTILKMGSAEGRHKAFSTCASHLTAITVFHGTVLSIYCRP
SSGNSGDADKVATVFYTVVPMNLNSVTYSLRNKDVKEALRKVMGSKIHS (SEQ ID NO: 9)

40 ATGGGCAAGGAAAACTGCACCACTGTGGCTGAGTTCATTCTCCTTGGACTATCAGATGTCC
CTGAGTTGAGAGTCTGCCTCTTCTGCTGTTCTCTCATCTATGGAGTCACGTTGTTAGCC
AACCTGGGCATGATTGCACTGATTCAAGTCTCAGCTCTCGGCTCCACACCCCCATGTACTTTT
TCCTCAGCCACTTGTCTCTGTAGATTTCTGCTACTCCTCAATAATTGTGCCAAAAATGTTG
GCTAATATCTTTAACAAGGACAAAGCCATCTCCTTCTAGGGTGCATGGTGCAATTCTACT
TGTTTTGCACTTGTGTGGTCACTGAGGTCTTCTGCTGGCCGTGATGGCCTATGACCGCTTT
45 GTGGCCATCTGTAACCCCTTGTCTATACACAGTCACCATGTCTTGAAGGTGCGTGTGGAGC
TGGCTTCTTGTGCTACTTCTGTGGGACGGTGTGTTCTCTGATTCAATTTGTGCTTAGCTCTT
AGGATCCCCCTTCTATAGATCTAATGTGATTAACCACTTTTCTGTGATCTACCTCCTGTCTT
AAGTCTTGCTTGTCTGATATCACTGTGAATGAGACACTGCTGTTCTGCTGGCCACTTTG
AATGAGAGTGTTACCATCATGATCATCCTCACTCCTACCTGCTAATTCTCACCACCATCCT
50 GAAGATGGGCTCTGCAGAGGGCAGGCACAAAGCCTTCTCCACCTGTGCTTCCCACCTCACA
GCTATCACTGTCTTCCATGGAACAGTCCTTTCCATTTATTGCAGGCCCAGTTCAGGCAATA
GTGGAGATGCTGACAAAGTGGCCACCGTGTCTACACAGTCGTGATTCTATGCTGAACCT
TGTGATCTACAGCCTGAGAAATAAAGATGTGAAAGAAGCTCTCAGAAAAGTGATGGGCTC
CAAAATTCACCTCTAG (SEQ ID NO: 10)

AOLFR6 sequences:

MMASERNQSSSTPTFILLGFSEYPEIQVPLFLVFLFVYTVTVVGNLGMIIIRLNSKLHTIMYFFLS
 HLSLTDFCSTVVPKLEENLVVEYRTISFSGCIMQFCFACIFGVTETFMLAAMAYDRFVAVCK
 PLLYTTIMSQKLCALLVAGSYTWGIVCSLILTYFLDLDFCESTFINNFICDHSVIVSASYSDPYIS
 5 QRLCFIIAIFNEVSSLIIILTSYMLIFTTIMKMRSASGRQKTFSTCASHLTATIFHGTILFLYCVPNP
 KTSSLIVTVASVFYTVAIPLMLNPLIYSLRNKDINNMFEKLVVTKLIYH (SEQ ID NO: 11)

ATGATGGCATCTGAAAGAAATCAAAGCAGCACACCCACTTTTATTCTCTTGGGTTTTTCAG
 AATACCCAGAAATCCAGGTTCCACTCTTTCTGGTTTTCTTGTTCGTCTACACAGTCACTGTA
 10 GTGGGGAACCTGGGCATGATAATAATCATCAGACTCAATTCAAACCTCCATACAATCATGT
 ACTTTTTCTTAGTCACTTGTCCTTGACAGACTTCTGTTTTTCCACTGTAGTTACACCTAAA
 CTGTTGGGAACTTGGTTGTGAATACAGAACCATCTCTTCTCTGTTGCATCATGCAAT
 TTTGTTTTGCTTGCATTTTTTGGAGTGACAGAACTTTCATGTTAGCAGCGATGGCTTATGAC
 CGTTTTGTGGCAGTTTGTAAACCTTGCTGTATACCACTATTATGTCTCAGAAGCTCTGTGC
 15 TCTTCTGGTGGCTGGGTCCTATACATGGGGGATAGTGTGCTCCCTGATACTCACATATTTT
 CTTCTTGACTTATCGTTTTGTGAATCTACCTTCATAAATAATTTTATCTGTGACCACTCTGT
 AATTGTTTTCTGCCTCCTACTCAGACCCCTATATCAGCCAGAGGCTATGCTTTATTATTGCCA
 TATTCAATGAGGTGAGCAGCCTAATTATCATTCTGACATCATATATGCTTATTTTCACTACC
 ATTATGAAGATGCGATCTGCAAGTGGGCGCCAGAAAACCTTCTCCACCTGTGCCTCCCACC
 20 TGACAGCCATCACTATCTCCATGGAACCTATCCTTTTCTTTACTGTGTTCCCTAATCCTAAA
 ACTTCTAGCCTCATAGTTACAGTGGCTTCTGTGTTTTACACAGTGGCGATTCCAATGCTGA
 ACCCATTGATCTACAGCCTTAGGAACAAAGATATCAATAACATGTTTGAAAAATTAGTTGT
 CACCAAATTGATTTACCACTGA (SEQ ID NO: 12)

25 **AOLFR7 sequences:**

MSYFYRLKLMKEAVLVKLPFTSLPLLLQTLRKSRLDMEIKNYSSSTSGFILLGLSSNPQLQKPLF
 AIFLIMYLLAAVGNVLIIPAIYSDPRLHTPMYFFLSNLSFMDICFTTVIVPKMLVNFLSETKVISY
 VGCLAQMYFFMAFGNTDSYLLASMAIDRLVAICNPLHYDVVMKPRHCLLMLLGSCSISHLHSL
 FRVLLMSRSLFCASHIHKHFFCDTQPVCLKSCSDTSSSQMVVMTETLAVIVTPFLCIIFSILRIMV
 30 TVLRPSAAGKWKAFSTCGSHLTAVALFYGSIHYVYFRPLSMYSVVRDRVATVMYTVVTPMLN
 PFYISLRNKDMKRGLKQLQDRIYR (SEQ ID NO: 13)

ATGAGCTATTTTTACAGGCTTAAGCTTATGAAAGAAGCTGTCTTGGTCAAACCTGCCCTTTA
 CATCTCTCCCACTGCTTCTCAAACCTATCCAGGAAGTCCAGAGACATGGAGATAAAGAA
 35 CTACAGCAGCAGCACTCAGGCTTCATCCTCCTGGGCCTCTCTTCCAACCTCAGCTGCAG
 AAACCTCTCTTTGCCATCTTCTCATCATGTACCTGCTCGCTGCGGTGGGGAATGTGCTCAT
 CATCCCGGCCATCTACTCTGACCCAGGCTCCACACCCCTATGTACTTTTTTCTCAGCAACT
 TGTCTTTTCATGGATATCTGCTTCACAACAGTCATAGTGCCTAAGATGCTGGTGAATTTTCTA
 TCAGAGACAAAGTTATCTCCTATGTGGGCTGCCTGGCCAGATGTACTTCTTTATGGCAT
 40 TTGGGAACACTGACAGCTACCTGCTGGCCTCTATGGCCATCGACCGGCTGGTGGCCATCTG
 CAACCCCTTACACTATGATGTGGTTATGAAACCACGGCATTGCCTGCTCATGCTATTGGGT
 TCTTGCAGCATCTCCACCTACATTCCCTGTTCCGCGTGCTACTTATGTCTCGCTTGTCTTT
 CTGTGCCTCTCACATCATTAAAGCACTTTTCTGTGACACCCAGCCTGTGCTAAAGCTCTCCT
 GCTCTGACACATCCTCCAGCCAGATGGTGGTGATGACTGAGACCTTAGCTGTCAATTGTGAC
 45 CCCCTTCTGTGTATCATCTTCTCCTACCTGCGAATCATGGTCACTGTGCTCAGAATCCCCT
 CTGCAGCCGGGAAGTGGAAGGCCTTCTCTACCTGTGGCTCCCACTCACTGCAGTAGCCCT
 TTTCTATGGGAGTATTATTTATGTCTATTTTAGGCCCCTGTCCATGTACTCAGTGGTTAGGG
 ACCGGGTAGCCACAGTTATGTACACAGTAGTGACACCCATGCTGAACCCCTTTCATCTACAG
 CCTGAGGAACAAAGATATGAAGAGGGGTTTGAAGAAATTACAGGACAGAATTTACCGGTA
 50 A (SEQ ID NO: 14)

AOLFR8 sequences:

MATSNHSSGAEFILAGLTQRPELQLPLFLFLGIYVTVVGNLGMIFLIALSSQLYPPVYYFLSH
 LSFIDLCSYSSVITPKMLVNFVPEENIISFLECTQLYFLIFVIAEGYLLTAMEYDRYVAICRPLLY
 55 NIVMSHRVCSIMMAVVYSLGFLWATVHTTRMSVLSFCRSHTVSHYFCDILPLLTLSCSSTHINEI

LLFIIGGVNTLATTALVLISYAFIFSSILGIHSTEGQSKAFGTCSSHLLAVGIFGSIITFMFKPPSS
TTMEKEKVSSVFYITIPMLNPLIYSLRNKDVKNALKKMTRGRQSS (SEQ ID NO: 15)

5 ATGGCTACTTCAAACCATTCCTTCAGGGGCTGAGTTTATCCTGGCAGGCTTGACACAACGCC
CAGAACTTCAACTGCCACTCTTCCTCCTGTTCCCTTGAATATATGTGGTCACAGTGGTGGG
GAACCTGGGCATGATCTTCTTAATTGCTCTCAGTTCTCAACTTTACCCCTCCAGTGTATTATT
TTCTCAGTCATTTGTCTTTTCATTGATCTCTGCTACTCCTCTGTCATTACCCCTAAGATGCTG
GTGAACCTTTGTTCCAGAGGAGAACATTATCTCCTTTCTGGAATGCATTACTCAACTTTATTT
CTTCCTTATTTTTGTAATTGCAGAAGGCTACCTTCTGACAGCCATGGAATATGACCGTTAT
10 GTTGCTATCTGTCGCCCACTGCTTTACAATATTGTCATGTCCACAGGGTCTGTTCCATAAT
GATGGCTGTGGTATACTCACTGGGTTTTCTGTGGGCCACAGTCCATACTACCCGCATGTCA
GTGTTGTCATTCTGTAGGTCTCATACGGTCAGTCATTATTTTTGTGATATTCTCCCTTATT
GACTCTGTCTTGCTCCAGCACCCACATCAATGAGATTCTGCTGTTCAATTATTGGAGGAGTT
AATACCTTAGCAACTACACTGGCGGTCTTATCTCTTATGCTTTTCATTTTCTTAGTATCCT
15 TGGTATTCACTCCACTGAGGGGCAATCCAAAGCCTTTGGCACTTGTAGCTCCCATCTCTTG
GCTGTGGGCATCTTTTTTGGGTCTATAACATTGATGATTTCAAGCCCCCTCCAGCACTAC
TATGGAAAAAGAGAAGGTGTCTTCTGTGTTCTACATCACAATAATCCCCATGCTGAATCCT
CTAATCTATAGCCTGAGGAACAAGGATGTGAAAAATGCACTGAAGAAGATGACTAGGGGA
AGGCAGTCATCCTGA (SEQ ID NO: 16)

20

AOLFR9 sequences:

MLARNNSLVTEFILAGLTDREPFWQPFFFLFLVIYIVTMVGNLGLITLFLNSHLHTPMYYFLFN
LSFIDL CYSSVFTPKMLMNFVSKKNIISNVGCMTRLFFFLFFVISECYMLTSMAYDRYVAICNPL
LYKVTMSHQVCSMLTFAAYIMGLAGATAHTGCMFRLTFCSANINHYLCDILPLLQLSCTSTYV
25 NEVVVLIVVGTNITVPSCITLISYVFIVTSILHIKSTQGRSKAFSTCSSHVIALSLFFGSAAFMYIKY
SSGSMEQKGVFSVFYTNVVPMLNPLIYSLRNKDVKVALRKALIKIQRRNIF (SEQ ID NO: 17)

ATGCTGGCTAGAAACAACTCCTTAGTGACTGAATTTATTCTTGCTGGATTAACAGATCGTC
CAGAGTTCTGGCAACCCCTCTTTTTCTGTTCTTAGTGATCTACATTGTCACCATGGTAGGC
30 AACCTTGGCTTGATCACTCTTTTCGGTCTAAATTCTCACCTCCACACACCAATGTACTATTT
CCTCTTCAATCTCTCCTTCATTGATCTCTGTTACTCCTCTGTTTTCACTCCCAAAATGCTAAT
GAACTTTGTGTCAAAAAAGAATATTATCTCCAATGTTGGGTGCATGACTCGGCTGTTTTTC
TTTCTCTTTTTCGTCATCTCTGAATGTTACATGTTGACCTCAATGGCATATGATCGCTATGT
GGCCATCTGTAATCCATTGCTGTATAAGGTCACCATGTCCCATCAGGTCTGTTCTATGCTCA
35 CTTTTGCTGCTTACATAATGGGATTGGCTGGAGCCACGGCCCAACCGGGTGCATGTTTAG
ACTCACCTTCTGCAGTGCTAATATCATTAAACCATTACTTGTGTGACATACTCCCCCTCCTCC
AGCTTTCCTGCACCAGCACCTATGTCAACGAGGTGGTGTGTTCTCATTGTTGTGGGTACTAA
TATCACGGTACCCAGTTGTACCATCCTCATTTCTTATGTTTTTATTGTCTACTAGCATCTTC
ATATCAAATCCACTCAAGGAAGATCAAAAGCCTTCAGTACTTGTAGCTCTCATGTCAATTGC
40 TCTGTCTCTGTTTTTGGGTGAGCGGCTCATGTATATTAATAATTCTTCTGGATCTATGG
AGCAGGGGAAAAGTTTTTCTGTTTTCTACACTAATGTGGTGCCCATGCTCAATCCCTCATC
TACAGTTTGAGGAACAAGGATGTCAAAGTTGCACTGAGGAAAGCTCTGATTAATAATTCAG
AGGAGAAATATATTCTAA (SEQ ID NO: 18)

45 **AOLFR10 sequences:**

MLARNNSLVTEFILAGLTDREPFQPLFFLFLVIYIVTMVGNLGLIILFGLNSHLHTPMYYFLFN
SFIDL CYSSVFTPKMLMNFVSKKNIISYVGCMTQLFFFLFFVISECYILTSMAYDRYVAICNPLLY
KVTMSHQVCSMLTFAAYIMGLAGATAHTGCMRLTLFCSANINHYLCDILPLLQLSCTSTYVN
EVVVVLIVVGINIMVPSCTILISYVFIVTSILHIKSTQGRSKAFSTCSSHVIALSLFFGSAAFMYIKYS
50 SGSMEQKGVFSVFYTNVVPMLNPLIYSLRNKDVKVALRKALIKIQRRNIF (SEQ ID NO: 19)

ATGCTGGCTAGAAACAACTCCTTAGTGACTGAATTTATTCTTGCTGGATTAACAGATCGTC
CAGAGTTCCGGCAACCCCTCTTTTTCTGTTTCTAGTGATCTACATTGTCACCATGGTAGGC
AACCTTGGCTTGATCATTCTTTTCGGTCTAAATTCTCACCTCCACACACCAATGTACTATTT
55 CCTCTTCAATCTCTCCTTCATTGATCTCTGTTACTCCTCTGTTTTCACTCCCAAAATGCTAAT
GAACTTTGTATCAAAAAAGAATATTATCTCCTATGTTGGGTGCATGACTCAGCTGTTTTTCT

TTCTCTTTTTTGTGCTCTCTGAATGCTACATATTGACCTCAATGGCATATGATCGCTATGTG
 GCCATCTGTAATCCATTGCTGTATAAGGTCACCATGTCCCATCAGGTCTGTTCTATGCTCAC
 TTTTGCTGCTTACATAATGGGATTGGCTGGAGCCACGGCCACACCGGGTGCATGCTTAGA
 CTCACCTTCTGCAGTGCTAATATCATCAACCATTACTTGTGTGACATACTCCCCCTCCTCCA
 5 GCTTTCCTGCACCAGCACCTATGTCAACGAGGTGGTTGTTCTCATTGTTGTGGGTATTAAT
 ATCATGGTACCCAGTTGTACCATCCTCATTCTTATGTTTTTCATTGTCACTAGCATTCTTCA
 TATCAAATCCACTCAAGGAAGATCAAAAGCCTTCAGTACTTGTAGCTCTCATGTCAATTGCT
 CTGTCTCTGTTTTTTGGGTGAGCGGCATTTCATGTATATTAATATTCTTCTGGATCTATGGA
 GCAGGGAAAAGTTTCTTCTGTTTTCTACACTAATGTGGTGCCCATGCTCAATCCTCTCATCT
 10 ACAGTTTGAGGAACAAGGATGTCAAAGTTGCACTGAGGAAAGCTCTGATTAATAATTCAGA
 GAAGAAATATATTCTAA (SEQ ID NO: 20)

AOLFR11 sequences:

MTLRNSSSVTEFILVGLSEQPELQLPLFLLFLGIYVFTVVGNLGLITLIGINPSLHTPMYFFLFNLS
 15 FIDLCYSCVFTPKMLNDFVSESIISYVGCMTQLFFFCFFVNSECYVLVSMAYDRYVAICNPPLY
 MVTMSPRVCFLLMFGSYVVGFAGAMAHTGSMRLRTFCDNSVIDHYLCDVLPQLSCTSTHV
 SELVFFIVGVITMLSSISIVISYALILSNILCIPSAEGRSKAFSTWGSIIAVALFFGSGTFTYLTTS
 FPGSMNHGRFASVFYTNVVPMLNPSIYSLRNKDDKLALGKTLKRVLF (SEQ ID NO: 21)

ATGACTCTGAGAAACAGCTCCTCAGTGAAGTTTATCCTTGTGGGATTATCAGAACAGC
 CAGAGCTCCAGCTCCCTCTTTTCTTCTATTCTTAGGGATCTATGTGTTCACTGTGGTGGGC
 AACTTGGGCTTGATCACCTTAATTGGGATAAATCCTAGCCTTCACACCCCATGACTTTT
 CCTCTTCAACTTGTCTTTATAGATCTCTGTTATTCCTGTGTGTTTACCCCCAAAATGCTGA
 ATGACTTTGTTTTAGAAAAGTATCATCTCTTATGTGGGATGTATGACTCAGCTATTTTCTTC
 20 TGTTTCTTTGTCAATTCTGAGTGCTATGTGTTGGTATCAATGGCCTATGATCGCTATGTGGC
 CATCTGCAACCCCTGCTCTACATGGTCACCATGTCCCCAAGGGTCTGCTTTCTGCTGATGT
 TTGGTTCCTATGTGGTAGGGTTTGTGTTGGGCCATGGCCCACTGGAAGCATGCTGCGACT
 GACCTTCTGTGATTCCAACGTCATTGACCATTATCTGTGTGACGTTCTCCCCCTCTTGCAGC
 TCTCCTGCACCAGCACCCATGTCAAGTGGTGGTATTTTTCATTGTTGTTGGAGTAATCACC
 25 ATGCTATCCAGCATAAGCATCGTCATCTCTTACGCTTTGATACTCTCCAACATCCTCTGTAT
 TCCTTCTGCAGAGGGCAGATCCAAAGCCTTTAGCACATGGGGCTCCACATAATTGCTGTT
 GCTCTGTTTTTTGGGTGAGGGACATTCACCTACTTAACAACATCTTTTCTGGCTCTATGAA
 CCATGGCAGATTGCTCAGTCTTTTACACCAATGTGGTCCCATGCTTAACCCCTTCGATCT
 30 ACAGTTTGAGGAATAAGGATGATAAACTTGCCCTGGGCAAAACCCTGAAGAGAGTGCTCT
 TCTAA (SEQ ID NO: 22)

AOLFR12 sequences:

MERNHNPDNPNVNLFFADKKNKRRNFGQIVSDVGRICYSVLSLGEPTTMGRNNLTPRSEFIL
 LGLSSRPEDQKPLFAVFLPIYLITVIGNLLILAIRSDTRLQTPMYFFLSILSFVDICYVTVIKMLV
 40 NFLSETKTISYGECLTQMYFFLAFGNTDSYLLAAMADRYVAICNPFHYTTIMSHRCCVLLLVL
 FCIPHFHSLHLLTNQLIFCASNVIHFFCDDQPVLLKSCSSHVKEITVMTEGLAVIMTPFSCIII
 SYLRILITVLKIPSAAGKRKAFSTCGSHLTVVTLFYGSISYVYFQPLSNYTVKDQIATIIYTVLTP
 MLNPFYISLRNKDMKQGLAKLMHRMKCQ (SEQ ID NO: 23)

ATGGAAAGAAACCACAATCCAGATAATTGTAATGTTTTAAATTTTTTCTTTGCTGATAAGA
 AGAATAAAAGGAGAAATTTTGACAGATTGTATCAGATGTTGGAAGAATCTGTTACAGTG
 TTAGTTTATCTTTAGGTGAACCCACAACCTATGGGAAGAAATAACCTAACAAGACCCTCTGA
 ATTCATCCTCCTTGGACTCTCCTCTCGACCTGAGGATCAGAAGCCGCTCTTTGCTGTGTTCC
 TCCCCATCTACCTTATCAGATGATAGGAAACCTGCTTATCATCCTGGCCATCCGCTCAGA
 45 CACTCGTCTCCAGACGCCCAGTACTTCTTTCTAAGCATCCTGTCTTTTGTGACATTTGCT
 ATGTGACAGTCATTATCCCTAAGATGCTGGTGAACCTCTTATCAGAGACAAAGACCATCTC
 TTACGGTGAGTGTCTGACCCAGATGTACTTTTCTTAGCCTTTGGAACACAGACAGTTAC
 CTGCTAGCAGCCATGGCCATTGACCGCTATGTGGCCATATGTAATCCCTTCCACTACATCA
 CCATTATGAGTACAGATGCTGTGCTGCTGTTCTGTTCTCTCCTTCTGCATTCCACATTTT
 50 CACTCCCTCCTGCACATTCTTCTGACTAATCAGCTCATCTTCTGTGCCTCCAATGTCATCCA
 TCACCTTTTTCTGCGATGATCAACCAGTGCTAAAATTGTCTGTTCTCTCCATTTTGTCAAAG

AAATCACAGTAATGACAGAAGGCTTGGCTGTCATAATGACCCCGTTTTCATGCATCATCAT
CTCTTATTTAAGAATCCTCATCACTGTTCTGAAGATTCCCTCAGCTGCTGGAAAGCGTAAA
GCATTTTCTACCTGTGGCTCTCATCTCACAGTGGTGACCCGTGTTTATGGAAGCATTAGCTA
TGTCTATTTTCAGCCCCTGTCCAATACTGTCAAGGATCAAATAGCAACAATTATCTAC
5 ACCGTAAGTACTCTATGCTAAATCCATTTATCTATAGTCTGAGGAACAAAGACATGAAGC
AGGGTTTGGCAAAGTTGATGCACAGGATGAAATGTCAGTAA (SEQ ID NO: 24)

AOLFR13 sequences:

MDQKNGSSFTGFILLGFSRDPQLELVLFVLLIFYIFTLLGNKTHIVLSHLDPHLHNP MYFFFSNL
10 SFLDLCYTTGIVPQLLVNLRGADKSISYGGCVVQLYISLGLGSTECVLLGVMAFDRYAAVCRPL
HYTVVMHPCLYVLMASWSWVIGFANSLLQTVLILLTLCGRNKLEHFLCEVPPLKLACVDTT
MNESELEFFSVIILLVPVALIIFSYSQIVRAVVRKISATGQRKVFGTCGSHLT VVSLFYGTAIYAY
LQPGNNYSQDQGXISLFYTHITPMINPLIYTLRNKDVKGALKKVLWKNYDSR (SEQ ID NO:
25)

15 ATGGATCAGAAAAATGGAAGTTCTTTCACTGGATTTATCCTACTGGGTTTCTCTGACAGGC
CTCAGCTGGAGCTAGTCCTCTTTGTGGTTTCTTTGATCTTCTATATCTTCACTTTGCTGGGG
AACAAAACCATCATTGTATTATCTCACTTGGACCCACATCTTCACAATCCTATGTATTTTTT
CTTCTCCAACCTAAGCTTTTTGGATCTGTGTTACACAACCGGCATTGTTCCACAGCTCCTGG
20 TTAATCTCAGGGGAGCAGACAAATCAATCTCCTATGGTGGTTGTGTAGTTCAGCTGTACAT
CTCTCTAGGCTTGGGATCTACAGAATGCGTTCTCTTAGGAGTGATGGCATTGACCGCTAT
GCAGCTGTTTGCAGGCCCCCTCCACTACACAGTAGTCATGCACCCCTGTCTGTATGTGCTGA
TGGCTTCTACTTCATGGGTCAATTGGTTTTGCCAACTCCCTATTGCAGACGGTGCTCATCTTG
CTTTTAACACTTTGTGGAAGAAATAAATTAGAACACTTTCTTTGTGAGGTTCTCCATTGCT
25 CAAGCTTGCCGTGTGTGACACTACTATGAATGAATCTGAACTCTTCTTTGTGAGTGTCTATTA
TTCTTCTGTACCTGTTGCATTAATCATATTCTCTATAGTCAGATTGTCAGGGCAGTCGTG
AGGATAAAGTCAGCAACAGGGCAGAGAAAAGTGTGTTGGGACATGTGGCTCCACCTCACA
GTGGTTTCCCTGTTCTACGGCACAGCTATCTATGCTACCTCCAGCCCGCAACAACACTCTC
TCAGGATCAGGGCAAGKTCATCTCTCTCTTCTACACCATCATTACCCCATGATCAACCCC
30 CTCATATATACACTGAGGAACAAGGATGTGAAAGGAGCACTTAAGAAGGTGCTCTGGAAG
AACTACGACTCCAGATGA (SEQ ID NO: 26)

AOLFR14 sequences:

MALPILLSPSCFASSQSLSSRMNSENLTAAVAPAEFVLLGITNRWDLRVALFLTCLPVYLVSL
35 LGNMGMALLIRMDARLHTPMYFFLANLSLLDACYSIAIGPKMLVDLLPRATIPYTACALQMF
VFAGLADTECCLLAAMAYDRYVAIRNPLLYTTAMSQRCLALLGASGLGGAVSAFVHTTLTF
RLSFCRSRKINSFFCDIPLLAISCSDTSLNELLFAICGFIQTATVLAITVSYGFIAGAVIHMRSVE
GSRRAASTGGSHLTAVAMMYGTLIFMYLRPSSSYALDTDKMASVFYTLVIPSLNPLIYSLRNKE
VKEALRQTWSRFHCPGQGSQ (SEQ ID NO: 27)

40 ATGGCCTTGCCATTGCTCTTATCTCCCTCCTGCTTTGCCTCTTCTCAGTCTCTGTCCAGTAG
GATGAACTCAGAGAACCTCACCCGGCCGCGGTTGCCCTGCTGAATTCGTCTCTCCTGGGC
ATCACAATCGCTGGGACCTGCGTGTGGCCCTCTTCTGACCTGCCTGCCTGTCTACCTGG.
TGAGCCTGCTGGGAAACATGGGCATGGCGCTGCTGATCCGCATGGATGCCCGGCTCCACA
45 CACCTATGTACTTCTTCTGCGCAACCTCTCCCTGCTGGATGCCTGCTATTCTCCGCCATC
GGCCCCAAGATGCTAGTGGACCTGCTGCTGCCCGAGCCACCATCCCTTACACAGCCTGTG
CCTCCAGATGTTTGTCTTTGCAGGTCTGGCTGATACTGAGTGTGCTTGTGCTGGCAGCCAT
GGCCTATGACCGCTACGTGGCCATCAGAAACCCACTTCTCTATACAACAGCTATGTGCGAG
CGTCTATGCCTGGCCTTGTGTTGGGAGCATCAGGCCTGGGTGGGGCAGTGAGTGCCTTTGTTT
50 ACACAACCTCACCTTCCGCTGAGCTTCTGCCGCTCCCGGAAGATCAATAGCTTCTTCTG
CGATATCCCTCCACTGCTGGCCATCTCGTGCAGTGACACCACTCTCAATGAACCTCTTCTCT
TCGCCATCTGTGGCTTCATCCAGACAGCCACGGTGTAGCTATCACGGTGTCTTATGGCTT
CATCGTGGGGCTGTGATCCACATCGCGTTCGGTCGAGGGCAGTCGGCGAGCAGCCTCCAC
CGTGGTTCCCACTCAGAGCCGTGGCCATGATGTACGGGACACTCATTTTCATGTACCTG
55 CGCCCCAGCTCCAGCTATGCCCTGGACACTGACAAGATGGCCTCTGTGTTCTATACCTGG

TCATCCCGTCTCTCAACCCACTCATCTACAGCCTCCGCAATAAGGAGGTCAAGGAGGCCCT
CAGGCAGACCTGGAGCCGATTCCACTGTCCAGGGCAGGGGTCCCAGTGA (SEQ ID NO: 28)

AOLFR15 sequences:

- 5 MRENNQSSTLEFILLGVTGQQEQEDFFYILFLFYPTITLIGNLLIVLAICSDVRLHNP MYFLLANLS
LVDIFFSSVTIPKMLANHLLGSKSISFGGCLTQMYFMIALGNTDSYLAAMAYDRAVAISHPLH
YTTIMSPRSCIWLIAGSWVIGNANALPHTLLTASLSFCGNQEVANFYCDITPLKLSCSDIHFHV
KMMYLGVGIFSVPLLCIIVSYIRVFSTVFQVPSTKGVLKAFSTCGSHLTVVSLYYGTVMGTYFR
PLTNYSLKDAVITVMYTA VTPMLNPFYSLRNRDMKAALRKLFNKRIS (SEQ ID NO: 29)
- 10 ATGAGGGAAAAATAACCACTCTCTACACTGGAATTCATCCTCCTGGGAGTTACTGGTCAGC
AGGAACAGGAAGATTTCTTCTACATCCTCTTCTGTTCAATTTACCCCATCACATTGATTGGA
AACCTGCTCATTGTCTAGCCATTTGCTCTGATGTTCCGCTTCACAACCCCATGTATTTTCT
CCTTGCCAACCTCTCCTTGGTTGACATCTTCTCTCATCGGTAACCATCCCTAAGATGCTGG
15 CCAACCATCTCTTGGGCAGCAAATCCATCTCTTTTGGGGGATGCCTAACGCAGATGTATTT
CATGATAGCCTTGGGTAACACAGACAGCTATATTTGGCTGCAATGGCATATGATCGAGCT
GTGGCCATCAGCCACCCACTTCACTACACAACAATTATGAGTCCACGGTCTTGTATCTGGC
TTATTGCTGGGTCTTGGGTGATTGGAATGCCAATGCCCTCCCCCACTCTGCTCACAGC
TAGTCTGTCTTCTGTGGCAACCAGGAAGTGGCCAACCTTCTACTGTGACATTACCCCTTG
20 CTGAAGTTATCCTGTTCTGACATCCACTTTCATGTGAAGATGATGTACCTAGGGGTTGGCA
TTTTCTCTGTGCCATTACTATGCATCATTGTCTCCTATATTCGAGTCTTCTCCACAGTCTTCC
AGGTTCTTCCACCAAGGGCGTGCTCAAGGCCTTCTCCACCTGTGGTTCCCACTCAGGT
TGTCTCTTTGTATTATGGTACAGTCATGGGCACGTATTTCCGCCCTTTGACCAATTATAGCC
TAAAAGACGCAGTGATCACTGTAATGTACACGGCAGTGACCCCAATGTTAAATCCTTTTCAT
25 CTACAGTCTGAGAAATCGGGACATGAAGGCTGCCCTGCGGAAACTCTTCAACAAGAGAAT
CTCCTCGTAA (SEQ ID NO: 30)

AOLFR16 sequences:

- 30 MRRNCTLVTEFILLGLTSRRELQILLFLFLAIYMTVAVAGNLGMIVLIQANAWLHMPMYFFLSH
LSFVDLCFSSNVTIPKMLEIFLSEKKSISYPACLVCYLFIALVHVEIFILAVMAFDRYMAICNPL
YGSRMKS SVCSFLITVPYVYGALTGLMETMWTYNLAFCGPNEINH FYCADPPLIKLACSDTYN
KELSMFIVAGWNLSFSLFICISYLYIFPAILKIRSTEGRQKAFSTCGSHLTAVTIFYATLFFMYLR
PPSKESVEQGMVA VFYTTVIPMLNLIYSLRNKNVKEALIKELSMKIYFS (SEQ ID NO: 31)
- 35 ATGAGAAGAAACTGCACGTTGGTGACTGAGTTTCATTCTCCTGGGACTGACCAGTCGCCGG
GAATTACAAATTCTCCTCTTCACGCTGTTTCTGGCCATTTACATGGTCACGGTGGCAGGGA
ACCTTGGCATGATTGTCTCATCCAGGCCAACGCCTGGCTCCACATGCCCATGTACTTTTCT
CTGAGCCACTTATCCTTCGTGGATCTGTGCTTCTCTCCAATGTGACTCCAAAGATGCTGG
40 AGATTTTCTTTTTCAGAGAAGAAAAGCATTTCTCTATCCTGCCTGTCTTGTGCAGTGTTACCTT
TTTATCGCCTTGGTCCATGTTGAGATCTACATCCTGGCTGTGATGGCCTTTGACCGGTACAT
GGCCATCTGCAACCTCTGCTTTATGGCAGCAGAATGTCCAAGAGTGTGTGCTCCTTCTC
ATCACGGTGCCTTATGTGTATGGAGCGCTCACTGGCCTGATGGAGACCATGTGGACCTACA
ACCTAGCCTTCTGTGGCCCCAATGAAATTAATCACTTCTACTGTGCGGACCCACCACTGAT
TAAGCTGGCTTGTCTGACACCTACAACAAGGAGTTGTCAATGTTTATTGTGGCTGGCTGG
45 AACCTTTCTTTTTCTCTCTTCATCATATGTATTTCTACCTTTACATTTTCCCTGCTATTTTA
AAGATTCGCTCTACAGAGGGCAGGCAAAAAGCTTTTCTACCTGTGGCTCCCATCTGACAG
CTGTCACTATATTTCTATGCAACCTTTTCTTCATGTATCTCAGACCCCCCTCAAAGGAATCT
GTTGAACAGGGTAAAATGGTAGCTGTATTTTATACACAGTAATCCCTATGCTGAACCTTA
TAATTTATAGCCTTAGAAATAAAAATGTAAAAGAAGCATTAATCAAAGAGCTGTCAATGA
50 AGATATACTTTTCTTAA (SEQ ID NO: 32)

AOLFR17 sequences:

- 55 MLNFTDVTEFILLGLTSRREWQVLFFIIFLVVYITMVGNI GMMVLIKVSPQLNNP MYFFLSHLS
FVDVWFSSNVTIPKMLENLFSDDKTTTYAGCLVCFFIALVHVEIFILAAMAFDRYMAIGNPL
YGSKMSRVVCIRLITFPYIYGFLTSLAATLWYGLYFCGKIEINH FYCADPPLIKMACAGTFVKE

YTMILAGINFTYSLTVIIISYLFILAILRMRSAGRQKAFSTCGSHLTAVIIFYGTLIFMYLRRPTE
ESVEQGMVAVFYTTVIPMLNPMIYSLRNKDVKKAMMKVISRSC (SEQ ID NO: 33)

5 ATGCTCAATTTACCGATGTGACAGAGTTCATTCTTTGGGGCTAACGAGCCGTCGAGAAT
GGCAAGTCTCTTCTTCATCATCTTTCTTGGTCTACATCATCACCATGGTGGGCAATATC
GGCATGATGGTGTAAATCAAGGTCAAGTCTCAGCTTAACAACCCCATGTACTTTTCTCTCA
GTCACCTTGTCATTTGTTGATGTGTGGTTTTCTTCCAATGTCACCCCTAAAAATGTTGGAAAAAC
CTGTTTTTCAGATAAAAAACAATTACTTATGCTGGTTGTTTAGTACAGTGTTTCTTCTTCAT
10 TGCTCTTGTCATGTGGAAATTTTATTCTTGCTGCGATGGCCTTTGATAGATACATGGCAA
TTGGGAATCCTCTGCTTTATGGCAGTAAAATGTCAAGGGTGTCTGTATTGACTGATTAC
TTTCCCTTACATTTATGGTTTTCTGACGAGTCTGGCAGCAACATTATGGACTTACGGCTTGT
ACTTCTGTGGAAAAATTGAGATCAACCATTTCTACTGTGCAGATCCACCTCTCATCAAAAT
GGCCTGTGCCGGGACCTTTGTAAAGAATATACAATGATCATACTTGCCGGCATTAACCTC
15 ACATATTCCCTGACTGTAATTATCATCTCTTACTTATTCATCCTCATTGCCATTCTGCGAAT
GCGCTCAGCAGAAGGAAGGCAGAAGGCCTTTTCCACATGTGGGTCCCATCTGACAGCTGT
CATTATATTCTATGGTACTCTGATCTTCATGTATCTCAGACGTCCACAGAGGAGTCTGTG
GAGCAGGGGAAGATGGTGGCTGTGTTCTATACCACAGTGATCCCCATGTTGAATCCCATGA
TCTACAGTCTGAGGAACAAGGATGTGAAAAAGGCCATGATGAAAGTGATCAGCAGATCAT
20 GTTAA (SEQ ID NO: 34)

AOLFR18 sequences:

MSNTNGSAITEFILLGLTDCPELQSLFLVFLVVYLVTLGNLGMIMLMRLDSRLHTPMYFFLT
NLAFLVLCYTSNATPQMSTNIVSEKTSIFAGCFTQCYFIALLLTEFYMLAAMAYDRYVAIYDP
LRYSVKTSRRVCICLATFPYVYGFSDGLFQAILTFRLTCRSNVINHFCADPLIKLSCDTYVK
25 EHAMPISAGFNLSSSLTIVLVSYAFILAILRIKSAEGRHKAFSTCGSHMMAVTLFYGTLFCMYI
RPPTDKTVEESKIIAVFYTFVSPVLNPLIYSLRNKDVKQALKNVLR (SEQ ID NO: 35)

30 ATGTCCAACACAAATGGCAGTGCAATCACAGAATTCATTTTACTTGGGCTCACAGATTGCC
CGGAATCCAGTCTCTGCTTTTTGTGCTGTTTCTGGTTGTTTACCTCGTCAOCTGCTAGGC
AACCTGGGCATGATAATGTTAATGAGACTGGACTCTCGCCTTCACACGCCCATGTACTTCT
TCCTCACTAACTTAGCCTTTGTGGATTTGTGCTATACATCAAATGCAACCCCGCAGATGTC
GACTAATATCGTATCTGAGAAGACCATTTCTTTGCTGGTTGCTTTACACAGTGCTACATTT
TCATTGCCCTTCTACTCACTGAGTTTACATGCTGGCAGCAATGGCCTATGACCGCTATGT
35 GGCCATATATGACCCTCTGCGCTACAGTGTGAAAACGTCCAGGAGAGTTTGCATCTGCTTG
GCCACATTTCCCTATGTCTATGGCTTCTCAGATGGACTCTTCCAGGCCATCCTGACCTTCCG
CCTGACCTTCTGTAGATCCAATGTCATCAACCACTTCTACTGTGCTGACCCGCCGCTCATT
AGCTTTCTTGTCTGATACTTATGTCAAAGAGCATGCCATGTTTCATATCTGCTGGCTTCAAC
CTCTCCAGTCCCTCACCATCGTCTTGGTGTCTTATGCCTTCATTCTTGTGCCATCCTCCG
40 GATCAAAATCAGCAGAGGGAAGGCACAAGGCATTCTCCACCTGTGGTTCCCATATGATGGC
TGTCACCTGTGTTTTATGGGACTCTCTTTTGCATGTATATAAGACCACCAACAGATAAGACT
GTTGAGGAATCTAAAATAATAGCTGTCTTTTACACCTTTGTGAGTCCGGTACTTAATCCAT
TGATCTACAGTCTGAGGAATAAAGATGTGAAGCAGGCCTTGAAGAATGTCTGAGATGA
(SEQ ID NO: 36)

AOLFR19 sequences:

45 METKNYSSSTSGFILLGLSSNPQLQKPLFAIFLIMYLLTAVGNVLILAIYSDPRLHTPMYFFLSNL
SFMDICFTTVIVPKMLVNFLSETKIISYVGCLIQMYFFMAFGNTDSYLLASMAIDRLVAICNPLH
YDVVMKPWHCLLMLLGSCSISHLHSLFRVLLMSRLSFCASHIHKHFFCDTQPVKLKSCSDTSSSQ
50 MVMVTETLAIVITPFLCTIFSYLQIIVTVLRIPSAAGKWKAFSTCGSHLTVVVLFGYSVIYVYFR
PLSMYSVMKGRVATVMYTVVTPMLNPFYIYSLRNKDMKRLKRLRHRIYS (SEQ ID NO: 37)

55 ATGGAGACAAAGAATTATAGCAGCAGCACCTCAGGCTTCATCCTCCTGGGCCTCTCTTCCA
ACCCTAAGCTGCAGAAACCTCTCTTTGCCATCTTCTCATCATGTACCTACTCACTGCGGTG
GGGAATGTGCTCATCATCCTGGCCATCTACTCTGACCCAGGCTCCACACCCCTATGTACT
TTTTTCTCAGCAACTGTCTTTTCATGGATATCTGCTTCAACACAGTCATAGTGCCTAAGATG
CTGGTGAATTTTCTATCAGAGACAAAGATTATCTCTTATGTGGGCTGCCTGATCCAGATGT

ACTTCTTCATGGCATTGTTGGGAACACTGACAGCTACCTGCTGGCCTCTATGGCCATCGACCG
 GCTGGTGGCCATCTGCAACCCCTTACACTATGATGTGGTTATGAAACCATGGCATTGCCTA
 CTCATGCTATTGGGTTCTTGCAGCATCTCCACCTACATTCCCTGTTCCGCGTGCTACTTAT
 GTCTCGCTTGTCTTTCTGTGCCTCTCACATCATTAAGCACTTTTTCTGTGACACCCAGCCTG
 5 TGCTAAAGCTCTCCTGCTCTGACACATCCTCCAGCCAGATGGTGGTGATGACTGAGACCTT
 AGCTGTCAATTGTGACCCCTTCCCTGTGTACCATCTTCTCCTACCTGCAAATCATCGTCACTG
 TGCTCAGAATCCCTCTGACAGCCGGGAAGTGAAGGCCTTCTCTACCTGTGGCTCCCACT
 CACTGTAGTGGTCTCTATGAGGAGTGTCATCTATGTCTATTTTAGGCCTCTGTCCATGT
 ACTCAGTGATGAAGGGCCGGGTAGCCACAGTTATGTACACAGTAGTGACACCCATGCTGA
 10 ACCCTTTCATCTACAGCCTGAGGAACAAAGATATGAAAAGGGGTTTGAAGAAATTAAGAC
 ACAGAATTTACTCATAG (SEQ ID NO: 38)

AOLFR20 sequences:

MVEENHTMKNEFILTGFTDHPCLKTLLFVFFAIYLLITVVGNISLVALIFTHCRLHTPMYIFLGN
 15 LALVDSCCACAITPKMLENFFSEGKRISLYECAVQFYFLCTVETADCFLLAAVAYDRYVAICNP
 LQYHIMMSKKLCIQMTTGAFIAGNLHSMIHVGLVFRLVFCGLNHINHFYCDTLPLYRLSCVDPF
 INELVLFIFFSGSVQVFTIGSVLISYLYILLTIFRMKSKEGRAKAFSTCASHFSSVSLFYGSIFFLYIRP
 NLLEEGNDIPAAILFTIVVPLNPFYSLRNKEVISVLRKILLKIKSQGSVNK (SEQ ID NO: 39)

20 ATGGTTGAAGAAAATCATACCATGAAAAATGAGTTTATCCTCACAGGATTTACAGATCACC
 CTGAGCTGAAGACTCTGCTGTTTGTGGTCTTCTTGCCATCTATCTGATCACCCTGGTGGG
 GAATATTAGTTTGGTGGCACTGATATTTACACACTGTCGGCTTCACACACCAATGTACATC
 TTTCTGGGAAATCTGGCTCTTGTGGATTCTTGCTGTGCCTGTGCTATTACCCCCAAAATGTT
 AGAGAACTTCTTTCTGAGGGCAAAGGATTTCCCTCTATGAATGTGCAGTACAGTTTTAT
 25 TTTCTTTGCACTGTGGAACTGCAGACTGCTTTCTTCTGGCAGCAGTGGCCTATGACCGCT
 ATGTGGCCATCTGCAACCCACTGCAGTACCACATCATGATGTCCAAGAACTCTGCATTCA
 GATGACCACAGGCGCCTTCATAGCTGGAATCTGCATTCCATGATTTCATGTAGGGCTTGTA
 TTTAGGTTAGTTTTCTGTGGATTGAATCACATCAACCACTTTTACTGTGATACTCTTCCCTT
 GTATAGACTCTCCTGTGTTGACCCCTTCATCAATGAACTGGTCTATTTCATCTTCTCAGGTT
 30 CAGTTCAAGTCTTTACCATAGGTAGTGTCTTAATATCTTATCTCTATATTCTTCTTACTATT
 TTCAGAATGAAATCCAAGGAGGGAAGGGCCAAAGCCTTTTCTACTTGTGCATCCCACTTTT
 CATCAGTTTCATTATTCTATGGATCTATTTTTTCTTATACATTAGACCAAAATTGCTTGAA
 GAAGGAGGTAATGATATACCAGCTGCTATTTTATTTACAATAGTAGTTCCTTACTAAATC
 CTTTCATTTATAGTCTGAGAAACAAGGAAGTAATAAGTGTCTTAAGAAAAATTCTGCTGAA
 35 AATAAAATCTCAAGGAAGTGTGAACAAATGA (SEQ ID NO: 40)

AOLFR21 sequences:

MEPRKNVTDVFLVGFTQNPKEQKVLVFMFLFYLLTMVGNLLIVVTVTVSETLGSPMSFFLAGL
 TFDIIYSSSIPRLISDLFFGNNSISQSFMAQLFIEHLFGGSEVFLLLVMAYDRYVAICKPLHYLV
 40 IMRQWVCVLLLVVSWVGGFLQSVFQLSIYGLPFCGPNVIDHFFCDMYPLKLAICTDTHVIGLL
 VVANGGLSCTIAFLLLISYGVLHSLKKLSQKGRQKAHSTCSSHITVVVFFVPCIFMCARPAR
 TFSIDKSVSVFYTVITPMLNPLIYTLRNSEMTSAMKKL (SEQ ID NO: 41)

45 ATGGAGCCAAGGAAAAATGTGACTGACTTTGTCCTCTTGGGCTTCACACAGAATCCAAAG
 GAGCAGAAAGTACTTTTTGTTATGTTCTTGCTCTTCTACATTTTGACCATGGTGGGCAACCT
 GCTCATTGTAGTGACCGTAACTGTCAGTGAGACCCCTGGGCTCACCATGTCCTTCTTCTT
 GCTGGCTTAACATTTATAGATATCATTTATTCTTCATCCATTTCCCCCAGATTGATTTTCA
 CTGTTCTTTGGGAATAATTCCATATCCTTCCAATCTTTCATGGCCAGCTCTTATCGAGC
 50 ACCTTTTTGGTGGGTGAGAGGTCTTCTCCTGTTGGTGATGGCCTATGACCGCTATGTGGC
 CATCTGTAAGCCCTTGCAATTATTTGGTTATCATGAGACAAATGGGTGTGTGTTTTGCTGCTG
 GTAGTGTCTGGGTTGGAGGATTTCTGCAATCAGTATTTCAACTTAGCATTATTTATGGGC
 TCCCATCTGTGGCCCCAATGTCATTGATCATTTTTCTGTGACATGTATCCCTTATTGAAA
 CTGGCCTGCACTGACACCCATGTTATTGGCCTCTTAGTGGTGGCCAATGGAGGACTGTCTT
 GCACTATTGCGTTTTCTGCTCTTACTCATCTCTTATGGTGTCTATCCTGCACTCTCTAAAGAAA
 55 CTTAGTCAGAAAGGGAGGCAAAAAGCCCACTCAACCTGCAGTTCACATCACTGTGGTTG
 TCTTCTTCTTTGTTCTTGTATTTTTATGTGTGCTAGACCTGCTAGGACCTTCTCCATTGAC

AAATCAGTGAGTGTGTTTTATACAGTCATAACCCCAATGCTGAACCCCTTAATCTACACTC
TGAGAAATCTGAGATGACAAGTGCTATGAAGAAGCTTTAG (SEQ ID NO: 42)

AOLFR22 sequences:

5 MRXXNXXTEFVLLGFSQDPGVXKALFVMFLLTYXXTVVGNLLIVVDIIASPLXGSPMYFFLAC
LSFIDAAYSTTISPKLIVGLFCDKKTISFQGCMGQLFIDHFFGGAEVFLVVMACDRYVAICKPL
HYLTIMNRQVCFLLLVXXMIGGFVHSAFQIVVYSLPFCGPXVIVHFSCDMHPLLELACTDITYFI
GLTVVVNSGAICMVIFNLLISYGVILSSLKTYSQEKRGKALSTCSSGSTVVVLFVPCIFIYVRP
VSNFPTDKFMTVFYTIITHMLSPLIYTLRNSEMRNAIEKLLGKKLTFIIGGVSVLM (SEQ ID NO:
10 43)

ATGAGACANNNNNAACAATATNACAGAATTTGTCCTCCTGGGCTTTTCTCAGGATCCTGGTG
TGNNNAAAGCATTATTTGTCATGTTTTTACTCACATACNNNNNNACAGTGGTGGGGAACCT
GCTCATTGTNGTGGATATTATTGCCAGCCCTTNNTTGGGTTCCCAATGTATTTCTTCTCTTG
15 CCTGCCTGTCATTTATAGATGCTGCATATTTCCACTACCATTTCTCCCAAGTTAATTGTAGGC
TTATTCTGTGATAAAAAGACTATTTCCCTTCCAAGGTTGCATGGGCCAGCTATTTATAGACC
ATTTCTTTGGTGGGGCTGAGGTCTTCCCTTCTGGTGGTGATGGCCTGTGATCGCTATGTGGC
CATCTGTAAGCCACTGCACTATTTGACCATCATGAATCGACAGGTTTGCTTCTCTGTGTGG
TNNNNCCATGATTGGAGGTTTTGTACATTCTGCGTTTCAAATTGTTGTGTACAGTCTCCCT
20 TTCTGTGGTCCCNAATGTCATTGTTTCATTTCAGTTGTGACATGCACCCATTACTGGAAGTGGC
ATGCACTGACACCTACTTTATAGGCCTCACTGTTGTTGTCAATAGTGAGCAATCTGTATG
GTCATTTTCAACCTTCTGTTAATCTCCTATGGAGTCATCCTAAGCTCCCTTAAACTTACAG
TCAGGAAAAGAGGGGTAAAGCCTTGTCTACCTGCAGCTCCGGCAGTACCGTTGTTGTCCTC
TTTTTGTACCTGTATTTTTCATATATGTTAGACCTGTTTCAAACCTTCTACTGATAAGTT
25 CATGACTGTGTTTTATACCATATCACACACATGCTGAGTCCTTTAATATATACGTTGAGA
AATTCAGAGATGAGAAATGCTATAGAAAACTCTTGGGTAAAAAGTTAACTATATTTATTA
TAGGAGGAGTGTCCTCATGTAG (SEQ ID NO: 44)

AOLFR23 sequences:

30 MAKNNLRTVTEFILMGFMDHPKLEIPLFLVFLSFYLVTLGNVGMIMLIQVDVKLYTPMYFFLS
HLSLLDACYTSVITPQILATLATGKTVISYGHCAAQFFLFTICAGTECFLLAVMAYDRYAAIRNP
LLYTVAMNPRLCWSLVVGAYVCGVSGAILRTTCTFTLSFCKDNQINFFCDLPLLKLACSDTA
NIEIUIFFGNFVILANASVILISYLLIKTILKVSSGGRKTFSTCASHITAVLFFGALFMYLQS
GSGKSLBEDKVVSFYTIVIPMLNPLIYSLRNKDVKDAFRKVARRLQVSLSM (SEQ ID NO: 45)

35 ATGGCCAAGAATAATCTCACCAGAGTAACCGAATTCATTCTCATGGGCTTTATGGACCACC
CCAAATTGGAGATTCCCCTCTTTCTGGTGTTTCTGAGTTTCTACCTAGTCACCCCTTCTTGGG
AATGTGGGGATGATTATGTTAATCCAAGTAGATGTCAAACCTCTACACCCCAATGTACTTCT
TCCTGAGCCACCTCTCCCTGCTGGATGCCTGTTACACCTCAGTCATCACCCCTCAGATCCCTA
40 GCCACATTGGCCACAGGCAAAACGGTCATCTCCTACGGCCACTGTGCTGCCAGTTCTTTT
TATTCACCATCTGTGCAGGCACAGAGTGCTTTCTGCTGGCAGTGATGGCCTATGATCGCTA
TGCTGCCATTGCAACCCACTGCTCTATACCGTGGCCATGAATCCCAGGCTCTGCTGGAGC
CTGGTGGTAGGAGCCTATGTCTGTGGGGTGTCAGGAGCCATCCTGCGTACCACTTGCACCT
TCACCCCTCCTTCTGTAAGGACAATCAAATAAACTTCTTCTTCTGTGACCTCCCAACCCCTG
45 CTGAAGCTTGCCTGCAGTGACACAGCAAACATCGAGATTGTCATCATCTTCTTTGGCAATT
TTGTGATTTTGGCCAATGCCTCCGTCATCCTGATTTCTATCTGCTCATCATCAAGACCATT
TTGAAAGTGAAGTCTTCAGGTGGCAGGGCCAAGACTTTCTCCACATGTGCCTCTCACATCA
CTGCTGTGGCCCTTTTCTTTGGAGCCCTTATCTTCATGTATCTGCAAAGTGGCTCAGGCAAA
TCTCTGGAGGAAGACAAAGTCGTGTCTGTCTTCTATACAGTGGTCATCCCCATGCTGAACC
50 CTCTGATCTACAGCTTAAGAAACAAAGATGTAAAAGACGCCTTCAGAAAGGTCGCTAGGA
GACTCCAGGTGTCCCTGAGCATGTAG (SEQ ID NO: 46)

AOLFR25 sequences:

55 METGNLTWVSDFVFLGLSQTRELRFLFLMFLFVYITTVMGNILIITVTSDSLHTPMYFLLRN
LAVLDLCFSSVTAPKMLVDLLSEKKTISYQGCMIFFHFLGGAMVFFLSVMAFDRLLAISRPL
RYVTVMNTQLWVGLVVATWVGGFVHSIVQLALMLPLPFCGPNILDNFYCDVPQVRLACTDT

SLLEFLKISNSGLLDVVWFFLLMSYLFILVMLRSHPGEARRKAASCTTHIIVVSMIFVPSIYLY
 ARPFTFPMDKLVSIGHTVMTPLNPMIYTLRNQDMQAAVRRRLGRHRLV (SEQ ID NO: 47)

5 ATGGAAACAGGGAACCTCACGTGGGTATCAGACTTTGTCTTCCTGGGGCTCTCGCAGACTC
 GGGAGCTCCAGCGTTTCCTGTTTCTAATGTTCCCTGTTTGTCTACATCACCAGTGTATGGGA
 AACATCCTTATCATCATCAGTACCTCTGATTCCCAGCTCCACACACCCATGTACTTTCT
 GCTCCGAAACCTGGCTGTCCTAGACCTCTGTTTCTCTTCAGTCACTGCTCCAAAATGCTAG
 TGGACCTCCTCTCTGAGAAGAAAACCATCTCTTACCAGGGCTGCATGGGTGAGATCTTCTT
 CTTCCACTTTTTGGGAGGTGCCATGGTCTTCTCCTCTCAGTGATGGCCTTTGACCGCTCA
 10 TTGCCATCTCCCGGCCCTCCGCTATGTCACCGTCATGAACACTCAGCTCTGGGTGGGGCT
 GGTGGTAGCCACCTGGGTGGGAGGCTTTGTCCACTCTATTGTCCAGCTGGCTCTGATGCTC
 CCACTGCCCTTCTGTGGCCCCAACATTTGGATAACTTCTACTGTGATGTTCCCCAAGTACT
 GAGACTTGCTGCACTGACACCTCACTGCTGGAGTTCCTCAAGATCTCCAACAGTGGGCTG
 CTGGATGTCGTCTGGTTCTTCTCCTCCTGATGTCCTACTTATTCATCCTGGTGATGCTGAG
 15 GTACATCCAGGGGAGGCAAGAAGGAAGGCAGCTTCCACCTGCACCAACCCACATCATCGT
 GGTTCATGATCTTTCGTTCCAAGCATTACCTCTATGCCCGGCCCTTCACTCCATTCCCTA
 TGGACAAGCTTGTGTCCATCGGCCACACAGTCATGACCCCCATGCTCAACCCCATGATCTA
 TACCCTGAGGAACCAGGACATGCAGGCAGCAGTGAGAAGATTAGGGAGACACCGGCTGGT
 TTGA (SEQ ID NO: 48)

20

AOLFR26 sequences:

MAAKNSSVTEFIEGLTHQPLRIPFLFLGFYTVTVVGNLGLITLIGLNSHLHTPMYFFLFNLS
 LIDFCSTTTTPKMLMSFVSRKNISFTGCMTQLFFCFVVSSEFILLSAMAYDRYVAICNPLLYT
 VTMSQVCLLLLLGAYGMGFAGAMAHTGSIMNLTFCADNLVNHFMCDILPLELSCNSSYMN
 25 ELVVFIVVAVDVGMPIVTVFISYALILSILHNSSTEGRSKAFSTCSSHIIIVSLFFGSGAFMYLKP
 LSILPLEQGVSSLFYTHVPVLNPLIYSLRNKDVKVALRRTLGRKIFS (SEQ ID NO: 49)

30 ATGGCAGCCAAAACTCTTCTGTGACAGAGTTTATCCTCGAAGGCTTAACCCACCAGCCGG
 GACTGCGGATCCCCCTCTTCTTCTGTTTCTGGGTTTCTACACGGTCACCGTGGTGGGGAA
 CCTGGGCTTGATAACCTGATTGGGCTGAACCTCTACCTGCACACTCCCATGTACTTCTTCC
 TTTTAACTCTCTTTAATAGATTTCTGTTTCTCCACTACCATCACTCCCCAAATGCTGATG
 AGTTTTGTCTCAAGGAAGAACATCATTTCCCTCACAGGGTGTATGACTCAGCTCTTCTTCTT
 CTGCTTCTTTGTCTCTCTGAGTCCTTCATCCTGTGACGATGGCGTATGACCGCTACGTGG
 CCATCTGTAACCACTGTTGTACACAGTCACCATGTCTTGCCAGGTGTGTTTGTCTCTTTG
 35 TTGGGTGCCTATGGGATGGGGTTTGTCTGGGGCCATGGCCACACAGGAAGCATAATGAAC
 CTGACCTTCTGTCTGACAACCTTGTCATCATTTTCATGTGTGACATCCTTCTCTCTTGA
 GCTCTCCTGCAACAGCTCTTACATGAATGAGCTGGTGGTCTTTATTGTGGTGGCTGTTGAC
 GTTGAATGCCCATGTGCACTGTCTTTATTTCTTATGCCCTCATCCTCTCCAGCATTCTACA
 CAACAGTTCTACAGAAGGCAGGTCCAAAGCCTTTAGTACTTGCAAGTCCCACATAATTGTA
 40 GTTTCTCTTTTCTTTGGTTCTGGTGCTTTTCATGTATCTCAAACCCCTTTCCATCCTGCCCTC
 GAGCAAGGGAAAAGTGTCTCCTCCTGTTCTATACCATAATAGTCCCCGTGTTAAACCCATTAA
 TCTATAGCTTGAGGAACAAGGATGTCAAAGTTGCCCTGAGGAGAACTTTGGGCAGAAAAA
 TCTTTTCTTAA (SEQ ID NO: 50)

AOLFR27 sequences:

45 MPSQNYSIIEFNLFGFSAFPQHLLPILFLYLLMFLFTLLGNLLIMATTWIEHRLHTPMYFLCTL
 SVSEILFTVAITPRMLADLLSTHHSITFVACANQMFFSFMFGFTHSFLLLVMGYDRYVAICHPLR
 YNVLMSPRDCAHLVACTWAGGSVMGMMVTTIVFHLTFCGSNVIHFFCHVLSLLKLACENKT
 SSVIMGVMLVCVTALIGCLFLILSYVFIVAAILRPSAEGRHKTFTSTCVSHLTVVVTHYSFASFTY
 50 LKPKGLHSMYSDALMATTYTVFTPLSPIIFSLRNKELKNAINKNFYRKFCPPSS (SEQ ID NO:
 51)

55 ATGCCTAGTCAGAACTATAGCATCATATCTGAATTTAACCTCTTTGGCTTCTCAGCCTTCCC
 CCAGCACCTCCTGCCCATCTTGTTCTGCTGTACCTCCTGATGTTCTGTTACATTGCTGG
 GCAACCTTCTCATCATGGCCACAATCTGGATTGAACACAGACTCCACACACCCATGTACCT
 CTTCTTGTGCACCCTCTCCGTCTCTGAGATTCTGTTCAGTGTGCCATCACCCCTCGCATGC

TGGCTGATCTGCTTTCCACCCATCATTCATCACCTTTGTGGCTTGTGCCAACCAGATGTTCT
 TTCTCCTTCATGTTTGGCTTCACTCACTCCTTCTCCTGGTCATGGGCTATGATCGCTA
 TGTGGCCATCTGCCACCCACTGCGTTACAATGTGCTCATGAGCCCCGTGACTGTGCCCAT
 CTTGTGGCCTGTACCTGGGCTGGTGGCTCAGTCATGGGGATGATGGTGACAACGATAGTTT
 5 TCCACCTCACTTTCTGTGGGTCTAATGTGATCCACCATTTTTTCTGTCATGTGCTTTCCCTCT
 TGAAGTTGGCCTGTGAAAACAAGACATCATCTGTCATCATGGGTGTGATGCTGGTGTGTGT
 CACAGCCCTGATAGGCTGTTTATTCCTCATCATCCTCTCCTATGTCITCATTGTGGCTGCCA
 TCTTGAGGATTCCCTCTGCCGAAGGCCGGCACAAGACATTTTCTACGTGTGTATCCACCT
 CACTGTGGTGGTCACGCACTATAGTTTTGCCTCCTTTATCTACCTCAAGCCCAAGGGCTCC
 10 ATTCTATGTACAGTGACGCCTTGATGGCCACCACCTATACTGTCTTCACCCCTTCCTTAGC
 CCAATCATTTTCAGCCTAAGGAACAAGGAGCTGAAGAATGCCATAAAATAAAACTTTTACA
 GAAAATTCTGTCTCCCAAGTTCCTGA (SEQ ID NO: 52)

AOLFR28 sequences:

15 MPNFTDVTEFTLLGLTCRQELQVLEFFVFLAVYMITLLGNIGMILLISISPQLQSPMYFFLSHLSF
 ADVCFSSNVTPKMLENLLSEKTIISYVGCLVQCYFFIAVVHVEVYLAVMAFDHYMAGCXPLL
 YGSKMSRTVCVRLISVXYXYGFSVSLICTLWYGLYFCGNFEINHFYCADPPLIACGRVHIKE
 ITMIVIAGINFTYSLSVLISYTLIVAVLRMRSDGRRKAFSTCGSHLTAVSMFYGTPIFMYLR
 RPTESVEQGMVAVFYTTVIPMLNPMIYSLRNKDVKEAVNKAITKTYVRQ (SEQ ID NO: 53)
 20
 ATGCCTAATTTACGGATGTGACAGAATTTACTCTCCTGGGGCTGACCTGTCGTGAGGAGC
 TACAGGTTCTCTTTTGTGGTGTTCCTAGCGGTTTACATGATCACTCTGTTGGGAAATATT
 GGTATGATCATTTTGATTAGCATCAGTCCTCAGCTTCAGAGTCCCATGTACTTTTCTGAG
 TCATCTGTCTTTTGCAGGACGTGTGCTTCTCCTCCAACGTTACCCCCAAAATGCTGGAAAAC
 25 TATTATCAGAGACAAAACCATTTCCTATGTGGGATGCTTGGTGACGTGCTACTTTTTCAT
 TGCCGTTGTCCACGTGGAGGTCTATATCCTGGCTGTGATGGCCTTTGACAGGTACATGGCC
 GGCTGCAANCTCTGCTTTATGGCAGTAAAATGTCTAGGACTGTGTGTGTTCCGGCTCATCT
 CTGTGNNTATGNNTATGGATTCTCTGTGACGCTAATATGCACACTATGGACTTATGGCTT
 ATACTTCTGTGGAACTTTGAAATCAATCACTTCTATTGTGCAGATCCCCCTCTCATCCAGA
 30 TTGCCTGTGGGAGAGTGACATCAAAGAAATCACAATGATTGTTATTGCTGGAATTAACCT
 CACATATTCCCTCTCGGTGGTCTCATCTCCTCACTCTCATTGTAGTAGCTGTGCTACGCA
 TCGCTCTGCGGATGGCAGGAGGAAGCGTTCTCCACCTGTGGGTCCCACTTGACGGCTGT
 TTCTATGTTTTATGGGACCCCCATCTTCATGTATCTCAGGAGACCCACTGAGGAATCCGTA
 GAGCAGGGCAAAATGGTGGCTGTGTTTTACACCACAGTAATTCCTATGTTGAATCCCATGA
 35 TCTACAGTCTGAGAAATAAGGATGTAAAAGAAGCAGTCAACAAAGCAATCACCAGACAT
 ATGTGAGGCAGTAA (SEQ ID NO: 54)

AOLFR29 sequences:

40 MMSFAPNASHSPVFLLLGFSTRANISYTLFFFLAIYLTTLGNVTVLLISWDSRLHSPMYLLR
 GLSVIDMGLSTVTLPLQLLAHLVSHYPTIPAARCLAQFFFFYAFGVTDLVIAMALDRYVAICD
 PLHYALVMNHQRCACLLALSWVVSILHTMLRVGLVPLCWTGDAGGNVNLPHFFCDHRPLLR
 ASCSDIHSNELAIFEGGFLMLGPCALIVLSYVRIGAAILRLPSAAGRRAVSTCGSHLTMVGFL
 YGTIICVYFQPPFQNSQYQDMVASVMYTAITPLANPFVYSLHNKDVKGALCRLLEWVKVDP
 (SEQ ID NO: 55)
 45
 ATGATGAGCTTTGCCCTAATGCTTCACACTCTCCGGTTTTTTTGTCTCCTTGGGTTCTCGAG
 AGCTAACATCTCCTACACTCTCCTCTTCTCTCTGTTCTCTGGCTATTTACCTGACCACCATA
 TGGGGAATGTGACACTGGTGTCTCATCTCCTGGGACTCCAGACTGCACTACCCCATGTA
 TTATCTGCTTCGTGGCCTCTCTGTGATAGACATGGGGCTATCCACAGTTACACTGCCCCAG
 50 TTGCTGGCCCCATTGGTCTCTCATTACCCAACCATTCCTGCTGCCCCGCTGCTTGGCTCAGTT
 CTTTTTCTTCTATGCATTTGGGGTTACAGATACTTGTCTATTGCTGTGCTGCTGCTGATC
 GCTATGTGGCCATCTGTGACCCCTGCACTATGCTTTGGTAATGAATCACCACGGTGTGC
 CTGCTTACTAGCCTTGAGCTGGGTGGTGTCCATACTGCACACCATGTTGCGTGTGGGACTC
 GTCCTGCTCTTTGCTGGACTGGGGATGCTGGGGGCAACGTTAACCTTCCTCACTTCTTTTG
 55 TGACCACCGGCCACTTCTGCGAGCCTCTTGTTCTGACATACATTCTAATGAGCTGGCCATA
 TTCTTTGAGGGTGGCTTCTTATGCTGGGCCCCCTGTGCCCTCATTGTACTCTCTTATGTCCG

AATTGGGGCCGCTATTCTACGTTTGCCTTCAGCTGCTGGTCGCCGCCGAGCAGTCTCCACC
 TGTGGATCCCACCTCACCATGGTTGGTTTCCCTCTACGGCACCATCATTTGTGTCTACTTCCA
 GCCTCCCTTCCAGAACTCTCAGTATCAGGACATGGTGGCTTCAGTAATGTATACTGCCATT
 ACACCTTTGGCCAAACCATTTGTGTATAGCCTCCACAATAAGGATGTCAAGGGTGCCTCT
 5 GCAGGCTGCTTGAATGGGTGAAGGTAGACCCCTGA (SEQ ID NO: 56)

AOLFR30 sequences:

MGFLSPMHPCRPPTQRRMAAGNHSTVTEFLKGLTKRADLQLPLFLLFLGIYLVTVGNLGMIT
 LCLNSQLHTPMYYFLSNLSLMDLCYSSVTPKMLVNFVSEKNISYAGCMSQLYFFLVFVIAEC
 10 YMLTVMAYDRYVXXCHPLLNYIMSHHTCLLLVAVVYAIGLIGSTTETGLMLKLPYCEHLISHY
 FCDILPLMKLSCSSTYDVENTVFPSAGFNIVTSLTVLVSYTFILSSILGISTTEGRSKAFSTCSSHL
 AAVGMFYGSTAFMYLKPSTISSLTQENVASVFYTTVIPMLNPLIYSLRNKEVKAQVQKTLRGK
 LF (SEQ ID NO: 57)

15 ATGGGGTTCTTGTCTCCCATGCATCCCTGCAGGCCTCCCACCCAGAGGAGAATGGCTGCAG
 GAAATCACTCTACAGTGACAGAGTTCATTCTCAAGGGTTTAACGAAGAGAGCAGACCTCC
 AGCTCCCCCTCTTTCTCCTCTTCCCTCGGGATCTACTTGGTCACCATCGTGGGGAACCTGGGC
 ATGATCACTCTAATTTGTCTGAACTCTCAGCTGCACACCCCATGTACTACTTTCTCAGCAA
 TCTGTCACTCATGGATCTCTGCTACTCCTCCGTCATTACCCCTAAGATGCTGGTGAACTTTG
 20 TGTCAGAGAAAAACATCATCTCCTACGCAGGGTGCATGTCACAGCTCTACTTCTTCTTGT
 TTTTGTCAATTGCTGAGTGTTACATGCTGACAGTGATGGCCTACGACCGCTATGTTGNCNTC
 TGCCACCCCTTTGCTTTACAACATCATTATGTCTCATCACACCTGCCTGCTGCTGGTGGCTGT
 GGTCTACGCCATCGGACTCATTTGGCTCCACAATAGAAACTGGCCTCATGTTAAACTGCC
 TATTGTGAGCACCTCATCAGTCACTACTTCTGTGACATCCTCCCTCTCATGAAGCTGTCTGT
 25 CTCTAGCACCTATGATGTTGAGATGACAGTCTTCTTTTGGGCTGGATTCAACATCATAGTC
 ACGAGCTTAACAGTTCTTGTCTTACACCTTCATTCTCTCCAGCATCCTCGGCATCAGCAC
 CACAGAGGGGAGATCCAAAGCCTTCAGCACCTGCAGCTCCACCTTGCAGCCGTGGGAAT
 GTTCTATGGATCAACTGCATTATGTAATTAACCCCTCCACAATCAGTTTCTTGACCCAG
 GAGAATGTGGCCTCTGTGTTCTACACCACGGTAATCCCCATGTTGAATCCCCTAATCTACA
 30 GCCTGAGGAACAAGGAAGTAAAGGCTGCCGTGCAGAAAACGCTGAGGGGTAAACTGTTTT
 GA (SEQ ID NO: 58)

AOLFR31 sequences:

MGTGNDTTVVEFTLLGLSEDTTVCAILFLVFLGIYVVTLMGNISIVLIRRSHTLHTPMYIFLCHL
 35 AFVDIGYSSSVTPVMLMSFLRKETSLPVAGCVAQLCSVVTFGTAECEFLAAMAYDRYVAICSP
 LLYSTCMSPGVCILVGMSYLGCCVNAWTFIGCLLRSLFCGPNKVNHHFFCDYSPLCLKACSHDF
 TFEIIPAISSGSIIVATVCVIAISYIYLITILKMHSTKGRHKAFSTCTSHLTAVTLFYGTITFIYVMP
 KSSYSTDQNKVVSVFYTVVIPMLNPLIYSLRNKEIKGALKRELRIKIFS (SEQ ID NO: 59)

40 ATGGGGACTGGAAATGACACCACTGTGGTAGAGTTTACTCTTTTGGGGTTATCTGAGGATA
 CTACAGTTTGTGCTATTTTATTTCTTGTGTTTCTAGGAATTTATGTTGTACCTTAATGGGT
 AATATCAGCATAATTGTATTGATCAGAAGAAGTCATCATCTTCATACACCCATGTACATTT
 TCCTCTGCCATTTGGCCTTTGTAGACATTGGGTAATCCTCATCAGTCACACCTGTCTGCTC
 ATGAGCTTCCTAAGGAAAGAAACCTCTCTCCCTGTTGCTGGTTGTGTGGCCAGCTCTGTT
 45 CTGTAGTGACGTTTGGTACGGCCGAGTGCTTCTGCTGGCTGCCATGGCCTATGATCGCTA
 TGTGGCCATCTGCTCACCCCTGCTCTACTCTACCTGCATGTCCCCTGGAGTCTGCATCATCT
 TAGTGGGCATGTCTACCTGGGTGGATGTGTGAATGCTTGGACATTCATTGGCTGCTTATT
 AAGACTGTCTTCTGTGGGCCAAATAAAGTCAATCACTTTTTCTGTGACTATTACCACTTT
 TGAAGCTTGCTTGTTCCCATGATTTTACTTTTGAAATAATTCCAGCTATCTCTTCTGGATCT
 50 ATCATTTGTGGCCACTGTGTGTGTCATAGCCATATCCTACATCTATATCCTCATCACCATCCT
 GAAGATGCACTCCACCAAGGGCCGCCACAAGGCCTTCTCCACCTGCACCTCCCACCTCACT
 GCAGTCACTCTGTTCTATGGGACCATACCTTCATTATGTGATGCCCAAGTCCAGCTACTC
 AACTGACCAGAACAAGGTGGTGTCTGTTCTACACCGTGGTGATTCCCATGTTGAACCCC
 CTGATCTACAGCCTCAGGAACAAGGAGATTAAGGGGGCTCTGAAGAGAGAGCTTAGAATA
 55 AAAATATTTTCTTGA (SEQ ID NO: 60)

AOLFR32 sequences:

MNSLKDGNHTALTGFILLGLTDDPILRVILFMILSGNLSIIILIRISSQLHHPMYFFLSHLAFADM
 AYSSSVTPNMLVNFLVERNTVSYLGCAIQLGSAFFATVECVLLAAMAYDRFVAICSPLLYSTK
 MSTQVSVQLLLVVYIAGFLIAVSYTTSFYFLLFCGPNQVNHFFCDFAPLLELSCSDISVSTVVLSE
 5 SSGSIIVTVCVIAVCYIYLITILKMRSTEGHHKAFSTCTSHLTVVTLFYGTTTFIYVMPNFSYST
 DQNKVSVLYTVVIPMLNPLIYSLRNKEIKGALKRELVRKILSHDACYFSRTSNNDIT (SEQ ID
 NO: 61)

ATGAATTCCTGAAGGACGGGAATCACACCGCTCTGACGGGGTTCATCCTATTGGGCTTAA
 10 CAGATGATCCAATCCTTCGAGTCATCCTCTTCATGATCATCCTATCTGGTAATCTCAGCATA
 ATTATTCTTATCAGAATTTCTTCTCAGCTCCATCATCCTATGTATTTCTTTCTGAGCCACTT
 GGCTTTTGCTGACATGGCCTATTCATCTTCTGTACACCCAACATGCTTGTAACCTCCTGG
 TGGAGAGAAATACAGTCTCCTACCTTGGATGTGCCATCCAGCTTGGTTCAGCGGCTTTCTT
 TGCAACAGTCGAATGCGTCCTTCTGGCTGCCATGGCCTATGACCGCTTTGTGGCAATTTGC
 15 AGTCCACTGCTTTATTCAACCAAAATGTCCACACAAGTCAGTGTCCAGCTACTCTTAGTAG
 TTTACATAGCTGGTTTTCTCATTGCTGTCTCCTATACTACTTCTCTATTTTTTACTCTTCT
 GTGGACCAAAATCAAGTCAATCATTTTTTCTGTGATTTTCGCTCCCTTACTTGAACCTCCTGT
 TCTGATATCAGTGTCTCCACAGTTGTTCTCTCATTTTCTTCTGGATCCATCATTGTGGTCAC
 TGTGTGTGTATGACCGTCTGCTACATCTATATCTCATCACCATCCTGAAGATGCGCTCCA
 20 CTGAGGGGACCACCAAGGCCTTCTCCACCTGCACCTCCACCTCACTGTGGTTACCCTGTT
 CTATGGGACCATTACCTTCATTTATGTGATGCCCAATTTTAGCTACTCAACTGACCAGAAC
 AAGGTGGTGTCTGTGTTGTACACAGTGGTGATTCCCATGTTGAACCCCTGATCTACAGCC
 TCAGGAACAAGGAGATTAAGGGGGCTCTGAAGAGAGAGCTTGTTAGAAAAATACTTTCTC
 ATGATGCTTGTTATTTTAGTAGAACTTCAAATAATGATATTACATAG (SEQ ID NO: 62)

AOLFR34 sequences:

MLEGVEHLLLLLLTDVNSKELOSGNQTSVSHFVLVGLHHPPLGAPLFLAFLVIYLLTVSGNG
 LIILTVDIRLHRPMCLFLCHLSFLDMTISCAIVPKMLAGFLLGSRISFGGCVIQLFSFHLGCT
 ECFLYTLMAYDRFLAICKPLHYATIMTHRVCNLSALGTWLGGTIHSFLQTSFVFRLPFCGPNRV
 30 DYIFCDIPAMRLACADTAINELVTFADIGFLALTCFMLILSYGYIVAAILRIPSADGRNFAST
 CAAHLTVVIVYVPCFTIYLRPCSQEPLDGVVAVFYTVITPLLSIYTLCKEMKAALQRLGG
 HKEVQPH (SEQ ID NO: 63)

ATGTTAGAGGGTGTGAGCATCTCCTTCTGCTACTTCTTTTGACAGATGTGAACAGCAAGG
 35 AACTGCAAAGTGGAAACCAGACTTCTGTGTCTCACTTCATTTTGGTGGGCCTGCACCACCC
 ACCACAGCTGGGAGCGCACTCTTCTTAGCTTTCTTGTATCTATCTCCTCACTGTTTCTG
 GAAATGGGCTCATCATCCTCACTGTCTTAGTGACATCCGGCTCCATCGTCCCATGTGCTT
 GTTCTGTGTACCTCTCCTTCTTGGACATGACCATTTCTTGTGCTATTGTCCCCAAGATGC
 TGGCTGGCTTTCTTCTTGGGTAGTAGGATTATCTCCTTTGGGGGCTGTGTAATCCAATATTT
 40 TCTTTCCATTTCTTGGGCTGTACTGAGTGCTTCTTTACACACTCATGGCTTATGACCGTTT
 CCTTGCCATTTGTAAGCCCTTACACTATGCTACCATCATGACCCACAGAGTCTGTAACCTCCC
 TGGCTTTAGGCACCTGGCTGGGAGGGAATCCATTCACTTTTCCAAACAAGTTTGTATT
 CCGGCTGCCCTTCTGTGGCCCCAATCGGGTGCAGTACATCTTCTGTGACATTCTGCCATGC
 TGGCTCTAGCCTGCGCCGATACGGCCATCAACGAGCTGGTCACCTTTGCAGACATTGGCTT
 45 CCTGGCCCTCACCTGCTTCATGCTCATCTCACTTCTATGGCTATATTGTAGCTGCCATCC
 TGCGAATTCCGTCAGCAGATGGGCGCCGCAATGCCTTCTCCACTTGTGCTGCCACCTCAC
 TGTGTGCTATTGTTTACTATGTGCCCTGCACCTTCATTTACCTGCGGCCTTGTTACAGGAGC
 CCTGGATGGGGTGGTAGCTGTCTTTACACTGTCTCATCACTCCCTTGCTTAACTCCATCATC
 TACACACTGTGCAACAAAGAAATGAAGGCAGCATTACAGAGGCTAGGGGGCCACAAGGAA
 50 GTGCAGCCTCACTGA (SEQ ID NO: 64)

AOLFR35 sequences:

MEPLNRTEVSEFFLKGFSGYPALHLLFPLCSAMYLVTLNGNTAIMAVSVLDIHLHTPVYFFLG
 NLSTLDICYTPTFVPLMLVHLLSSRKTISSFAVCAIQMCLSLSTGSTECLLAITAYDRYLAICQPL
 55 RYHVLMSHRLCVLLMGAAWVLCLKSVTEMVISMRLPFCGHHVVSHTCKILAVLKLACGNT
 SVSEDFLLAGSILLPLVPLAFICLSYLLILATILRVPSAARCKAFSTCLAHLAVVLLFYGTIFMY

LKPKSKEAHISDEVFTVLYAMVTTMLNPTIYSLRNKEVKEAARKVWGRSRASR (SEQ ID NO: 65)

5 ATGGAGCCGCTCAACAGAACAGAGGTGTCCGAGTTCTTTCTGAAAGGATTTTCTGGCTACC
CAGCCCTGGAGCATCTGCTCTTCCCTCTGTGCTCAGCCATGTACCTGGTGACCCCTCCTGGG
GAACACAGCCATCATGGCGGTGAGCGTGCTAGATATCCACCTGCACACGCCCCTGTACTTC
TTCCTGGGCAACCTCTCTACCCTGGACATCTGCTACACGCCCACCTTTGTGCCCTCTGATGCT
GGTCCACCTCCTGTCTATCCCGGAAGACCATCTCCTTTGCTGTCTGTGCCATCCAGATGTGTC
10 TGAGCCTGTCCACGGGCTCCACGGAGTGCCTGCTACTGGCCATCACGGCCTATGACCGCTA
CCTGGCCATCTGCCAGCCACTCAGGTACCACTGCTCATGAGCCACCGGCTCTGCGTGCTG
CTGATGGGAGCTGCCTGGGTCTCTGCCTCCTCAAGTCGGTGACTGAGATGGTCATCTCCA
TGAGGCTGCCCTTCTGTGGCCACCACGTGGTCAGTCACTTACCTGCAAGATCCTGGCAGT
GCTGAAGCTGGCATGCGGCAACACGTCCGTGAGCGAAGACTTCTGCTGGCGGGCTCCAT
CCTGCTGCTGCCTGTACCCCTGGCATTCTGCTGCTCTACTTGCTCATCTGCGCCACCA
15 TCCTGAGGGTGCCCTCGGCCGCCAGGTGCTGCAAGCCTTCTCCACCTGCTTGGCACACCT
GGCTGTAGTGCTGCTTTTCTACGGCACCATCATCTTCACTTGAAGCCCAAGAGTAAG
GAAGCCACATCTCTGATGAGGTCTTACAGTCCTCTATGCCATGGTCACGACCATGCTGA
ACCCACCATCTACAGCCTGAGGAACAAGGAGGTGAAGGAGGCCGCCAGGAAGGTGTGGG
GCAGGAGTCGGGCCTCCAGGTGA (SEQ ID NO: 66)

20

AOLFR36 sequences:

MYLVTVLRNLLSILAVSSDHPHTPMYFFLSNLCWADIGFTLATVPKMIVDMGSHSKVISYGG
CLTQMSFLVLFACIVDMFLTVMAYDCFVAICRPLHYVIVNPHLCVFFVLVSFFLSLLDSQLHS
WIVLQFTFFKNVEISNFVCEPSQLKLASYDSVINSIFYFDNTMFGFLPISGILLSYKIVPSILRIS
25 SSDGKYKAFSACGCHLAVVCLFYGTGIGVYLTSAVAPPLRNGMVASVMYAVVTPMLNPFYIS
LRNRDIQSALWRVCNKTVESHDLFHPFSCVVEKGQPHSIPTSANPAP (SEQ ID NO: 67)

ATGTATCTGGTCACGGTGCTGAGGAACCTGCTCAGCATCCTGGCTGTCAGCTCTGACTCCC
ACCCCCACACCCCATGTACTTCTTCCCTCTCCAACCTGTGCTGGGCTGACATCGGTTTCACC
30 TTGGCCACGGTTCCCAAAATGATTGTGGACATGGGGTGCATAGCAAAGTCATCTCTTATG
GGGGCTGCCTGACACAGATGTCTTTCTTGGTACTTTTTGCATGTATAGTAGACATGTTCTT
GACTGTGATGGCTTATGACTGCTTTGTAGCCATCTGTCGCCCTCTGCACTACCCAGTCATC
GTGAATCCTCACCTCTGTGTCTTCTTCGTTTTGGTGTCCTTTTTCTTAGCCTGTTGGATTCC
CAGCTGCACAGTTGGATTGTGTTACAATTCACCTTCTTCAAGAATGTGGAAATCTCTAATT
35 TTGTCTGTGAGCCATCTCAACTTCTCAAGCTTGCCCTTATGACAGCGTCATCAATAGCATA
TTCATATATTTTGATAATACTATGTTTGGTTTTCTTCCCATTTTCAGGGATCCTTTTGTCTTAC
TATAAAATTGTCCCCTCCATTCTAAGGATTTTCATCATCAGATGGGAAGTACAAAGCCTTCT
CAGCCTGTGGCTGTACCTGGCAGTTGTTTGCTTATTTTATGGAACAGGCATTGGCGTGTA
CCTGACTTCAGCTGTGGCACCACCCCTCAGGAATGGTATGGTGGCGTCAGTGATGTCGCT
40 GTGGTCACCCCCATGCTGAACCCCTTTCATCTACAGCCTGAGAAACAGGGACATTCAAAGTG
CCCTGTGGAGGGTGTGCAACAAAACAGTCGAATCTCATGATCTGTTCCATCCTTTTTCTTG
TGTGGTTGAGAAAGGGCAACCACATTCAATCCCTACATCTGCAAATCCTGCCCTTAG
(SEQ ID NO: 68)

45 **AOLFR37 sequences:**

MEKANETSPVMGFVLLRLSAHPELEKTFVLLMYLVILLGNGVLILVTILDSRLHTPMYFFLG
NLSFLDICFTTSSVPLVLDSFLTPQETISFSACAVQMALSFAMAGTECLLSMMAFDYVAICNP
LRYSVIMSKAAYMPMAASSWAIGGAASVVHTSLAIQLPFCGDNVINHFTCEILAVLKLACADIS
INVISMEVTNVIFLGVPLFISFSYVFIITILRIPSAEGRKKVFSTCSAHLTVVIVFYGTLFMYG
50 KPKSKDSMGADKEDLSKLIPLFYGVVTPMLNPIIYSLRNKDVKA AVRRLRPKGFTQ (SEQ ID
NO: 69)

ATGGAAAAAGCCAATGAGACCTCCCCTGTGATGGGGTTCGTTCTCCTGAGGCTCTCTGCCC
ACCCAGAGCTGGAAAAGACATTCTTCGTGCTCATCCTGCTGATGTACCTCGTGATCCTGCT
55 GGGCAATGGGGTCCCTCATCCTGGTGACCATCCTTGACTCCCGCCTGCACACGCCCCTGTAC
TTCTTCTAGGGAACCTCTCCTTCTGACATCTGCTTCACTACCTCCTCAGTCCCACTGGT

CCTGGACAGCTTTTGAAGTCCCCAGGAAACCATCTCCTTCTCAGCCTGTGCTGTGCAGATG
 GCACTCTCCTTTGCCATGGCAGGAACAGAGTGCTTGCTCCTGAGCATGATGGCATTGTGATC
 GCTATGTGGCCATCTGCAACCCCTTAGGTACTCCGTGATCATGAGCAAGGCTGCCTACAT
 GCCCATGGCTGCCAGTCCCTGGGCTATTGGTGGTGCTGCTTCCGTGGTACACACATCCTTG
 5 GCAATTCAGCTGCCCTTCTGTGGAGACAATGTCATCAACCACTTCACCTGTGAGATTCTGG
 CTGTTCTAAAGTTGGCCTGTGCTGACATTTCCATCAATGTGATCAGCATGGAGGTGACGAA
 TGTGATCTTCTAGGAGTCCCGGTTCTGTTTCATCTCTTTCTCCTATGTCTTCATCATACCA
 CCATCCTGAGGATCCCCTCAGCTGAGGGGAGGAAAAAGGTCTTCTCCACCTGCTCTGCCCA
 CCTCACCGTGGTGATCGTCTTCTACGGGACCTTATTCTTCATGTATGGGAAGCCTAAGTCT
 10 AAGGACTCCATGGGAGCAGACAAAGAGGATCTTTCAGACAAACTCATCCCCCTTTTCTATG
 GGGTGGTGACCCCGATGCTCAACCCCATCATCTATAGCCTGAGGAACAAGGATGTGAAGG
 CTGCTGTGAGGAGACTGCTGAGACCAAAAGGCTTCACTCAGTGA (SEQ ID NO: 70)

AOLFR38 sequences:

15 MYLVTVLRLNLLILAVSSDSLHTPMCFFLSNLCWADIGFTSAMVPMIVDMQSHSRVISYAGC
 LTQMSFFVLFIACIEDMLLTVMAYDRFVAICHPLHYVPMNPHLGVLVLSFFLSLLDSQLHSW
 IVLQFTFFKNVVISNFVCDPSQLLNACSDSVINSIFTYLDSIMFGFLPISGILLSYANNVPSILRISS
 SDRKSKAFSTCGSHLAVVCLFYGTGIGVYLTSAVSPPRNGVVASVMYAVVTPMLNPFYISLR
 NRDIQSALWRLRSRTVESHDLLSQDLLHPFSCVGEKGQPH (SEQ ID NO: 71)
 20
 ATGTACCTGGTCACGGTGCTGAGGAACCTGCTCATCATCCTGGCTGTCAGCTCTGACTCCC
 ACCTCCACACCCCCATGTGCTTCTTCTCTCCAACCTGTGCTGGGCTGACATCGGTTTCACC
 TCGGCCATGGTTCCCAAGATGATTGTGGACATGCAGTCGCATAGCAGAGTCATCTCTTATG
 CGGGCTGCCTGACACAGATGTCTTTCTTTGTCCTTTTGCATGTATAGAAGACATGCTCCTG
 25 ACAGTGATGGCCTATGACCGATTTGTGGCCATCTGTCAACCCCTGCACTACCCAGTCATCA
 TGAATCCTCACCTTGGTGTCTTCTTAGTTTGGTGTCCTTTTCTCAGCCTGTTGGATTCC
 CAGCTGCACAGTTGGATTGTGTTACAATTCACCTTCTTCAAGAATGTGGAAATCTCCAATT
 TTGTCTGTGACCCATCTCAACTTCTCAACCTTGCCTGTTCTGACAGTGTCAATAGCATA
 TTCATATATTTAGATAGTATTATGTTTGGTTTTCTTCCCATTTCAAGGATCCTTTTGTCTTAC
 30 GCTAACAATGTCCCCTCCATTCTAAGAATTTTCATCATCAGATAGGAAGTCTAAAGCCTTCT
 CCACCTGTGGCTCTCACCTGGCAGTTGTTTGTCTTATTTTATGGAACAGGCATTGGCGTGTA
 CCTGACTTCAGCTGTGTCAACCCCCCAGGAATGGTGTGGTGGCATCAGTGATGTACGCT
 GTGGTCACCCCCATGCTGAACCCCTTTCATCTACAGCCTGAGAAATAGGGACATTCAAAGTG
 CCCTGTGGAGGCTGCGCAGCAGAACAGTCGAATCTCATGATCTGTTATCTCAAGATCTGCT
 35 CCATCCTTTTCTTGTGTGGGTGAGAAAGGTCAACCACATTAA (SEQ ID NO: 72)

AOLFR39 sequences:

MGVKNHSTVTEFLLSGLTEQAEQLPLFLFLGIYTVTVVGNLSMISIRLNRLHTPMYYFLSS
 LSFLDFCYSSVITPKMLSGFLCRDRSISYSGCMIQLFFFCVVISSECYMLAAMACDRYVAICSP
 40 LYRVIMSPRVCSLLVAAVFSVGFTDAVIHGGCILRLSFCGSNIKHIFCDIVPLIKLSCSSTYIDEL
 LIFVIGGFNMVATSLTHISYAFILTSILRIHKKGRCKAFSTCSSHLTAVLMFYGSLMSMYLKPAS
 SSSLTQEKVSSVFYTTVILMLNPLIYSLRNNEVRNALMKLLRRKISLSPG (SEQ ID NO: 73)
 ATGGGTGTAAAAAACCATTCACAGTGACTGAGTTTCTTCTTTCAGGATTAACTGAACAAG
 45 CAGAGCTTCAGCTGCCCCTCTTCTGCCTCTTCTTAGGAATTTACACAGTTACTGTGGTGGG
 AAACCTCAGCATGATCTCAATTATTAGGCTGAATCGTCAACTTCATACCCCATGTACTAT
 TTCTGAGTAGTTTGTCTTTTTTAGATTCTGCTATTCTTCTGTCAATTACCCCTAAAATGCT
 ATCAGGGTTTTTATGCAGAGATAGATCCATCTCCTATTCTGGATGCATGATTAGCTGTTTT
 TTTTCTGTGTTTGTGTTATTTCTGAATGCTACATGCTGGCAGCCATGGCCTGCGATCGCTAC
 50 GTGGCCATCTGCAGCCCACTGCTCTACAGGGTCATCATGTCCCTAGGGTCTGTTCTCTGC
 TGGTGGCTGCTGTCTTCTCAGTAGGTTTCACTGATGCTGTGATCCATGGAGGTTGTATACT
 CAGGTTGTCTTTCTGTGGATCAAACATCATTAACATTATTTCTGTGACATTGTCCCTCTTA
 TTAAACTCTCCTGCTCCAGCACTTATATTGATGAGCTTTTGATTTTGTCAATTGGTGATT
 AACATGGTGGCCACAAGCCTAACAACTATTATTTTCATATGCTTTTATCCTCACCAGCATCCT
 55 GCGCATCCACTCTAAAAAGGGCAGGTGCAAGCGTTTAGCACCTGTAGCTCCACCTGACA
 GCTGTTCTTATGTTTTATGGGTCTCTGATGTCCATGTATCTCAACCTGCTTCTAGCAGTTC

ACTCACCCAGGAGAAAAGTATCCTCAGTATTTTATACCACTGTGATTCTCATGTTGAATCCC
TTGATATATAGTCTGAGGAACAATGAAGTAAGAAATGCTCTGATGAAACTTTTAAGAAGA
AAAATATCTTTATCTCCAGGATAA (SEQ ID NO: 74)

5 **AOLFR40 sequences:**

MSNATLLTAFILTGLPHAPGLDAPLFGIFLVVYVLTVLGNLILLVIRVDSHLHTPMYYFLTNLS
FIDMWFSTVTVPKMLMTLVSPSGRTISFHSCVAQLYFFHFLGSTECFLYTVMSYDRYLAISYPL
RYTNMMTGRSCALLATGTWLSGSLHSAVQTLTFHLPYCGPNQIQHYFCDAPPILKLACADTS
ANEMVIFVNI GLVASGCFVLIVLSYVSVIVCSILRRTSEGRHRAFQTCASHCIVVLCFFGPGFLFIYL
10 RPSGRDALHGVA VFYTTLTPLFNPVVYTLRNKEVKALLKLKNGSVFAQGE (SEQ ID NO:
75)

ATGTCCAACGCCACCCTACTGACAGCGTTCATCCTCACGGGCCTTCCCCATGCCCCAGGGC
TGGACGCCCCCTCTTTGGAATCTTCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
15 CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCCATGTACTACTTCTCTCA
CCAACCTGTCCTTCATTGACATGTGGTTCTCCACTGTCACGGTGCCCAAAATGCTGATGAC
CTTGGTGTCCCCAAGCGGCAGGACTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTT
TCCACTTCTGGGGAGCACCGAGTGTTCCTCTACACAGTCATGTCCTATGATCGCTACCT
GGCCATCAGTTACCCGCTCAGGTACACCAACATGATGACTGGGCGCTCGTGTGCCCTCCTG
20 GCCACCGGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCC
ATTTGCCCTACTGTGGACCCAACAGATCCAGCACTACTTCTGTGACGCACCGCCCATCCT
GAAACTGGCCTGTGCAGACACCTCAGCCAACGAGATGGTCATCTTTGTGAATATTGGGCTA
GTGGCCTCGGGCTGCTTTGTCTGATAGTGCTGTCTATGTGTCCATCGTCTGTTCCATCCT
GCGGATCCGCACCTCAGAGGGGAGGCACAGAGCCTTTCAGACCTGTGCCTCCCACTGTATC
25 GTGGTCTTTGCTTCTTTGGCCCTGGTCTTTTCACTTACCTGAGGCCAGGCTCCAGGGACGC
CTTGATGGGGTTGTGGCCGTTTCTACACCACGCTGACTCCTCTTTCAACCCTGTTGTGT
ACACCCTGAGAAACAAGGAGGTAAAGAAAGCTCTGTTGAAGCTGAAAAATGGGTCACTAT
TTGCTCAGGGTGAATAG (SEQ ID NO: 76)

30 **AOLFR41 sequences:**

MNPENWTQVTSFVLLGFPSSHLIQFLVFLGLMVTYIVTATGKLLIIVLSWIDQRLHIQMYFFLRN
FSFLELLLVTVVVPKMLVVILTGDHTISFVSCIQSYLYFFLGTTDFLLAVMSLDRLAICRPLR
YETLMNGHVCSQLVLASWLAGFLWVLCPTVLMASLPFCGPNIDHFFRDSWPLRLSCGDTH
LLKLVAFMLSTLVLLGSLALTSVSYACILATVLRAPTAABERRKAFSTCASHLTVVVIYSSIFY
35 IRMSEAQSKLLNKGASVLSCTIPLLNPFIFTLRNDKVQQALREALGWPRLTAVMKLRVTSQRK
(SEQ ID NO: 77)

ATGAACCCTGAAAACTGGACTCAGGTAACAAGCTTTGTCCTTCTGGGTTTCCCCAGTAGCC
ACCTCATACAGTTCTGGTGTTCTGGGGTTAATGGTGACCTACATTGTAACAGCCACAGG
40 CAAGCTGCTAATTATTGTGCTCAGCTGGATAGACCAACGCCTGCACATACAGATGTACTTC
TTCCTGCGGAATTTCTCCTTCTGGAGCTGTTGCTGGTAACTGTTGTGGTTCCCAAGATGCT
TGTCGTCATCCTCACGGGGGATCACACCATCTCATTGTGCTGCTCATCCAGTCCCTACC
TCTACTTCTTTCTAGGCACCACTGACTTCTTCTCTGGCCGTCATGTCTCTGGATCGTTAC
CTGGCAATCTGCCGACCACTCCGCTATGAGACCCTGATGAATGGCCATGTCTGTTCCCAAC
45 TAGTGCTGGCCTCCTGGCTAGCTGGATTCTCTGGGTCCTTTGCCCCACTGTCCTCATGGCC
AGCCTGCCCTTTCTGTGGCCCCAATGGTATTGACCACTTCTTTCTGTGACAGTTGGCCCTTGCT
CAGGCTTTCTGTGGGGACACCCACCTGCTGAAACTGGTGGCTTTTCACTGCTCTCTACGTTG
GTGTTACTGGGCTCACTGGCTCTGACCTCAGTTTCTATGCCTGCATTCTTGCCACTGTTCT
CAGGGCCCCCTACAGCTGCTGAGCGAAGGAAAGCGTTTTCCACTTGCGCCTCGCATCTTACA
50 GTGGTGGTCATCATCTATGGCAGTTCCATCTTTCTCTACATTGCTATGTCAGAGGCTCAGTC
CAAACCTGCTCAACAAAGGTGCCCTCCGTCCTGAGCTGCATCATCACACCCCTCTTGAACCCA
TTCATCTTCACTCTCCGCAATGACAAGGTGCAGCAAGCACTGAGAGAAGCCTTGGGGTGGC
CCAGGCTCACTGCTGTGATGAACTGAGGGTCACAAGTCAAAGGAAATGA (SEQ ID NO:
78)

55

AOLFR42 sequences:

MNPANHSQVAGFVLLGLSQVWELRFVFFTVFSAVYFMTVVGNLLIVVIVTSDPHLHTTMYFLL
 GNLSFLDFCYSSITAPRMLVDLLSGNPTISFGGCLTQLFFHFHFIGGIKIFLLTVMAYDRYIAISQPL
 HYTLIMNQTVCALLMAASWVGGFHSIVQIALTIQLPFCGPDKLDNFYCDVPQLKLACTDITFV
 5 LELLMVSNNGLVTLMCFLVLLGSYTAALLVMLRSHSREGRSKALSTCASHIAVVTLIFVPCIYVY
 TRPFRTPMDKAVSVLYTTVTPMLNPAIYTLRNKEVIMAMKKLWRRKKDPIGPLEHRPLH
 (SEQ ID NO: 79)

ATGAATCCAGCAAATCATTCCCAGGTGGCAGGATTTGTTCTACTGGGGCTCTCTCAGGTTT
 10 GGGAGCTTCGGTTTGTITTTCTTCACTGTTTTCTCTGCTGTGTAATTTATGACTGTAGTGGGA
 AACCTTCTTATTGTGGTCATAGTGACCTCCGACCCACACCTGCACACAACCATGTATTTTCT
 CTTGGGCAATCTTTCTTCTGGAATTTTGTACTCTTCCATCACAGCACCTAGGATGCTGG
 TTGACTTGCTCTCAGGCAACCCTACCATTTCCTTTGGTGGATGCCTGACTCAACTCTTCTTC
 TTCCACTTCATTGGAGGCATCAAGATCTTCTGCTGACTGTCATGGCGTATGACCGCTACA
 15 TTGCCATTTCCCAGCCCTGCACTACACGCTCATTATGAATCAGACTGTCTGTGCACTCCTT
 ATGGCAGCCTCCTGGGTGGGGGGCTTCATCCACTCCATAGTACAGATTGCATTGACTATCC
 AGCTGCCATTCTGTGGGCCTGACAAGCTGGACAACCTTTTATTGTGATGTGCCTCAGCTGAT
 CAAATTGGCCTGCACAGATACCTTTGTCTTAGAGCTTTTAATGGTGTCTAACAATGGCCTG
 GTGACCTGTATGTGTTTTCTGGTGCTTCTGGGATCGTACACAGCACTGCTAGTCTAGTCTC
 20 GAAGCCACTGACGGGAGGGCCGACGCAAGGCCCTGTCTACCTGTGCCTCTCACATTGCTGT
 GGTGACCTTAATCTTTGTGCCTTGCTCTACGTCTATACAAGGCCCTTTTCGGACATTCCCCA
 TGGACAAGGCCGTCTCTGTGCTATACACAATTGTCAACCCCATGCTGAATCCTGCCATCTA
 TACCCTGAGAAACAAGGAAGTGATCATGGCCATGAAGAAGCTGTGGAGGAGGAAAAAGG
 ACCCTATTGGTCCCCTGGAGCACAGACCTTACATTAG (SEQ ID NO: 80)

25

AOLFR43 sequences:

MQKPQLLVPIIATSNGLVHAAYFLLVGIPGLPTIHFWLAFPLCFMYALATLGNLTIVLIIRVE
 RRLHEPMYLFLAMLSTIDLVLSSITMPKMASLFLMGIQIEFNICLAQMFLIHALSAVESAVLLA
 MAFDRFVAICHPLRHASVLTGCTVAKIGLSALTRGFVFFPLPFILKWLSYQTHTVTHSFCLHQ
 30 DIMKLSCTDTRVNVVYGLFILLSVMGVDSLFIGFSYILILWAVLELSSRAALKAFNTCISHLCAV
 LVFYVPLIGLSVVHRLGGPTSLHVVMANTYLLPPVNVNPLVYGAKTKEICSRVLCMFSQGGK
 (SEQ ID NO: 81)

ATGCAGAAGCCCCAGCTCTTGGTCCCTATCATAGCCACTTCAAATGGAAATCTGGTCCACG
 35 CAGCATACTTCCTTTTGGTGGGTATCCCTGGCCTGGGGCCTACCATACACTTTTGGCTGGCT
 TTCCCACTGTGTTTTATGTATGCCTTGGCCACCCTGGGTAACCTGACCATTGTCCTCATCAT
 TCGTGTGGAGAGGGCGACTGCATGAGCCCATGTACCTCTTCTGGCCATGCTTTCCACTATT
 GACCTAGTCCTCTCCTCTATCACCATGCCCAAGATGGCCAGTCTTTTCTGATGGGCATCCA
 GGAGATCGAGTTCAACATTTGCCTGGCCAGATGTTCTTATCCATGCTCTGTGAGCCGTG
 40 GAGTCAGCTGTCTGTGCTGACAGGGGTACTGTGGCCAAGATTGGACTATCTGCCCTGACCAG
 GCCATGCTTCTGTGCTGACAGGGGTACTGTGGCCAAGATTGGACTATCTGCCCTGACCAG
 GGGGTTTGTATTCTTCTTCCCACTGCCCTTATCCTCAAGTGGTTGTCTACTGCCAAACAC
 ATACTGTACACACTCCTTCTGTCTGCACCAAGATATTATGAAGCTGTCTGTACTGACAC
 CAGGGTCAATGTGGTTTATGGACTCTTCATCATCCTCTCAGTCATGGGTGTGGACTCTCTCT
 45 TCATTGGCTTCTCATATATCCTCATCCTGTGGGCTGTTTTGGAGCTGTCTCTCGGAGGGCA
 GCACTCAAGGCTTTCAACACCTGCATCTCCACCTCTGTGCTGTTCTGGTCTTCTATGTACC
 CCTCATTTGGGCTCTCGGTGGTGCATAGGCTGGGTGGTCCCACCTCCCTCCTCCATGTGGTT
 ATGGCTAATACCTACTTGCTGCTACCACCTGTAGTCAACCCCTTGTCTATGGAGCCAAGA
 CCAAAGAGATCTGTTCAAGGGTCTCTGTATGTTCTCACAAGGTGGCAAGTGA (SEQ ID
 50 NO: 82)

AOLFR44 sequences:

MSSCNFTHATFVLIGIPGLEKAHFVWGFPLLSMYVVMFGNCIVVFIVRTERSLHAPMYLFLC
 MLAAIDLALSTSTMPKILALFWFDSREISFEACLTQMFFIHALSAIESTILLAMAFDRYVAICHPL
 55 RHA AVLNNVTVAQIGIVAVVRGSLFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYADTLP
 NVVYGLTAILLVMGVDMFISLSYFLIRTVLQPLPSKSERAKAFGTCVSHIGVVLAIFYVPLIGLS

VVHRFGNSLHPVIRVVMGDIYLLLPVINPIYGA TKQIRTRVLAMFKISCDKDLQAVGGK
(SEQ ID NO: 83)

5 ATGAGTTCCTGCAACTTCACACATGCCACCTTTGTGCTTATTGGTATCCCAGGATTAGAGA
AAGCCCATTCTGGGTGGCTTCCCCCTCCTTTCCATGTATGTAGTGGCAATGTTTGAAAC
TGCATCGTGGTCTTCATCGTAAGGACGGAACGCAGCCTGCACGCTCCGATGTACCTCTTTC
TCTGCATGCTTGACGCCATTGACCTGGCCTTATCCACATCCACCATGCCTAAGATCCTTGCC
CTTTTCTGGTTTGATTCCCGAGAGATTAGCTTTGAGGCCTGTCTTACCCAGATGTTCTTTAT
TCATGCCCTCTCAGCCATTGAATCCACCATCCTGCTGGCCATGGCCTTTGACCGTTATGTGG
10 CCATCTGCCACCCACTGCGCCATGCTGCAGTGCTCAACAATACAGTAACAGCCCAGATTGG
CATCGTGGCTGTGGTCCGCGGATCCCTCTTTTTTTTCCCACTGCCTCTGCTGATCAAGCGGC
TGGCCTTCTGCCACTCCAATGTCTCTCGCACTCCTATTGTGTCCACCAGGATGTAATGAA
GTTGGCCTATGCAGACACTTTGCCCAATGTGGTATATGGTCTTACTGCCATTCTGCTGGTC
ATGGGCGTGGACGTAATGTTTCATCTCCTTGTCTTATTTCTGATAATACGAACGGTTCTGC
15 AACTGCCTTCCAAGTCAGAGCGGGCCAAGGCCTTTGGAACCTGTGTGTACACATTGGTG
GGTACTCGCCTTCTATGTGCCACTTATTGGCCTCTCAGTGGTACACCGCTTTGGAACAGC
CTTCATCCCATTTGTGCGTGTGTGCATGGGTGACATCTACCTGCTGCTGCCTCCTGTCACTAA
TCCCATCATCTATGGTGCCAAAACCAAACAGATCAGAACACGGGTGCTGGCTATGTTCAAG
ATCAGCTGTGACAAGGACTTGCAGGCTGTGGGAGGCAAGTGA (SEQ ID NO: 84)

20

AOLFR45 sequences:

MLPSNITSTHPAVLLVGIPGLEHLHAWISIPFCFAYTLALLGNCTLLFIQADAALHEPMYLFLA
MLATIDLVLSTTLPKMLAIFWFRDQENFFACLVMFFLHSFSIMESAVLLAMAFDRYVAICKP
LHYTTVLTGSLITKIGMAAVARAVTLMPLPFLRRFHYCRGPVIAHCYCEHMAVVRLACGDT
25 SFNNIYGIAVAMFSVVDLLFVILSYVFILQAVLQLASQEARYKAFGTCVSHIGAILSTYTPVVIS
SVMHRVARHAAPRVHILLAIFYLLFPPMVNPIYGVKTKQIREYVLSLFQRKNM (SEQ ID NO:
85)

30 TGGAAACAAGAGGTAATCTTTGCAGGTGGGATAGCACAGGTTGAACTCTAATCATATATA
CTGTAGAAGGTATATATAGAAGGTGAAGAAGCCCTGTAAAAATTGACAAGGAGATTTCCA
GGAGCCATGCTTCCCTCTAATATCACCTCAACACATCCAGCTGTCTTTTTGTTGGTAGGAAT
TCCTGGTTTGGAACACCTGCATGCCTGGATCTCCATCCCCTTCTGCTTTGCTTATACTCTGG
CCCTGCTAGGCAACTGTACCCCTTCTCTTCATATCCAGGCTGATGCAGCCCTCCATGAACCC
ATGTACCTCTTTCTGGCCATGTTGGCAACCATTGACTTGGTTCTTTCTTCTACAACGCTGCC
35 CAAAATGCTTGCCATATTCTGGTTCAGGGATCAGGAGATCAACTTCTTTGCCTGTCTGGTC
CAGATGTTCTTCTTCACTCCTTCTCCATCATGGAGTCAGCAGTGCTGCTGGCCATGGCCTT
TGACCGCTATGTGGCCATCTGCAAGCCATTGCCTACTACACGACGGTCCCTGACTGGGTCCCTC
ATCACCAAGATTGGCATGGCTGCTGTGGCCCCGGCTGTGACACTAATGACTCCACTCCCCT
TCCTGCTCAGACGCTTCCACTACTGCCGAGGCCAGTGATTGCCATTGCTACTGTGAACA
40 CATGGCTGTGGTAAGGCTGGCGTGTGGGACACTAGCTTCAACAATATCTATGGCATTGCT
GTGGCCATGTTTAGTGTGGTGTGGACCTGCTCTTTGTTATCCTGTCTTATGTCTTCATCCT
TCAGGCAGTTCTCCAGCTTGCTCTCAGGAGGCCGCTACAAAGCATTTGGGACATGTGTG
TCTCACATAGGTGCCATCCTGTCCACCTACACTCCAGTAGTCATCTCTTCAGTCATGCACCG
TGTAGCCCGCCATGCTGCCCCCTCGTGCCACATACTCCTTGCTATTTTCTATCTCCTTTTCC
45 CACCCATGGTCAATCCTATCATATATGGAGTCAAGACCAAGCAGATTCTGTGAGTATGTGCT
CAGTCTATTCCAGAGAAAGAACATGTAGATGGATAGTTCTCTTTTTTATCCCACCTTGCCA
AGTAATGAGAATGCTGGATTGGGGTTGAGGGGAAAAATCTAAATAGGAAAAATTGCAGAGT
ATCTTTGACAATTCTCTAGTATGATAAGGAAAATGAGGTTTCATTCTCACAGATCTACGA
GTCAGGTCAAACCAGGAGTGCACCTATAGTCTGGTCTGATAGTAGAGGTTTGACCTTCCCA
50 TTGTCATAGACTCATCATATGGCTAAGGAAGACAAACCTCTCAAAGTGGTATTGTAATCTG
GGTGAAAGACAGTAGGACCTTTATTGGCTGAGATTGGCCCAAACAGCTGAGTC (SEQ ID
NO: 86)

AOLFR46 sequences:

55 MNIKHCGWHMIHTWLNIREDDSDFKNFQIQGLSGNPHSTTSRMYFLCFCTSLLGFKVHWV
SRLIXKLYMASPNNDSTAPVSEFLICFPNFQSWQHWLSLPLSLFLAMGANTLLITIQLEAS

LHQPLYLLSLLSLLDIVLCLTVIPKVLAIWFDFLRISIFPACFLQMFIMNSFLTMESECTFMVMA
YDRYVAICHPLRYPSTTDQFVARAVVFIARNAFVSLPVPMLSARLRYCAGNIKNKICSNLSVS
KLSCDDITFNQLYQFVAGWTLGSDLILIVISYFSLKVVLRKAEGAVAKALSTCGSHFILIFFS
TVLLVLVITNLARKRIPPDVPILLNLHHLIPPALNPVYGVRTKEIKQGIQNLLKRL (SEQ ID NO:
5 87)

ATGAATATAAAACATTGTGGCTGGCATATGATACATACTTGGTTAAATATAAGGGAGGAT
GATGACAGTGATTTTAAAACTTTATTGGACAGATACAGGGCCTCAGTGGAACCCACACT
CTACTACGTCTAGAATGTACTTTTATGTTTCTGTACTTCTCTACTAGGTTTAAAGGTACAC
10 TGGGTCTCCAGATTGATCANGAACTTTACATGGCATCTCCCAACAATGACTCCACTGCCC
CAGTCTCTGAATTCCTCCTCATCTGCTTCCCCAACTTCCAGAGCTGGCAGCACTGGTTGTCT
CTGCCCCCTCAGCCTTCTCTTCTCCTGGCCATGGGAGCTAACACCACCTCCTGATCACCAT
CCAGCTGGAGGCCTCTCTGCACCAGCCCCGTGACTACCTGCTCAGCCTCCTCTCCCTGCTGG
ACATCGTGCTCTGCCTCACCGTCATCCCCAAGGTCCTGGCCATCTTCTGGTTTGACCTCAGG
15 TCGATCAGCTTCCCAGCCTGCTTCCCTCCAGATGTTTCATCATGAACAGTTTTTGGACCATGGA
GTCCTGCACGTTTCATGGTCATGGCCTATGACCGTTATGTGGCCATCTGCCATCCATTGAGA
TACCCGTCTATCATCACTGACCAGTTTGTGGCTAGGGCCGTGGTCTTTGTTATAGCCCGGA
ATGCCCTTGTCTTCTCTTCTGTTCCCATGCTTCTGCGAGGCTCAGATACTGTGCAGGAAAC
ATAATCAAGAACTGCATCTGCAGTAACCTGTCTGTGTCCAACTCTCTTGTGATGACATCA
20 CTTTCAATCAGCTCTACCAGTTTGTGGCAGGCTGGACTCTGTTGGGCTCTGATCTTATCCTT
ATTGTTATCTCCTATTCTTTTATATTGAAAGTTGTGCTTAGGATCAAGGCCGAGGGTGTGT
GGCCAAGGCCTTGAGCACGTGTGGTTCCCACTTCATCCTCATCCTCTTCTTCAGCACAGTCC
TGCTGGTTCTGGTCATCACTAACCTGGCCAGGAAGAGAATTCCTCCAGATGTCCCCATCCT
GCTCAACATCCTGCACCACCTCATCCCCCAGCTCTGAACCCCATGTGTTATGGTGTGAGA
25 ACCAAGGAGATCAAGCAGGGAATCCAAAACCTGCTGAAGAGGTTGTAA (SEQ ID NO: 88)

AOLFR47 sequences:

MSASNITLTHPTAFLLVGIPGLEHLHIWISIPFCLAYTLALLGNCTLLLIQADAALHEPMYLFLA
MLAAIDLVLSSSALPKMLAIFWFRDREINFFACLAQMFFLHSFSIMESAVLLAMAFDRYVAICK
30 PLHYTKVLTGSLITKIGMAAVARAVTLMTPPLPFLRCFHYCRGPVIAHCYCEHMAVVRACGD
TSFNNIYGIAMFIVVLDLLVLVLSYIFILQAVLLASQEARYKAFGTCVSHIGAILAFYTTVVIS
SVMHRVARHAAPHVHILLANFYLLFPPMVNPITYGVKTKQIRESILGVFPRKDM (SEQ ID NO:
89)

ATGTCAGCCTCCAATATCACCTTAACACATCCAACCTGCCCTTCTTGTGGTGGGGATTCCAG
GCCTGGAACACCTGCACATCTGGATCTCCATCCCTTTCTGCTTAGCATATACACTGGCCCTG
CTTGGAACCTGCACTCTCCTTCTCATCATCCAGGCTGATGCAGCCCTCCATGAACCCATGT
ACCTCTTTCTGGCCATGTTGGCAGCCATCGACCTGGTCCTTTCTCCTCAGCACTGCCAAA
ATGCTTGCCATATTCTGGTTCAGGGATCGGGAGATAAACTTCTTTGCCTGTCTGGCCAA
40 TGTCTTCTCCTTCACTCCTTCTCCATCATGAGTCAGCAGTGCTGCTGGCCATGGCCTTTGAC
CGCTATGTGGCTATCTGCAAGCCACTGCACTACACCAAGGTCCTGACTGGGTCCCTCATCA
CCAAGATTGGCATGGCTGCTGTGGCCCGGGCTGTGACACTAATGACTCCACTCCCCTTCT
GCTGAGATGTTTCCACTACTGCCGAGGCCAGTGATCGCTCACTGCTACTGTGAACACATG
GCTGTGGTGAGGCTGGCGTGTGGGGACACTAGCTTCAACAATATCTATGGCATCGCTGTGG
45 CCATGTTTATTGTGGTGTGGACCTGCTCCTTGTATCCTGTCTTATATCTTTATTCTTCAG
GCAGTTCTACTGCTTGCCTCTCAGGAGGCCCGCTACAAGGCATTTGGGACATGTGTCTCTC
ATATAGGTGCCATCTTAGCCTTCTACACAACTGTGGTTCATCTCTTCAGTCATGCACCGTGA
GCCCCCATGCTGCCCCCTCATGTCCACATCCTCCTTGCCAATTTCTATCTGCTCTTCCACC
CATGGTCAATCCCATAATCTATGGTGTCAAGACCAAGCAAATCCGTGAGAGCATCTTGGGA
50 GTATTCCCAAGAAAGGATATGTAG (SEQ ID NO: 90)

AOLFR48 sequences:

MMVDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFL
CMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFIAHSLSGMESTVLLAMAFDRYVAICH
55 PLRHATVLTLPRTVKIGVAAVVRGAALMAPLPVFIKQLPFCRSNLSHSYCLHQDVMKLCADDI
RVNVVYGLIVIIISAIGLDSLLISFSYLLILKTVLGLTREAQAKAFGTCVSHVCAVFIFYVPFIGLSM

VHRFSKRRDSPLPVILANIYLLVPPVLNPVYGVKTKRILRLFHVATHASEP (SEQ ID NO: 91)

5 ATGATGGTGGATCCCAATGGCAATGAATCCAGTGCTACATACTTCATCCTAATAGGCCTCC
CTGGTTTAGAAGAGGCTCAGTTCTGGTTGGCCTTCCCATTGTGCTCCCTCTACCTTATTGCT
GTGCTAGGTAACCTTGACAATCATCTACATTGTGCGGACTGAGCACAGCCTGCATGAGCCCA
TGTATATATTTCTTTGCATGCTTTCAGGCATTGACATCCTCATCTCCACCTCATCCATGCCC
AAAATGCTGGCCATCTTCTGGTTCAATTCCACTACCATCCAGTTTGATGCTTGTCTGCTACA
10 GATGTTTGCCATCCACTCCTTATCTGGCATGGAATCCACAGTGCTGCTGGCCATGGCCTTTT
GACCGCTATGTGGCCATCTGTCAACCACTGCGCCATGCCACAGTACTTACGTTGCCTCGTG
TCACCAAAATGGTGTGGCTGCTGTGGTGCAGGGGGCTGCACTGATGGCACCCCTTCTCTGT
CTTCATCAAGCAGCTGCCCTTCTGCCGCTCCAATATCCTTTCCCATTCCTACTGCCTACACC
AAGATGTCATGAAGCTGGCCTGTGATGATATCCGGGTCAATGTCGTCTATGGCCTTATCGT
CATCATCTCCGCCATTGGCCTGGACTCACTTCTCATCTCCTTCTCATATCTGCTTATTCTTA
15 AGACTGTGTTGGGCTTGACACGTGAAGCCAGGCCAAGGCATTTGGCATTGCGTCTCTCA
TGTGTGTGCTGTGTTTCATATTCTATGTACCTTTCATTGGATTGTCCATGGTGCATCGCTTTA
GCAAGCGGCGTGACTCTCCGCTGCCCGTCATCTTGCCAATATCTATCTGCTGGTTCCTCCT
GTGCTCAACCCAATTGTCTATGGAGTGAAGACAAAGGAGATTCGACAGCGCATCCTTCGA
CTTTTCCATGTGGCCACACACGCTTCAGAGCCCTAG (SEQ ID NO: 92)

20

AOLFR49 sequences:

MLTFHNVCSPVSSFWL TGIPGLES LHVWLSIPFGSMYLVAVVGNVTILAVVKIERSLHQPMYFF
LCMLAAIDLVLSTSTIPKLLGIFWFGACDIGLDACLGQMFLIHC FATVESGIFLAMA FDRYVAIC
NPLRHS MVLT YTVVGR LGLVSLLRGVLYIGPLPLMIRLRLPLYKTHVISHSYCEHMAVVALTC
25 GDSRVNNVYGLSIGFLVLILDSVAIAASYVMIFRAVMGLATPEARLKT LGTCASHLCAILFYVP
IAVSSLIHRFGQCVPPPVTLLANFYLLIPPILNPVYAVRTKQIRESLLQIPRIEMKIR (SEQ ID
NO: 93)

30 ATGCTCACTTTTTCATAATGTCTGCTCAGTACCCAGCTCCTTCTGGCTCACTGGCATCCCAGG
GCTGGAGTCCCTACACGTCTGGCTCTCCATCCCCTTTGGCTCCATGTACCTGGTGGCTGTG
GTGGGGAATGTGACCATCCTGGCTGTGGTAAAGATAGAACGCAGCCTGCACCAGCCCATG
TACTTTTCTTGTGCATGTTGGCTGCCATTGACCTGGTTCTGTCTACTTCCACTATACCCAA
ACTTCTGGGAATCTTCTGGTTCGGTGCTTGTGACATTGGCCTGGACGCCTGCTTGGGCCAA
ATGTTCTTATCCACTGCTTTGCCACTGTTGAGTCAGGCATCTTCCTTGCCATGGCCTTTGA
35 TCGCTACGTGGCCATCTGCAACCCACTACGTCATAGCATGGTGCTCACTTATACAGTGGTG
GGTCGTTTGGGGCTGTTTCTCTCCTCCGGGTGTTCTCTACATTGGACCTCTGCCTCTGAT
GATCCGCTGCGGCTGCCCTTTATAAAACCCATGTTATCTCCACTCCTACTGTGAGCAC
ATGGCTGTAGTTGCCTTGACATGTGGCGACAGCAGGGTCAATAATGTCTATGGGCTGAGC
ATCGGCTTTCTGGTGTGATCCTGGACTCAGTGGCTATTGCTGCATCCTATGTGATGATTTT
40 CAGGGCCGTGATGGGGTTAGCCACTCCTGAGGCTAGGCTTAAACCCCTGGGGACATGCGC
TTCTCACCTCTGTGCCATCCTGATCTTTTATGTTCCCATTTGCTGTTTCTTCCCTGATTCACCG
ATTTGGTCAGTGTGTGCTCCTCCAGTCCACACTCTGCTGGCCAACCTTCTATCTCCTCATTC
CTCCAATCCTCAATCCCATTTGTCTATGCTGTTGCGACCAAGCAGATCCGAGAGAGCCTTCT
CCAAATACCAAGGATAGAAATGAAGATTAGATGA (SEQ ID NO: 94)

45

AOLFR50 sequences:

MNLD SFFSFLKSLIMALSNSSWRLPQPSFVLV GIPGLEESQHWIALPLGILYLLALVGNVTILFII
WMDPSLHQSMYFLSMLAIDL VVASSTAPKALAVLLVRAQEIGYTVCLIQMFFTHAFSSMES
GVLVAMALDRYVAICHPLHSTILHPGVIGHIGMVVLVRGLLLLPFLILLRKLIFCQATIIGHAY
50 CEHMAVVKLACSETTVNRAYGLTVALLVVG L DVL AIGVSYAHILQAVLKVPGNEARLKAFST
CGSHVCVILVFYIPGMFSFLTHRFGHHVPHHVHLLAILYRLVPPALNPLVYRVKTQKIQ
(SEQ ID NO: 95)

55 ATGAATTTGGATTCTTTTTTCTCTTTCCTCCTCAAGTCATTGATAATGGCACTTAGCAATTC
CAGCTGGAGGCTACCCAGCCTTCTTTTTCTGGTAGGAATCCGGGTTTAGAGGAAAGC
CAGCACTGGATCGCACTGCCCTGGGCATCCTTTACCTCCTTGCTCTAGTGGGCAATGTTA

CCATTCTCTTCATCATCTGGATGGACCCATCCTTGACCAATCTATGTACCTCTTCTGTCC
 ATGCTAGCTGCCATCGACCTGGTTGTGGCCTCCTCCACTGCACCCAAAGCCCTTGCACTGC
 TCCTGGTTTCGTGCCCAAGAGATTGGTTACACTGTCTGCCTGATCCAGATGTTCTTACCCAT
 GCATTCTCCTCCATGGAGTCAGGGGTACTTGTGGCCATGGCTCTGGATCGCTATGTAGCCA
 5 TTTGTACCCCTTGACCAATCCACAATCCTGCATCCAGGGGTCATAGGGCACATCGGAAT
 GGTGGTGTGGTGCAGGGGATTACTACTCCTCATCCCTTCTCATTCTGTTGCGAAACTT
 ATCTTCTGCCAAGCCACCATCATAGGCCATGCCTATTGTGAACATATGGCTGTTGTGAAAC
 TTGCCTGCTCAGAAACCACAGTCAATCGAGCTTATGGGCTGACTGTGGCCTTGCTTGTGGT
 TGGGCTGGATGTCTGGCCATTGGTGTTCCTATGCCACATTCTCCAGGCAGTGTGAAG
 10 GTACCAGGAAATGAGGCCCGACTTAAGGCCTTTAGCACATGTGGCTCTCATGTTTGTGTCA
 TCCTGGTCTTCTATATCCCGGGAATGTTCTCCTTCTCACTACCGCTTTGGTCATCATGTA
 CCCCATCACGTCCATGTTCTTCTGGCCATACTGTATCGCCTTGTGCCACCTGCACCTCAATCC
 TCTTGTCTATAGGGTGAAGACCCAGAAGATCCACCAAGTGA (SEQ ID NO: 96)

15 **AOLFR51 sequences:**

MCQQLRDCILLIHLCLNRKKVSLVMLGPAYNHTMETPASFLLVGIPGLQSSHLWLAIISLAM
 YIALLGNTIIVTAIWMDSTRHEPMYCFLCVLAAVDIVMASSVVPKMVSIFCSGDSSISFSACFTQ
 MFFVHLATAVETGLLLTMAFDTRYVAICKPLHYKRILTPQVMLGMSMAITIRAIATPLSWMVS
 HLPFCGSNVVVHSHYCEHIALARLACADVPSSLYSLIGSSLMVGSVDVAFIAASYILILKAVFLSS
 20 KTAQLKALSTCGSHVGMALYYLPGMASIYAAWLQDVPVPLHTQVLLADLYVIIPATLNPITY
 GMRTKQLRERIWSYLMHVLFDHNSLGS (SEQ ID NO: 97)

ATGTGTCAACAAATCTTACGGGATTGCATTCTTCTCATACATCATTTGTGCATTAACAGGA
 AAAAAGTCTCACTTGTGATGCTGGGTCCAGCTTATAACCACACAATGGAAACCCCTGCCTC
 25 CTTCCTCCTTGTGGGTATCCCAGGACTGCAATCTTCACATCTTGGCTGGCTATCTCACTGA
 GTGCCATGTACATCATAGCCCTGTTAGGAAACACCATCATCGTGACTGCAATCTGGATGGA
 TTCCACTCGGCATGAGCCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTA
 TGGCCTCCTCGGTGGTACCCAAGATGGTGAGCATCTTCTGCTCAGGAGACAGCTCAATCAG
 CTTTAGTGCTTGTTCCTCACTCAGATGTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGG
 30 CTGCTGCTGACCATGGCTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGA
 GAATTCTCACGCCTCAAGTGATGCTGGGAATGAGTATGGCCATCACCATCAGAGCTATCAT
 AGCCATAACTCCACTGAGTTGGATGGTGAGTCATCTACCTTTCTGTGGCTCCAATGTGGTT
 GTCCACTCCTACTGTGAGCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCCA
 GCAGTCTCTACAGTCTGATTGGTTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCT
 35 GCCTCCTATATCTTAATTCTCAAGGCATATTGTTGCTCTCCTCAAAGACTGCTCAGTTGAA
 AGCATTAAGCACATGTGGCTCCCATGTGGGGGTTATGGCTTTGTACTATCTACCTGGGATG
 GCATCCATCTATGCGGCCTGGTTGGGGCAGGATGTAGTGCCCTTGACACCCCAAGTCTGCTC
 TAGCTGACCTGTACGTGATCATCCCAGCCACCTTAAATCCCATCATCTATGGCATGAGGAC
 CAAACAACCTGCGGGAGAGAATATGGAGTTATCTGATGCATGTCCTCTTTGACCATTCCAAC
 40 CTGGGTTTCATGA (SEQ ID NO: 98)

AOLFR52 sequences:

MLGPAYNHTMETPASFLLVGIPGLQSSHLWLAIISLAMYTTALLGNTLIVTAIWMDSTRHEPMY
 CFLCVLAAVDIVMASSVVPKMVSIFCSGDSSISFSACFTQMFFVHLATAVETGLLLTMAFDTRYV
 45 AICKPLHYKRILTPQVMLGMSMAVTIRAVTFMTPLSWMMNHLFPFCGSNVVVHSHYCKHIALAR
 LACADVPSSLYSLIGSSLMVGSVDVAFIAASYILILRAVFDLSSKTAQLKALSTCGSHVGMALY
 YLPGMASIYAAWLQDIVPLHTQVLLADLYVIIPATLNPITYGMRTKQLLEGIWSYLMHFLFDH
 SNLGS (SEQ ID NO: 99)

ATGCTGGGTCCAGCTTACAACCACACAATGGAAACCCCTGCCTCCTCCTCCTTGTGGGTA
 TCCCAGGACTGCAATCTTCACATCTTTGGCTGGCTATCTCACTGAGTGCCATGTACATCAC
 AGCCCTGTTAGGAAACACCCCTCATCGTGACTGCAATCTGGATGGATTCCACTCGGCATGAG
 CCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTATGGCCTCCTCCGTGGT
 ACCCAAGATGGTGAGCATCTTCTGCTCGGGAGACAGCTCCATCAGCTTTAGTGCTTGTTC
 55 ACTCAGATGTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGGCTGCTGTGACCATGG
 CTTTGGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGAGAATTCTCACGCCTCA

AGTGATGCTGGGAATGAGTATGGCCGTCACCATCAGAGCTGTCACATTCATGACTCCACTG
 AGTTGGATGATGAATCATCTACCTTTCTGTGGCTCCAATGTGGTTGTCCACTCCTACTGTAA
 GCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCAGCAGTCTCTACAGTCTG
 ATTGGTTCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCTGCCTCCTATATCTTAAT
 5 TCTCAGGGCAGTATTTGATCTCTCCTCAAAGACTGCTCAGTTGAAAGCATTAAAGCACATGT
 GGCTCCCATGTGGGGGTTATGGCTTTGTACTATCTACCTGGGATGGCATCCATCTATGCGG
 CCTGGTTGGGGCAGGATATAGTGCCCTTGACACCCAAAGTGCTGCTAGCTGACCTGTACGT
 GATCATCCCAGCCACTTTAAATCCCATCATCTATGGCATGAGGACCAACAATTGCTGGAG
 10 GGAATATGGAGTTATCTGATGCACCTTCTCTTTGACCACTCCAACCTGGGTTTCATGA (SEQ
 ID NO: 100)

AOLFR54 sequences:

MSDSNLSDNHLPDTFFLTGIPGLEAAHFVIAIPFCAMYLVALVGNAALILVIAMDNALHAPMY
 LFLCLLSLTDLALSSTTVPKMLAILWLHAGEISFGGCLAQMFCVHSIYALESSILLAMAFDRYVA
 15 ICNPLRYTTILNHAVIGRIGFVGLFRSVAIVSPFIFLLRRLPYCGHRVMTHTYCEHMGARLACA
 NITVNIVYGLTVALLAMGLDSILIAISYGFIHAFVHLPASHDAQHKALSTCGSHIGIILVFYIPAFF
 SFLTHRFGHHEVPKHVHIFLANLYVLVPPVLNPILYGARTKEIRSRLKLLHLGKTSI (SEQ ID
 NO: 101)

20 ATGTCAGATTCCAACCTCAGTGATAACCATCTTCCAGACACCTTCTTCTTAACAGGGATCC
 CAGGGCTGGAGGCTGCCACTTCTGGATTGCCATCCCTTTCTGTGCCATGTATCTTGTAGC
 ACTGGTTGGAATGCTGCCCTCATCTGGTCAATTGCCATGGACAATGCTCTTCATGCACCT
 ATGTACCTCTTCTCTGCTTCTCTCACTCACAGACCTGGCTCTCAGTTCTACCACTGTGCC
 CAAGATGCTGGCCATTTTGTGGCTCCATGCTGGTGAGATTTCTTTGGTGGATGCCTGGCC
 25 CAGATGTTTTGTGTCCATTCTATCTATGCTCTGGAGTCTCGATTCTACTTGCCATGGCCTT
 TGATAGGTATGTGGCTATCTGTAACCCATTAAGGTATACAACCATTCTCAACCATGCTGTC
 ATAGGCAGAATTGGCTTTGTTGGGCTATTCCGTAGTGTGGCTATTGTCTCCCCCTTCATCTT
 CTTGCTGAGGCGACTCCCCTACTGTGGTCAACCGTGTGCATGACACACATACTGTGAGCAT
 ATGGGCATCGCCCGACTGGCCTGTGCCAACATCACTGTCAATATTGTCTATGGGCTAACTG
 30 TGGCTCTGCTGGCCATGGGACTGGATTCCATTCTCATTGCCATTTCTATGGCTTTATCCTC
 CATGCAGTCTTTACCTTCCATCTCATGATGCCAGCACAAAGCTCTGAGTACCTGTGGCT
 CCCCATTTGGCATCATCTGGTTTTCTACATCCCTGCCTTCTTCTCCTTCCTCACCCACCGC
 TTTGGTCAACGAAAGTCCCCAAGCATGTGCACATCTTTCTGGCTAATCTCTATGTGCTGG
 TGCCTCCTGTACTCAATCCTATTCTCTATGGAGCTAGAACCAAGGAGATTTCGGAGTCGACT
 35 TCTAAAACTGCTTCACCTGGGGAAGACTTCAATATGA (SEQ ID NO: 102)

AOLFR57 sequences:

MSFQVTYMFYHLWTFMEKSNNSTLFIILLGFSQKNIEVLFCVLFVLCYIAIWMGNLLIMISITCTQ
 LIHQPMYFFLNYSLSLDCYTSTVTPKLMVDLLAERKTISYNNCMQLFTTHFFGGIEFILFTGM
 40 AYDRYVAICKPLHYTIIMSROKCNTHIVCCTGGFIHSASQFLLTIFVFPFCGPNEIDHYFCDVYPLL
 KLACSNHIMIGLLVIANSGLIALVTFVLLSYVFILYTRAYSERRSKALATCSSHVIVVVLFF
 APALFIYIRPVTTFSEDKVFALFYTHAPMFNPLIYTLRNTEMKNAMRKVWCCQILLKRNQLF
 (SEQ ID NO: 103)

45 ATGTCATTTTCAGGTGACTTATATGTTCTATCTACACTGGACCATGGAAAAAAGCAATAATA
 GCACTTTGTTTATTCTCTTGGGGTTTTCCCAAAATAAGAACATTGAAGTCCTCTGCTTTGTA
 TTATTTTTGTTTTGCTACATTGCTATTTGGATGGGAACTTACTCATAATGATTTCTATCAC
 GTGCACCCAGCTCATTACCAACCCATGTATTTCTTCTCAATTACCTCTCACTCTCCGACC
 TTTGCTACACATCCACAGTGACCCCAAATTAATGGTTGACTTACTGGCAGAAAGAAAGAC
 50 CATTTCTATAATAACTGTATGATACAACTCTTACCACCCATTTTTTTGGAGGCATAGAGA
 TCTTCATTCTCACAGGGATGGCCTATGACCGCTATGTGGCCATTTGCAAGCCCTGCACTA
 CACCATTATTATGAGCAGGCAAAAGTGAACACAATCATCATAGTTTGTGTACTGGGGGA
 TTTATACATTCTGCCAGTCAGTTTCTTCTCACCATCTTTGTACCATTTTGTGGCCCAAATGA
 GATAGATCACTACTTCTGTGATGTGTATCCTTTGCTGAAATTGGCCTGTTCTAATATACACA
 55 TGATAGGTCTCTTAGTCATTGCTAATTCAGGCTTAATTGCTTTGGTGACATTTGTTGTCTTG
 TTGTTGCTTATGTTTTTATATTGTATACCATCAGAGCATACTCTGCAGAGAGACGCAGCA

5 AAGCTCTTGCCACTTGTAGTTCTCATGTAATTGTTGTGGTCCTGTTTTTGTCTCCTGCATTG
 TTCATTTACATTAGACCGGTCAACAATTCTCAGAAGATAAAGTGTGGCCCTTTTTTATAC
 CATCATTGCTCCCATGTTCAACCTCTCATATACACGCTGAGAAACACAGAGATGAAGAAC
 GCCATGAGGAAAGTGTGGTGTGTCAAATACTCCTGAAAAGAAATCAACTTTTCTGA (SEQ
 ID NO: 104)

AOLFR58 sequences:

10 MFSMTTEALNNFALGCTNLLMTMPQIDLKQIFLCPNCRLYMIPVGAFIFSLGNMQNQSFVTEF
 VLLGLSQPNVQEIVFVFLFVYIATVGGNMLIVVTILSSPALLVSPMYFFLGFLSFLDACFSSVI
 TPKMIVDSLYVTKTISFEGCMMQLFAEHFFAGVEVIVLTAMAYDRYVAICKPLHYSSIMNRR
 CGILMGVAWTGGLLHSMIQLFTFQLPFCGPNVINHFMCPLYLLELACTDTHIFGLMVVINS
 FICIINFSLLLVSYAVILLSLRTHSSEGRWKALSTCGSHIAVVILFFVPCIFVYTRPPSAFSLDKMA
 AIFYIILNPLLNPLIYTFRNKEVKQAMRRIWNRLMVVSDEKENIKL (SEQ ID NO: 105)

15 ATGTTCTCAATGACAACAGAAGCACTCAATAATTTTGCACTTGGATGTACCAACTTGTAA
 TGACTATGATACCACAAATTGATCTGAAGCAAATTTTCCTTTGTCCTAATTGCAGACTATA
 CATGATCCCTGTTGGAGCTTTCATCTTTTCCTTGGGAAACATGCAAAACCAAAGCTTTGTA
 ACTGAGTTTGTCTCCTGCGGACTTTCACAGAATCCAAATGTTTCAGGAAATAGTATTTGTG
 TATTTTTGTTTGTCTACATTGCAACTGTTGGGGGCAACATGCTAATTGTAGTAACCATTCCT
 20 AGCAGCCCTGCTCTTCTGGTGTCTCCTATGTACTTCTTCTTGGGCTTCTGTCTTCTCTGGA
 TGGGTGCTTCTCATCTGTCTATCAACCCAAAGATGATTGTAGACTCCCTCTATGTGACAAA
 ACCATCTCTTTTGAAGGCTGCATGATGCAGCTCTTTGCTGAACACTTCTTTGCTGGGGTGG
 AGGTGATTGTCTCACAGCCATGGCCTATGATCGTTATGTGGCCATTGCAAGCCCTTGCA
 TTACTCTTCTATCATGAACAGGAGGCTCTGTGGCATTCTGATGGGGGTAGCCTGGACAGGG
 25 GGCTCTTGCATTCCATGATACAAATTCCTTTTACTTTCAGCTTCCCTTTTGTGGCCCCAA
 TGTCAATCACTTTATGTGTGACTTGTACCCGTTACTGGAGCTTGCCTGCACTGATACTC
 ACATCTTTGGCCTCATGGTGGTCATCAACAGTGGGTTTATCTGCATCATAAACTTCTCCTTG
 TTGCTTGTCTCCTATGCTGTCTCTCTCTGAGAACACACAGTTCTGAAGGGCGCTG
 GAAAGCTCTCTCCACCTGTGGATCTCACATTGCTGTTGTGATTTTGTCTTTGTCCCATGCA
 30 TATTTGTATATACACGACCTCCATCTGCTTTTCCCTTGACAAAATGGCGGCAATATTTTAT
 ATCATCTTAAATCCCTTGCTCAATCCTTTGATTTACACTTTCAGGAATAAGGAAGTAAAC
 AGGCCATGAGGAGAATATGGAACAGACTGATGGTGGTTTCTGATGAGAAAGAAAATATTA
 AACTTTAA (SEQ ID NO: 106)

35 **AOLFR59 sequences:**

MGDWNNSDAVEPIFILRGFPGLLEYVHSWLSILFCLAYLVAFMGNVTILSVIWISSLHQPMYFYI
 SILAVNDLGMSTLPTMLAVLWDAPEIQASACYAQLFFIHTFTFLESSVLLAMAFDRFVAICH
 PLHYPTILTNSVIGKIGLACLLRSLGVVLPPTLLRHYHYCHGNALSHAFCLHQDVLRLSCTDA
 RTNSIYGLCVIATLGVDSIFILLSYVLILNTVLDIASREEQLKALNTCVSHICVVLFFVPIGV
 40 MVHRFGKHLSPIVHILMADIYLLPVLNPIVYSVRTKQIRLGILHKFVLRRLF (SEQ ID NO:
 107)

ATGGGAGACTGGAATAACAGTGATGCTGTGGAGCCCATATTTATCCTGAGGGGTTTTCCTG
 GACTGGAGTATGTTTCATTCTTGGCTCTCCATCCTCTTCTGTCTTGCAATTTGGTAGCATT
 45 ATGGGTAATGTTACCATCCTGTCTGTCAATTTGGATAGAATCCTCTCTCCATCAGCCCATGTA
 TTACTTTATTTCCATCTTAGCAGTGAATGACCTGGGGATGTCCCTGTCTACACTTCCACCA
 TGCTTGCTGTGTTATGGTTGGATGCTCCAGAGATCCAGGCAAGTGCTTGCTATGCTCAGCT
 GTTCTTCATCCACACATTCACATTCCTGGAGTCCCTCAGTGTTGCTGGCCATGGCCTTTGACC
 GTTTTGTGCTATCTGCCATCCACTGCACTACCCACCATCCTCACCACAGTGTAATTGGC
 50 AAAATTGGTTTGGCCTGTTTGCTACGAAGCTTGGGAGTTGTACTTCCACACCTTTGCTACT
 GAGACACTATCACTACTGCCATGGCAATGCCCTCTCTCACGCCCTTCTGTTTGACACAGGAT
 GTTCTAAGATTATCCTGTACAGATGCCAGGACCAACAGTATTTATGGGCTTTGTGTAGTCA
 TTGCCACTAGGTGTGGATTCAATCTTCATACTTCTTTCTTATGTTCTGATTCTTAATACT
 GTGCTGGATATTGCATCTCGTGAAGACAGCTAAAGGCACTCAACACATGTGTATCCCAT
 55 TCTGTGTGGTGCTTATCTTCTTGTGCCAGTTATTGGGGTGTCAATGGTCCATCGCTTTGGG
 AAGCATCTGTCTCCCATAGTCCACATCCTCATGGCAGACATCTACCTTCTTCTCCCCCAGT

CCTTAACCCTATTGTCTATAGTGTGTCAGAACAAAGCAGATTCGTCTAGGAATTCTCCACAAG
TTTGTCTTAAGGAGGAGGTTTTAA (SEQ ID NO: 108)

AOLFR60 sequences:

5 MFLPNDTQFHPSSFLLLGIPGLETLHTWIGFFCAVYMIALIGNFTILLVIKTDSSLHQPMFYFLA
MLATTDVGLSTATIPKMLGIFWINLRGIIFEACLTQMFFIHNFTLMESAFLVAMAYDSYVAICN
PLQYSAILTNKVSVIGLVFVRALIFVIPSILLRLPFCGNHVIPHTYCEHMGHLASCAIKINI
IYGLCAICNLVFDITVIALSYVHLCAVFLRPTHEPRLKSLSTCGSHVCVILAFYTPALFSFMTHC
FGRNVPRYIHILLANLYVVPPMLNPVIYGVRTKQIYKCVKKILLQEQGMEKEEYLIHTRF
10 (SEQ ID NO: 109)

ATGTTCCCTTCCCAATGACACCCAGTTTCACCCCTCCTCCTTCTGTTGCTGGGGATCCCAGG
ACTAGAAACACTTCACATCTGGATCGGCTTTCCCTTCTGTGCTGTGTACATGATCGCACTC
ATAGGGAACCTTCACTATTCTACTTGTGATCAAGACTGACAGCAGCCTACACCAGCCCATGT
15 TCTACTTCCCTGGCCATGTTGGCCACCACTGATGTGGGTCTCTCAACAGCTACCATCCCTAA
GATGCTTGGAATCTTCTGGATCAACCTCAGAGGGATCATCTTGAAGCCTGCCTCACCCAG
ATGTTTTTTATCCACAACCTTCACACTTATGGAGTCAGCAGTCTTGTGGCAATGGCTTATG
ACAGCTATGTGGCCATCTGCAATCCACTCCAATATAGCGCCATCCTCACCACAAAGGTTGT
TTCTGTGATTGGTCTTGGTGTGTTGTGAGGGCTTTAATTTTCGTCAATCCCTCTATACTTC
20 TTATAATTGCGGTTGCCCTTCTGTGGGAATCATGTAATCCCCACACCTACTGTGAGCACAT
GGGTCTTGCTCATCTATCTTGTGCCAGCATCAAAATCAATATTATTTATGGTTTATGTGCCA
TTTGTAACTCGGTGTTTGACATCAGTCATTGCCCTCTCTTATGTGCATATTCTTTGTGCT
GTTTCCCGTCTTCCCTACTCATGAGCCCCGACTCAAGTCCCTCAGCACATGTGGTTTCAATGT
GTGTGTAATCCTTGCTTCTATACACCAGCCCTCTTTCCCTTATGACTCATTGCTTTGGCC
25 GAAATGTGCCCCGCTATATCCATATACTCCTAGCCAATCTCTATGTTGTGGTGCCACCAAT
GCTCAATCCTGTCTATATATGGAGTCAGAACCAAGCAGATCTATAAATGTGTAAAGAAAAT
ATTATTGCAGGAACAAGGAATGGAAAAGGAAGAGTACCTAATACATACGAGGTTCTGA
(SEQ ID NO: 110)

30 **AOLFR61 sequences:**

MSIINTSYVEITTFVLVGMPLGLEIAHIWISIPICSMYLIAILGNGTILFIKTEPSLHGPMYYFLSML
AMSDLGLSLSLPTVLSIFLNPETSSSACFAQEFFIHGFSVLESSVLLIMSFDRLAIHNPLRYT
SILTTVRVAQIGIVFSFKSMMLVLPFPFTLRSRLRYCKKNQLSHSYCLHQDVMKLACSDNRIDVIY
GFFGALCLMVDFILIAVSYTLILKTVPGIASKKEELKALNTCVSHICAVIIFYLPINLAVVHRFAG
35 HVSPLINVLMANVLLLVPPLMKPIVYCVKTKQIRVRVVAKLCQWKI (SEQ ID NO: 111)

ATGTCCATTATCAACACATCATATGTTGAAATCACCACCTTCTTCTTGGTTGGGATGCCAG
GGCTAGAATATGCACACATCTGGATCTCTATCCCCATCTGCAGCATGTATCTTATTGCTATT
CTAGGAAATGGCACCATTCTTTTATCATCAAGACAGAGCCCTCCTTGCATGGGCCCATGT
40 ACTATTTTCTTTCCATGTTGGCTATGTCAGACTTGGGTTTGTCTTATCATCTCTGCCCCACT
GTGTTAAGCATCTTCTGTTCAATGCCCTGAAACTTCTTCTAGTGCCTGCTTTGCCAGGA
ATTCTTCATTCATGGATTCTCAGTACTGGAGTCCTCAGTCCTCCTGATCATGTCAATTTGATA
GATTCCTAGCCATCCACAATCCTCTGAGATACACCTCAATCCTGACAACTGTCAGAGTTGC
CCAAATAGGGATAGTATTCTCCTTTAAGAGCATGCTCCTGGTTCTTCCCTTCCCTTTCACTT
45 TAAGAAGCTTGAGATATTGCAAGAAAAACCAATTATCCCATTCCTACTGTCTCCACCAGGA
TGTCATGAAGTTGGCCTGTTCTGACAAACAGAATTGATGTTATCTATGGCTTTTGGAGCA
CTCTGCCTTATGGTAGACTTTATTCTCATTGCTGTGTCTTACACCCTGATCCTCAAGACTGT
ACCGGGAATTGCATCCAAAAAGGAGGAGCTTAAGGCTCTCAATACTTGTGTTTACACATC
TGTGCAGTGATCATCTTCTACCTGCCATCATCAACCTGGCCGTTGTCCACCGCTTTGCCGG
50 GCATGTCTCTCCCTCATTAAATGTTCTCATGGCAAATGTTCTCCTACTTGTACCTCCGCTGA
TGAAACCAATTGTTTATTGTGTAAAACTAAACAGATTAGAGTGAGAGTTGTAGCAAAATT
GTGTCAATGGAAGATTAA (SEQ ID NO: 112)

AOLFR62 sequences:

55 MFYHNKSIFHPVTFFLIGIPGLEDFHWMWISGPFCSVYLVALLGNATILLVIKVEQTLREPMFYFL
AILSTIDLALSATSVPRMLGIFWFDAHEINYGACVAQMFLIHAFTGMEAEVLLAMAFDRYVAIC

APLHYATILTSVLVVGISMCIIVRPVLLTLPVYLIYRLPFCQAHIAHSYCEHMGIAKLSCGNIRI
 NGIYGLFVVVSFFVLNLVLIGISYVYILRAVFRLP SHDAQLKALSTCGAHVGVICVFYIPSVFSFLT
 HRFQHQIPGYIHILVANLYLIPPSLNPITYGVRTKQIRERVLYVFTKK (SEQ ID NO: 113)

5 ATGTTTTATCACAACAAGAGCATATTTACCCAGTCACATTTTTCTCATTGGAATCCCAGG
 TCTGGAAGACTTCCACATGTGGATCTCCGGGCCTTTCTGCTCTGTTTACCTTGTGGCTTTGC
 TGGGCAATGCCACCATTCTGCTAGTCATCAAGGTAGAACAGACTCTCCGGGAGCCCATGTT
 CTACTTCTGGCCATTCTTTCCACTATTGATTTGGCCCTTTCTGCAACCTCTGTGCCTCGCA
 TGCTGGGTATCTTCTGGTTTGTGCTCAGCAGATTAACATGGAGCTTGTGTGGCCAGAT
 10 GTTTCTGATCCATGCCTTCACTGGCATGGAGGCTGAGGTCTTACTGGCTATGGCTTTTGAC
 CGTTATGTGGCCATCTGTGCTCCACTACATTACGCAACCATTCTTGACATCCCTAGTGTGGT
 GGGCATTAGCATGTGCATTGTAATTCGTCCCCTTTTACTTACACTTCCCATGGTCTATCTTA
 TCTACCGCCTACCCCTTTTGTGAGGCTCACATAATAGCCCATTCTACTGTGAGCACATGGG
 CATTGCAAAATTGTCTGTGGAAACATTTCGTATCAATGGTATCTATGGGCTTTTTGTAGTTT
 15 CTTTCTTTGTTCTGAACCTGGTGCTCATTGGCATCTCGTATGTTTACATTCTCCGTGCTGTC
 TTCCGCCTCCCATCACATGATGCTCAGCTAAAAGCCCTAAGCACGTGTGGCGCTCATGTTG
 GAGTCATCTGTGTTTTCTATATCCCTTCAGTCTTCTCTTCTTACTCATCGATTGAGACAC
 CAAATACCAGGTTACATTACATTCTTGTGCAATCTCTATTTGATTATCCACCCTCTCT
 CAACCCCATCATTTATGGGGTGAGGACCAACAGATTGAGAGCGAGTGCTCTATGTTTTT
 20 ACTAAAAAATAA (SEQ ID NO: 114)

AOLFR63 sequences:

MSIINTSYVEITTFVLVGMPLGEYAHIWISIPICSMYLIAILGNGTILFIKTEPSLHEPMMYYFLSML
 AMSDLGLSSLPTVLISIFLNAPEISSNACFAQEFFIHGFSVLESSVLLMSFDRFLAIHNPLRYTS
 25 ILTTVRVAQIGIVFSFKSMMLLVLPFPFTLRNLRYCKKNQLSHSYCLHQDVMKLACSDNRIDVTY
 GFFGALCLMVDFILIAVSYTLILKTVLGIASKKEQLKALNTCVSHICAVIIFYLPIINLAVVHRFAR
 HVSPLINVLMANVLLVPPLTNPIVYCVKTKQIRVRVAVAKLCQRKI (SEQ ID NO: 115)

ATGTCCATTATCAACACATCATATGTTGAAATCACCACCTTCTTCTTGGTTGGGATGCCAG
 30 GGCTAGAATATGCACACATCTGGATCTCTATCCCCATCTGCAGCATGTATCTTATTGCTATT
 CTAGGAAATGGCACCATTCTTTTATCATCAAGACAGAGCCCTCCTTGCATGAGCCCATGT
 ACTATTTTCTTCCATGTTGGCTATGTCAGACTTGGGTTTGTCTTTATCATCTCTGCCCACT
 GTGTTAAGCATCTTCCGTGTTCAATGCTCCTGAAATTTTCATCCAATGCCTGCTTTGCCAGGA
 ATTCTTCATTCATGGATTCTCAGTACTGGAGTCTCAGTCTCCTGATCATGTCAATTGATA
 35 GATTCTAGCCATCCACAACCCTCTGAGATACACCTCAATCCTGACAACTGTGAGAGTTGC
 CCAAATAGGGATAGTATTCTCCTTTAAGAGCATGCTCCTGGTTCTTCCCTTCCCTTTCACTT
 TAAGAAACTTGAGATATTGCAAGAAAAACCAATTATCCCATTCCTACTGTCTCCACCAGGA
 TGTCATGAAGTTGGCCTGTTCTGACAAACAGAAATTGATGTTATCTATGGCTTTTTTGGAGCA
 CTCTGCCTTATGGTAGACTTTATTCTCATTGCTGTGTCTTACACCCTGATCCTCAAGACTGT
 40 ACTGGGAATTGCATCCAAAAAGGAGCAGCTTAAGGCTCTCAATACTGTGTTTACACATC
 TGTGCAGTGATCATCTTCTACCTGCCCATCATCAACCTGGCCGTTGTCCACCGCTTTGCCCG
 GCATGTCTCTCCCCTCATTAAATGTTCTCATGGCAAATGTTCTCCTACTTGTACCTCCACTGA
 CGAACCCAATTGTTTATTGTGTAATAAATAACAGATTAGAGTGAGAGTTGTAGCAAAATT
 GTGTCAACGGAAGATTAA (SEQ ID NO: 116)

45

AOLFR64 sequences:

MTILLNSSLQRATFFLTGFQGLEGLHGWISIPFCFIYLTVILGNLTILHVICTDATLHGPMYYFLG
 MLAVTDLGLCLSTLPTVLGIFWFDTREIGIPACFTQLFFIHTLSSMESSVLLSMSIDRSVAVCNPL
 HDSTVLTPACIVKMGLSSVLRSAALLPLPFLKRFQYCHSHVLAHAYCLHLEIMKLACSSIYN
 50 HIYGLFVVACTVGVDLLIFLSYALILRTVLSIASHQERLRALNTCVSHICAVLLFYIPMIGLSLV
 HRFGEHLPRVHLFMSYVYLLVPPLMNPPIYSIKTKQIRQRIKKFQFIKSLRCFWKD (SEQ ID
 NO: 117)

ATGACAATTCTTCTTAATAGCAGCCTCCAAAGAGCCACTTTCTTCTGACGGGCTTCCAAG
 55 GTCTAGAAGGTCTCCATGGCTGGATCTCTATTCCCTTCTGCTTCATCTACCTGACAGTTATC
 TTGGGGAACCTCACCATTCTCCACGTCATTTGTAAGTATGCACTCTCCATGGACCCATGT

ACTATTTCTTGGGCATGCTAGCTGTACAGACTTAGGCCTTTGCCTTTCCACACTGCCCACT
 GTGCTGGGCATTTTCTGGTTTGATACCAGAGAGATTGGCATCCCTGCCTGTTTCACTCAGC
 TCTTCTTCATCCACACCTTGTCTTCAATGGAGTCATCAGTTCTGTTATCCATGTCCATTGAC
 CGCTCCGTGGCCGTCTGCAACCCACTGCATGACTCCACCGTCCTGACACCTGCATGTATTG
 5 TCAAGATGGGGCTAAGCTCAGTGCTTAGAAGTGCTCTCCTCATCCTCCCCTTGCCATTCCCT
 CTGAAGCGCTTCCAATACTGCCACTCCCATGTGCTGGCTCATGCTTATTGTCTTCACCTGGA
 GATCATGAAGCTGGCCTGCTCTAGCATCATTGTCAATCACATCTATGGGCTCTTTGTTGTG
 GCCTGCACCGTGGGTGTGGACTCCCTGCTCATCTTTCTCTCATACGCCCTCATCCTTCGCAC
 CGTGCTCAGCATTGCCTCCCACAGGAGCGACTCCGAGCCCTCAACACCTGTGTCTCTCAT
 10 ATCTGTGCTGTACTGCTCTTCTACATCCCCATGATTGGCTTGTCTCTTGTGCATCGCTTTGG
 TGAACATCTGCCCCGCGTTGTACACCTCTTCATGTCTATGTGTATCTGCTGGTACCACCCC
 TTATGAACCCCATCATCTACAGCATCAAGACCAAGCAAATTCGCCAGCGCATCATTAAGAA
 GTTTCAGTTTATAAAGTCACTTAGGTGTTTTTGAAGGATTAA (SEQ ID NO: 118)

15 **AOLFR65 sequences:**

MAGRMSTSNHTQFHPSSFLLLGIPGLEDVHIWIGVPPFFVYLVALLGNTALLFVIQTEQSLHEPM
 YYFLAMLDSIDLGLSTATIPKMLGIFWFNTKEISFGGCLSHMFFIHFHTAMESIVLVAMAFDRYI
 AICKPLRYTMILTSKIIISLIAGIAVLRSLYMVPLVFLLLRLPFCGHRIPHTYCEHMGIA RLACAS
 IKVNIRFGLGNISLLLLDVILIISYVRILYAVFCLPSWEARLKALNTCGSHIGVILAFFTPAFFSFL
 20 THRFGHNPQYIHIILANLYVVVPPALNPVIYGVRTKQIRERVLRIFLKTNH (SEQ ID NO: 119)

ATGGCAGGAAGAATGTCTACGTCTAATCACACCCAGTTCCATCCTTCTTCATTCCCTACTGCT
 GGGTATCCCAGGGCTAGAAGATGTGCACATTTGGATTGGAGTCCCTTTTTTCTTTGTGTAT
 CTTGTTGCACTCCTGGGAAACACTGCTCTCTTGTGTTGTGATCCAGACTGAGCAGAGTCTCC
 25 ATGAGCCTATGTACTACTTCTGGCCATGTTGGATTCCATTGACCTGGGCTTGTCTACAGC
 CACCATCCCCAAAATGTTGGGCATCTTCTGGTTCAATACCAAAGAAATATCTTTTGGAGGC
 TGCCCTTCTCACATGTTCTTCATCCATTTCTTCACTGCTATGGAGAGCATTGTGTTGGTGGC
 CATGGCCTTTGACCGCTACATTGCCATTTGAAACCTCTTCGGTACACCATGATCCTCACCA
 GCAAATCATCAGCCTCATTGCAGGCATTGCTGTCTGAGGAGCCTGTACATGGTTGTTC
 30 ACTGGTGTTTCTCCTTCTGAGGCTGCCCTTCTGTGGGCATCGTATCATCCCTCATACTTAT
 GTGAGCACATGGGCATTGCCGTCTGGCCTGTGCCAGCATCAAAGTCAACATTAGGTTTGG
 CCTTGGCAACATATCTCTCTTGTACTGGATGTTATCCTTATTATTCTCTCCTATGTACAGGA
 TCCTGTATGCTGTCTTCTGCCTGCCCTCCTGGGAAGCTCGACTCAAAGCTCTCAACACCTGT
 GGTCTCATATTGGTGTTATCTTAGCCTTTTTTACACCAGCATTTTTTTTCATTCTTGACACA
 35 TCGTTTTGGCCATAATATCCACAGTATATACATATTATATTAGCCAACTGTATGTGGTTG
 TCCCACAGCCCTCAATCCTGTAATCTATGGAGTCAGGACAAAGCAGATTGAGAGAGAG
 TGCTGAGGATTTTTCTCAAGACCAATCACTAA (SEQ ID NO: 120)

AOLFR66 sequences:

40 MSFLNGTSLTPASFILNGIPGLEDVHLWISFPLCTMYSIAITGNFGLMYLIYCDEALHRPMYVFL
 ALLSFTDVLMTSTLPNTLFILWFNLKEIDFKACLAQMFFVHTFTGMESGVLMLMALDHCVAI
 CFPLRYATILTNSVIAKAGFLTFLRGVMLVPSTFLTKRLPYCKGNVIPHTYCDHMSVAKISCGN
 VRVNAIYGLIVALLIGGFDILCITISYTMILQAVVSLSSADARQKAFSTCTAHFCAIVLTYVPAFF
 TFFTHHFGGHTIPLHHIIMANLYLLMPPTMNPVYGVKTRQVRESVIRFFLKGDNSHNF (SEQ
 45 ID NO: 121)

ATGTCATTTCTAAATGGCACCAGCCTAACTCCAGCTTCATTTCATCCTAAATGGCATCCCTG
 GTTTGGAAGATGTGCATTTGTGGATCTCCTTCCCACTGTGTACCATGTACAGCATTGCTATT
 ACAGGGAACCTTCGGCCTTATGTACCTCATCTACTGTGATGAGGCCTTACACAGACCTATGT
 50 ATGCTCTCCTTGGCCTTCTTCTTCAAGATGTGCTCATGTGCACACGACCCCTCCCAAC
 ACTCTCTCATATTTGTGGTTAATCTCAAGGAGATTGATTTTAAAGCCTGCCTCGCCAGAT
 GTTCTTTGTGCACACCTTCACAGGGATGGAGTCTGGGGTGCTCATGCTCATGGCCCTGGAC
 CACTGTGTGGCCATCTGCTTCCCTCTGCGTTATGCCACCATCCTCACTAATTCAGTCATTGC
 TAAAGCTGGGTTCTCACTTTTCTTAGGGGTGTGATGCTTGTATCCCTTCCACTTCTCTCA
 55 CCAAGCGCCTTCCATACTGCAAGGGCAACGTCATACCCACACCTACTGTGACCACATGTC
 TGTGGCCAAGATATCTTGTGGTAATGTCAGGGTTAACGCCATCTATGGTTTGATAGTTGCC

CTGCTGATTGGGGGCTTTGATATCCTGTGCATTACAATCTCCTACACTATGATTCTTCAAGC
 AGTTGTGAGTCTATCATCAGCAGATGCTCGACAGAAGGCCTTCAGCACCTGCACTGCCCCAC
 TTCTGTGCCATAGTCCCTCACCTATGTTCCAGCCTTCTTTACCTTCTTTACACACCATTTTGG
 GGGACACACCATTCCCTCTACACATACATATTATTATGGCTAATCTCTACCTACTAATGCCTC
 5 CCACAATGAACCCTATTGTGTATGGGGTGAAAACCAGGCAGGTACGAGAAAGTGTCTTA
 GGTTCTTTCTTAAGGGAAAGGACAATTCTCATAACTTTTAA (SEQ ID NO: 122)

AOLFR67 sequences:

MSGDNSSSLTPGFFILNGVPGLEATHIWISLPFCFMYIIA VVGNCGLICLISHEEALHRPMYYFLA
 10 LLSFTDVTLCCTMVPNMLCIFWFNLKEIDFNACLAQMFFVHMLTGMESGVLMLMALDRYVAI
 CYPLRYATILTNPVIAKAGLATFLRNVMLIIPFTLLTKRLPYCRGNFIPHTYCDHMSVAKVSCGN
 FKVNAIYGLMVALLIGVFDICCSVSYTMILQAVMSLSSADARHKAFSTCTSHMCSIVITYVAAF
 FTFFTHRFVGHNPNIHIIIVANLYLLLPPTMNPVYGVKTKQIQEGVIKFLLDKVSFTYDK
 (SEQ ID NO: 123)

15 ATGTCTGGGGACAACAGCTCCAGCCTGACCCCAGGATTCTTTATCTTGAATGGCGTTCCTG
 GGCTGGAAGCCACACACATCTGGATCTCCCTGCCATTCTGCTTTATGTACATCATTGCTGTC
 GTGGGGAAGTGTGGGCTCATCTGCCTCATCAGCCATGAGGAGGCCCTGCACCGGCCCATGT
 ACTACTTCTGCGCCCTGCTCTCCTTCACTGATGTACCTTGTGCACCACCATGGTACCTAAT
 20 ATGCTGTGCATATTCTGGTTCAACCTCAAGGAGATTGACTTTAACGCCTGCCTGGCCCAGA
 TGTTTTTTGTCCATATGCTGACAGGGATGGAGTCTGGGGTGCTCATGCTCATGGCCCTGGA
 CCGCTATGTGGCCATCTGCTACCCCTTACGCTATGCCACCATCCTTACCAACCCTGTCATCG
 CCAAGGCTGGTCTTGCCACCTTCTTGAGGAATGTGATGCTCATCATCCATTCACTCTCCTC
 ACCAAGCGCCTGCCCTATTGCCGGGGGAACCTTCATCCCCACACCTACTGTGACCATATGT
 25 CTGTGGCCAAGGTATCCTGTGGCAATTCAAGGTCAATGCTATTTATGGTCTGATGGTTGC
 TCTCCTGATTTGGTGTGTTTGATATCTGCTGTATCTCTGTATCTTACACTATGATTTTGCAGG
 CTGTTATGAGCCTGTCTATCAGCAGATGCTCGTCACAAAGCCTTCAGCACCTGCACATCTCA
 CATGTGTTCCATTGTGATCACCTATGTTGCTGCTTTTTTCACTTTTTTCACTCATCGTTTTGT
 AGGACACAATATCCCAAACCACATACATCATCGTGGCCAACCTTTATCTGCTACTGCCT
 30 CCTACCATGAACCCAATTGTTTATGGAGTCAAGACCAAGCAGATTACAGGAAGGTGTAATTA
 AATTTTACTTGGAGACAAGGTTAGTTTTACCTATGACAAATGA (SEQ ID NO: 124)

AOLFR68 sequences:

MTTHRNDTLSTEASDFLLNCFVRSPSWQHWLSLPLSLLFLLAVGANTTLLMTTWLEASLHQPL
 35 YYLLSLLSLLDIVLCLTVIPKVLTFWFDLRPISFPACFLQMYIMNCF LAMBESCTFMVMAYDRY
 VAICHPLRYPSTIDHFVVKAAAMFILTRNVMLTLPILSAQLRYCGRNVIENCICANMSVSRSLSC
 DDVTINHL YQFAGGWTL LGS DLILFLSYTELRAVLRLKAEGAVAKALSTCGSHFMLILFFSTIL
 LVFVLTHVAKKKVSPDVPVLLNVLHHVIPAALNPITYGVRTQEI KQGMQRLLKKGC (SEQ ID
 NO: 125)

40 ATGACAACACACCGAAATGACACCCTCTCCACTGAAGCTTCAGACTTCCTCTTGAATTGTT
 TTGTCAGATCCCCCAGCTGGCAGCACTGGCTGTCCCTGCCCCCTCAGCCTCCTTTTCTCTTG
 GCGTAGGGGGCCAACACCACCCTCCTGATGACCATCTGGCTGGAGGCCTCTCTGCACCAGC
 CCTGTACTACCTGCTCAGCCTCCTCTCCCTGCTGGACATCGTGCTCTGCCTCACTGTCATC
 45 CCAAGGTCCTGACCATCTTCTGGTTTGACCTCAGGCCCATCAGCTTCCCTGCCTGCTTCCT
 CCAGATGTACATCATGAATTGTTTCTAGCCATGGAGTCTTGACATTTCATGGTTCATGGCC
 TATGATCGTTATGTAGCCATCTGCCACCCATGAGATATCCATCAATCATCACTGATCACTT
 TGTAAGTCAAGGCTGCCATGTTTATTTTGACCAGAAATGTGCTTATGACTCTGCCATCCCC
 ATCCTTTTCAGCACAACTCCGTTATTGTGGAAGAAATGTCATTGAGAACTGCATCTGTGCCA
 50 ATATGTCTGTTTCCAGACTCTCCTGCGATGATGTCACCATCAATCACCTTTACCAATTTGCT
 GGAGGCTGGACTCTGCTAGGATCTGACCTCATCCTTATCTTCTCTCCTACACCTTCATTCT
 GCGAGCTGTGCTGAGACTCAAGGCAGAGGGTGCCGTGGCAAAGGCCCTAAGCACATGTGG
 CTCCCACTTCATGCTCATCCTCTTCTTCAGCACCATCCTTCTGGTTTTTGTCTCACACATGT
 GGCTAAGAAGAAAGTCTCCCTGATGTGCCAGTCTTGCTCAATGTTCTCCACCATGTCATT
 55 CTGTCAGCCCTTAACCCCATCATTTACGGGGTGAGAACCAAGAAATTAAGCAGGGGAATG
 CAGAGGTTGTTGAAGAAAGGGTGCTAA (SEQ ID NO: 126)

AOLFR69 sequences:

- MSYSIYKSTVNIPLSHGVVHSFCHNMNCNFMHIFKVLDFNMKNVTEVTLFVLKGFTDNLELQ
 TIFFFLFLAIYLFITLMGNLGLILVVIRDSQLHKPMYYFLSMLSSVDACYSSVITPNMLVDFTTKN
 5 KVISFLGCVAQVFLACSFGTTECFLLAAMAYDRYVAIYNPLLYSVMSPRVYVYMLINASYVAGI
 LHATHTVATFSLFCGANEIRRVFCDIPLLAISYSDHTNQLLLFYFVGSIELVTILIVLISYGLIL
 LAILKMYSABGRRKVFSTCGAHLTGVSIIYGTILFMYVRPSSSYASDHDMIVSIFYTTVIPLLPV
 IYSLRNKDVKDSMKKMFGKNQVINKVYFHTKK (SEQ ID NO: 127)
- 10 ATGTCGTACAGTATATACAAGAGCACAGTTAACATCCCCTTGAGTCATGGTGTTGTTTCATT
 CTTTTTGTGATAATATGAACTGTAACCTTATGCATATCTTCAAGTTTGTTCTAGATTTC AAC
 ATGAAGAATGTCACTGAAGTTACCTATTTGTAAGTGAAGGGCTTCACAGACAATCTTGAAC
 TGCAGACTATCTTCTTCTTCTGTTTCTAGCAATCTACCTCTTCACTCTCATGGGAAATTTA
 GGACTGATTTTAGTGGTCATTAGGGATTCCCAGCTCCACAAACCCATGTACTATTTTCTGA
 15 GTATGTTGTCTTCTGTGGATGCCTGCTATTCTCAGTTATTACCCCAAATATGTTAGTAGAT
 TTTACGACAAAGAATAAAGTCATTTTATTCTTGGATGTGTAGCACAGGTGTTTCTTGCTT
 GTAGTTTGGAAACCACAGAATGCTTTCTTGGCTGCAATGGCTTATGATCGCTATGTAGC
 CATCTACAACCTCTCCTGTATTCACTGAGCATGTCAACCCAGAGTCTACATGCCACTCATC
 AATGCTTCTATGTTGCTGGCATTTTACATGCTACTATACATACAGTGGCTACATTTAGCCT
 20 ATCCTTCTGTGGAGCCAATGAAATTAGGCGTGTCTTTGTGATATCCCTCCTCTCCTTGCTA
 TTTCTTATTCTGACACTCACACAAACAGCTTCTACTCTTCTACTTTGTGGGCTCTATCGAG
 CTGGTCACTATCCTGATTGTTCTGATCTCCTATGTTGTTGATTCTGTTGGCCATTCTGAAGAT
 GTATTCTGCTGAAGGGAGGAGAAAAGTCTTCTCCACATGTGGAGCTCACCTAACTGGAGT
 GTCAATTTATTATGGGACAATCCTCTTCATGTATGTGAGACCAAGTTCAGCTATGCTTCG
 25 GACCATGACATGATAGTGTCAATATTTTACACCATTGTGATTCCCTTGCTGAATCCCGTCAT
 CTACAGTTTGAGGAACAAAGATGTAAAAGACTCAATGAAAAAATGTTTGGGAAAAATCA
 GGTTATCAATAAAGTATATTTTCATACTAAAAAATAA (SEQ ID NO: 128)

AOLFR70 sequences:

- MDSTFTGYNLYNLQVKTEMDKLSSGLDIYRNPLKNKTEVTMFILTGFTDDFELQVFLFFFAI
 YLFTLIGNLGLVVLVIEDSWLHNPMMYYFLSVLSFLDACYSTVVT PKMLVNFLAKNKSISFIGCA
 TQMLLFVTFGTTECFLLAAMAYDHYVAIYNPLLYSVMSPRVYVPLITASYVAGILHATIHIVA
 TFSLSFCGSNEIRHVFCMPPLLAISCSDHTNQLLLFYFVGSIEIVTILIVLISCD FILL SILKMHSA
 KGRQKAFSTCGSHLTGVITYHGTLVS YMRPSSSYASDHDIIVSIFYTTVIPKLNPIIYSLRNKEVK
 35 KAVKKMLKLVYK (SEQ ID NO: 129)
- ATGGACTCCACTTTCACAGGCTATAACCTTTATAACCTGCAAGTAAAAACTGAAATGGACA
 AGTTGTGCATCAGTTTGGATATATACAGGAATCCACTGAAGAACAAGACTGAAGTCACCA
 TGTTTATATTGACAGGCTTCACAGATGATTTTGAGCTGCAAGTCTTCTTATTTTACTATTT
 40 TTTGCAATCTATCTCTTTACCTTGATAGGCAATTTAGGGCTGGTTGTGTTGGTCATTGAGG
 ATTCTGGCTCCACAACCCCATGTATTATTTCTTAGTGTGTTTATCATTCTTGGATGCTTGC
 TATTCTACAGTTGTCACTCCAAAAATGTTGGTCAATTTCTGGCAAAAAATAAATCCATTT
 CATTTATCGGATGTGCAACACAGATGCTTCTTTTGTACTTTTGGAACTACAGAATGTTTT
 CTCTGGCTGCAATGGCTTATGATCACTATGTAGCCATCTACAACCTCTCCTGTATTCACT
 45 GAGCATGTCAACCCAGAGTCTATGTGCCACTCATCACTGCTTCTACGTTGCTGGCATTTTAC
 ATGCTACTATACATATAGTGGCTACATTTAGCCTGTCTTCTGTGGATCCAATGAAATTAG
 GCATGTCTTTTGTGATATGCCTCCTCTCCTTGCTATTTCTTGTCTGACACTCACACAAACC
 AGCTTCTACTCTTCTACTTTGTGGGTCTATTGAGATAGTCACTATCCTGATTGCTCCTCATT
 TCCTGTGATTTTATTCTGTTGTCCATTCTGAAGATGCATTCTGCTAAGGGAAGGCAAAAGG
 50 CCTTCTCTACATGTGGCTCTCACCTAACTGGAGTGACAATTTATCATGGAACAATTCTCGTC
 AGTTATATGAGACCAAGTTCAGCTATGCTTCAGACCATGACATCATAGTGTCAATATTTT
 ACACAATTGTGATTCCCAAGTTGAATCCCATCATCTATAGTTTGAGGAACAAAGAAGTAA
 AAAGGCAGTGAAGAAAATGTTGAAATTGGTTTACAAATGA (SEQ ID NO: 130)

AOLFR71 sequences:

MGRNRNNTNVPDFILTGLSDSEEVQMALFILFLIYLLITMLGNVGMILIRLDLQLHTPMYFFLTH
 LSFIDLSYSTVITPKTLANLLTSNYISFMGCFAQMFFVFLGAAECFLSSMAYDRYVAICSPRLY
 PVIMSKRLCCALVTGPYVISFINSFVNVMWSRLHFCDSNVVRHFFCDTSPILALSCMDTYDIEI
 5 MIHILAGSTLMVSLITISASYVSILSTILKINSTSGKQKALSTCASHLLGVTFYGTMIFTYLKPRK
 SYSLGRDQVASVFYTTIVPMLNPLIYSLRNKEVKNALIRVMQRRQDSR (SEQ ID NO: 131)

ATGGGTTAGAAGAAATAACACAAATGTGCCTGACTTCATCCTTACGGGACTGTCAGATTCTG
 AAGAGGTCCAGATGGCCCTCTTTATACTATTTCTCCTGATATACCTAATTACTATGCTGGGC
 10 AATGTGGGGATGATATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTATTTTT
 TCCTTACTCACTTGTCATTTATTGACCTCAGTTACTCAACTGTCATCACACCTAAAACCTTA
 GCGAACTTACTGACTTCCAATAATTTCTCTCATGGGCTGCTTTGCCAGATGTTCTTTTT
 TGTCTTCTTGGGAGCTGCTGAATGTTTTCTCTCATCAATGGCCTATGATCGCTACGTAG
 CTATCTGCAGTCTCTACGTTACCCAGTTATTATGTCCAAAAGGCTGTGTTGCGCTCTTGTC
 15 ACTGGGCCCTATGTGATTAGCTTTATCAACTCCTTTGTCAATGTGGTTTGGATGAGCAGAC
 TGCATTTCTGCGACTCAAATGTAGTTCGTCACTTTTTCTGCGACACGTCTCCAATTTTAGCT
 CTGTCTGCTGCATGGACACATACGACATTGAAATCATGATACACATTTTAGCTGGTTCCACCC
 TGATGGTGTCCTTTATCACAATATCTGCATCCTATGTGTCCATTCTCTCTACCATCTGAAA
 ATTAATTCCACTTCAGGAAAGCAGAAAGCTTTGTCTACTTGTGCCTCTCATCTCTGGGAG
 20 TCACCATCTTTTATGGAATATGATTTTTACTTATTTAAAACCAAGAAAGTCTTATTCTTTG
 GGAAGGGATCAAGTGGCTTCTGTTTTTATACTATTGTGATTCCCATGCTGAATCCACTCAT
 TTATAGTCTTAGAAACAAAGAAGTTAAAAATGCTCTCATTAGAGTCATGCAGAGAAGACA
 GGACTCCAGGTAA (SEQ ID NO: 132)

25 **AOLFR72 sequences:**

MAPENFTRVTEFILTGVSSEPELQIPFLVFLVLYGLTMAGNLGITLTSVDSRLQTPMYFFLQHL
 ALINLGNSTVIAPKMLINFLVKKKTTSFYECATQLGGFLFFIVSEVIMLALMACDRYVAICNPLL
 YMVVVSRRCLLLVSLTYLYGFSTAIVVSSYVFSVSYCSSNIINHFCYCDNVPLLALSCSDTYLPE
 TVVFISAATNVVGSLLIIVLSYFNIVLSILKICSEGRKKAFSTCASHMMAVTIFYGTLLFMYVQP
 30 RSNHSLDITDDKMASVFYTLVIPMLNPLIYSLRNKDVKTALQRFMTNLCYSFKTM (SEQ ID NO:
 133)

ATGGCTCCTGAAAATTTACCAGGGTCACTGAGTTTATTCTTACAGGTGTCTCTAGCTGTC
 CAGAGCTCCAGATTCCCCTCTTCCTGGTCTTTCTGGTGCTCTATGGGCTGACCATGGCAGG
 35 GAACCTGGGCATCATCACCTCACCAGTGTGACTCTCGACTTCAAACCCCATGTACTTTT
 TCCTGCAACATCTGGCTCTCATTAACTCTTGGTAACTCTACTGTCATTGCCCTAAAATGCTG
 ATTAACCTTTTAGTAAAGAAGAAACTACCTCATTTCTATGAATGTGCCACCCAACTGGGAG
 GGTCTTGTTCTTTATTGTATCGGAGGTAATCATGCTGGCTTTGATGGCCTGTGACCGCTAT
 GTGGCTATTTGTAACCTCTGCTGTACATGGTGGTGGTGTCTCGGCGGCTCTGCCTCCTGCT
 40 GGTCTCCCTCACATACCTCTATGGCTTTTCTACAGCTATTGTGGTTTCATCTTATGTATTCT
 CTGTGTCTTATTGCTCTTCTAATAATCAATCATTTTTACTGTGATAATGTTCTCTGTTA
 GCATTATCTTGCTCTGATACTTACTTACCAGAAACAGTTGTCTTTATATCTGCAGCAACAA
 ATGTGGTTGGTTCCCTGATTATAGTTCTAGTATCTTATTTCAATATTGTTTTGTCTATTTTA
 AAAATATGTTTCATCAGAAGGAAGGAAAAAGCCTTTTCTACCTGTGCTTCACATATGATGG
 45 CAGTCACAATTTTTATGGGACATTGCTATTCTATGTATGTGCAGCCCCGAAGTAACCATT
 ATTGGATACTGATGATAAGATGGCTTCTGTGTTTACACGTTGGTAATTCCTATGCTGAAT
 CCCTTGATCTACAGCCTGAGGAATAAGGATGTGAAGACTGCTCTACAGAGATTCATGACA
 AATCTGTGCTATTCCTTTAAACAATGTAA (SEQ ID NO: 134)

50 **AOLFR73 sequences:**

MNHVVKHNHTAVTKVTEFILMGITDNPGLQAPLFLGLIYLVTVIGNLGMVILTYLDSKLHTP
 MYFFLRHLSITDLGYSTVIAPKMLVNFIVHKNTISYNWYATQLAFFEIFIISLFIISAMAYDRYV
 AICKPLLYVIMAEKVLWVLVIVPYLYSTFVSLFTIKLFKLSFCGSNIISYFYCDCIPLMSILCSDT
 NELELILIFSGCNLLFSLSVLISYMFILVAILRMNSRKGRYKAFSTCSSHLTVVIMFYGTLLFIYL
 55 QPKSHTLAIDKMASVFYTLIPMLNPLIYSLRNKEVKDALKRTLNRFKIPI (SEQ ID NO: 135)

ATGAATCATGTGGTAAAACACAATCACACGGCAGTGACCAAGGTGACTGAATTTATTCTCA
 TGGGGATTACAGACAACCCTGGGCTGCAGGCTCCACTGTTTGGACTCTTCCTCATCATATA
 TCTGGTACAGTGATAGGCAATCTGGGCATGGTTATCTTGACCTACTTGGACTCCAAGCTA
 CACACCCCATGTACTTTTCTTAGACATTTGTCAATCACTGATCTTGGTTACTCCACTGT
 5 CATTGCCCGAAGATGTTAGTAACTTCATAGTGCACAAAAACACAATTTCTTACAATTGG
 TATGCCACTCAGCTAGCATTCTTGAGATTTTCATCATCTCTGAGCTCTTTATTCTATCAGC
 AATGGCCTATGATCGCTACGTAGCCATCTGTAAACCTCTTCTGTACGTGATCATCATGGCA
 GAGAAAGTACTTTGGGTGCTGGTAATTGTTCCCTATCTCTATAGCACGTTTGTGTCACTATT
 TCTCACAATTAAGTTATTTAACTGTCCCTCTGTGGCTCAAACATAATCAGCTATTTTACT
 10 GTGACTGTATCCCTCTGATGTCCATACTCTGTTCTGACACAAATGAATTAGAATTAATAAT
 TTTGATCTTCTCAGGCTGTAATTTGCTCTTCTCCCTCTCAATTGTTCTCATATCCTACATGTT
 TATTCTAGTGGCATTCTCAGAATGAACCTCAAGGAAAGGGAGGTACAAAGCCTTCTCCACC
 TGTAGCTCTCATCTGACAGTGGTGATCATGTTCTATGGGACATTGTTATTTATTTACTTGCA
 ACCCAAGTCCAGTCATACTTTGGCTATTGATAAAATGGCCTCAGTGTTTTATACCCTGTTG
 15 ATTCCTATGCTGAATCCGTTGATCTACAGCCTAAGGAACAAAGAAGTAAAAGATGCTCTAA
 AGAGAACTTTAACCAATCGATTCAAAATTCCCATTTAA (SEQ ID NO: 136)

AOLFR74 sequences:

MEQHNLTTVNEFILTGITDIAELQAPLFALFLMYVISVMGNLGMIVLTKLDSRLQTPMYFFLRH
 20 LAFMDLGYSTTVGPKMLVNFVVDKNIISYFCATQLAFFLVFIGSELFILSAMSVDLYVAICNPL
 LYTVIMSRRCVQLVAIPYLYCTFISLLVTIKIFLSFCGYNVISHFYCDLPLPLCSNTHIEILI
 ILFAAIDLISLLIVLLSYLLLVAILRMNSAGRQKAFSTCGAHLTVVIVFYGTLLFMYVQPKSSH
 SFDTDKVASIFYTLVIPMLNPLIYSLRNKDKYALRRTWNNLCNIFV (SEQ ID NO: 137)

25 ATGGAACAACACAATCTAACAACGGTGAATGAATTCATTCTTACGGGAATCACAGATATC
 GCTGAGCTGCAGGCACCATTATTTGCATTGTTCCCTCATGATCTATGTGATCTCAGTGATGG
 GCAATTTGGGCATGATTGTCCTACCAAGTTGGACTCCAGGTTGCAAACCCCTATGTACTT
 TTTTCTCAGACATCTGGCTTTTCATGGATCTTGGTTATTCAACAACTGTGGGACCCAAAATG
 TTAGTAAATTTTGTGTGGATAAGAATATAATTTCTTATTATTTTGTGCAACACAGCTAGC
 30 TTTCTTTCTTGTGTTTATTGGTAGTGAACCTTTTATTCTCTCAGCCATGTCCTACGACCTCT
 ATGTGGCCATCTGTAACCCCTCTGCTATACACAGTAATCATGTACGAAGGGTATGTCAGGT
 GCTGGTAGCAATCCCTTACCTCTATTGCACATTCATTCTCTCTAGTCACCATAAAGATTT
 TTAATTTATCCTTCTGTGGCTACAACGTCATTAGTCATTTCTACTGTGACAGTCTCCCTTG
 TTACCTTTGCTTTGTTCAAATACACATGAAATTGAATTGATAATTCTGATCTTTGCAGCTAT
 35 TGATTTGATTTTCATCTCTTCTGATAGTTCTTTTATCTTACCTGCTCATCCTTGTAGCCATTCT
 CAGGATGAATTCTGCTGGCAGACAAAAGGCTTTTCTACCTGTGGAGCCACCTGACAGTG
 GTCATAGTGTCTATGGGACTTTGCTTTTCATGTACGTGCAGCCCAAGTCCAGTCATTCCCTT
 TGACACTGATAAAGTGGCTTCCATATTTTACACCCTGGTTATCCCATGTTGAATCCCTTGA
 TCTATAGTTTACGAAACAAAGATGTAAATATGCCCTACGAAGGACATGGAATAACTTATG
 40 TAATATTTTGTTTAA (SEQ ID NO: 138)

AOLFR75 sequences:

MEGKNQTNISEFLLGFSSWQQQVLLFALFLCLYLTLGLFGNLLILLAIGSDHCLHTPMYFFLA
 NLSLVDLCLPSATVPKMLLNITQTQTISYPGCLAQMYFCMMFANMDNFLTVMAYDRYVAI
 45 CHPLHYSTIMALRLCASLVAAPWVIAILNPLLHTLMMMAHLHFCSDNVIHFFCDINSLPLSCSD
 TSLNQLSVLATVGLFVVPVSVCLVSYLIVSAVMKVPSAQGKLFKAFSTCGSHLALVILFYGANT
 GVYMSPLSNHSTEKDSAASVIFMVVAPVLNPFYISLRNNELKGTLLKKTLSRPGAVAHACNPSTL
 GGRGGWIMRSGDRDHPG (SEQ ID NO: 139)

50 ATGGAAGGGAAAAATCAAACCAATATCTCTGAATTTCTCCTCCTGGGCTTCTCAAGTTGGC
 AACAACAGCAGGTGCTACTCTTTGCACTTTTCTGTGTCTCTATTAAACAGGGCTGTTTGA
 AACTTACTCATCTTGTGGCCATTGGCTCGGATCACTGCCTTCACACACCCATGTATTTCTT
 CCTTGCCAACTCTGCTTGGTAGACCTCTGCTTCCCTCAGCCACAGTCCCCAAGATGCTAC
 TGAACATCCAAACCCAAACCCAAACCATCTCCTATCCCGGCTGCCTGGCTCAGATGTATTT
 55 CTGTATGATGTTTGCCAATATGGACAATTTTCTTCTCACAGTGATGGCATATGACCGTTAC
 GTGGCCATCTGTACCCTTTACATTACTCCACCATTATGGCCCTGCGCCTCTGTGCTCTCT

GGTAGCTGCACCTTGGGTCATTGCCATTTTGAACCCTCTCTTGACACTCTTATGATGGCCC
 ATCTGCACCTTCTGCTCTGATAATGTTATCCACCATTTCTTCTGTGATATCAACTCTCTCCTC
 CCTCTGTCTGTTCCGACACCAGTCTTAATCAGTTGAGTGTCTGGCTACGGTGGGGCTGA
 TCTTTGTGGTACCTTCAGTGTGTATCCTGGTATCCTATATCCTCATTGTTTCTGCTGTGATG
 5 AAAGTCCCTTCTGCCCAAGGAAAACCAAGGCTTTCTCTACCTGTGGATCTCACCTTGCCTT
 GGTCACTTCTTTTCTATGGAGCAAACACAGGGGTCTATATGAGCCCCTTATCCAATCACTCT
 ACTGAAAAAGACTCAGCCGCATCAGTCATTTTTATGGTTGTAGCACCTGTGTTGAATCCAT
 TCATTTACAGTTTAAGAAACAATGAAGTGAAGGGGACTTTAAAAAAGACCCTAAGCCGGC
 CGGGCGCGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCA
 10 TGAGGTCAGGAGATCGAGACCATCCTGGCTAA (SEQ ID NO: 140)

AOLFR76 sequences:

MENNTEVSEFILLGLTNAPELQVPLFIMFTLIYLITLTGNLGMILLDDSHLHTPMYFFLSNLSLA
 GIGYSSAVTPKVLTLGLIEDKAISYSACAAQMFFCAVFATVENYLLSSMAYDRYAAVCNPLHY
 15 TTTMTTRVCACLAIGCYVIGFLNASIQIGDTFRLSFCMSNVIIHFFCDKPAVITLTCSEKHISELIL
 VLISSENVFFALLVTLISYLFILITILKRHTGKGYQKPLSTCGSHLIAIFLYITVIIMYIRPSSSHSM
 DTDKIASVFYTMIPMLSPIVYTLRNKDVKNAFMKVVEKAKYSLDSVF (SEQ ID NO: 141)

ATGGAGAATAATACAGAGGTGAGTGAATTCATCCTGCTTGGTCTAACCAATGCCCCAGAA
 20 CTACAGGTTCCCTCTTTATCATGTTTACCCTCATCTACCTCATCACTCTGACTGGGAACCT
 GGGGATGATCATATTAATCCTGCTGGACTCTCATCTCCACACTCCCATGTACTTTTTCTCA
 GTAACCTGTCTCTTGCAGGCATTGGTTACTCCTCAGCTGTCACTCCAAAGGTTTAACTCG
 GTTGCTTATAGAAGACAAAGCCATCTCCTACAGTGCCTGTGCTGCTCAGATGTTCTTTGT
 GCAGTCTTTGCCACTGTGGAAAATTACCTCTTGTCTCAATGGCCTATGACCGCTACGCAG
 25 CAGTGTGTAAACCCCTACATTATACCACCACCATGACAACACGTGTGTGTGCTTGTCTGGC
 TATAGGCTGTTATGTCATTGGTTTTCTGAATGCTTCTATCCAAATTGGAGATACATTTCCGC
 TCTCTTTCTGCATGTCCAATGTGATTATCACTTTTTCTGTGACAAACCAGCAGTCATTACT
 CTGACCTGCTCTGAGAAACACATTAGTGAGTTGATTCTTGTCTTATATCAAGTTTAAATGT
 CTTTTTGCACCTTCTTGTACCTTGATTTCCTATCTGTTTCATATTGATCACCATTCTTAAGAG
 30 GCACACAGGTAAGGGATACCAGAAGCCTTTATCTACCTGTGGTTCTCACCTCATTGCCATT
 TTCTTATTTTATATAACTGTCATCATCATGTACATACGACCAAGTTCCAGTCATTCCATGGA
 CACAGACAAAATTGCATCTGTGTTCTACACTATGATCATCCCCATGCTCAGTCCTATAGTCT
 ATACCCTGAGGAACAAAGACGTGAAGAATGCATTATGAAGGTTGTTGAGAAGGCAAAAT
 ATTCTCTAGATTCACTCTTTAA (SEQ ID NO: 142)

AOLFR77 sequences:

MGDVNQSVASDFILVGLFSHSGSRQLLFSLVAVMFVIGLLGNTVLLFLIRVDSRLHTPMYFLLS
 QLSLFDIGCPMVTIPKMASDFLRGEGATSYGGGAAQIFFLTLMGVAEGVLLVMSYDRYVAVC
 QPLQYPVLMRRQVCLLMGSSWVGVNLASIQTSITLHFPYCASRIVDHFCEVPALLKLSA
 40 DTCAYEMALSTSGVLILMLPLSLIATSYGHVLAFLSMRSEEARHKAVTTCSSHITVVGIFYGA
 AVFMYMVPCAYHSPQQDNVVSIFYSLVTPTLNPLIYSLRNPEVWMAVVKVLSRAGLRQMC
 (SEQ ID NO: 143)

ATGGGGGATGTGAATCAGTCGGTGGCCTCAGACTTCATTCTGGTGGGCCTCTTCAGTCACT
 45 CAGGATCACGCCAGCTCCTCTTCTCCCTGGTGGCTGTCATGTTTGCATAGGCCTTCTGGGC
 AACACCGTTCTTCTCTTCTTGATCCGTGTGGACTCCCGGCTCCACACACCCATGTACTTCT
 GCTCAGCCAGCTCTCCCTGTTTGACATTGGCTGTCCCATGGTCACCATCCCCAAGATGGCA
 TCAGACTTTCTGCGGGGAGAAGGTGCCACCTCCTATGGAGGTGGTGCAGCTCAAATATTCT
 TCCTCACACTGATGGGTGTGGCTGAGGGCGTCTGTTGGTCCTCATGTCTTATGACCGTTA
 50 TGTGCTGTGTGCCAGCCCCTGCAGTATCCTGTACTTATGAGACGCCAGGTATGTCTGCTG
 ATGATGGGCTCCTCCTGGGTGGTAGGTGTGCTCAACGCCTCCATCCAGACCTCCATCACCC
 TGCATTTTCCCTACTGTGCCTCCCGTATTGTGGATCACTTCTTCTGTGAGGTGCCAGCCCTA
 CTGAAGCTATCCTGTGCAGATACCTGTGCCTACGAGATGGCGCTGTCCACCTCAGGGGTGC
 TGAACCTAATGCTCCCTCTTTCCCTCATCGCCACCTCCTACGGCCACGTGTTGCAGGCTGTT
 55 CTAAGCATGCGCTCAGAGGAGGCCAGACACAAGGCTGTACCCACCTGCTCCTCGCACATCA
 CGGTAGTGGGGCTCTTTATGGTGGCGCCGTGTTTCATGTACATGGTGCCTTGGCGCTACCA

CAGTCCACAGCAGGATAACGTGGTTTCCCTCTTCTATAGCCTTGTCAACCCCTACACTCAAC .
CCCCTTATCTACAGTCTGAGGAATCCGAGGTGTGGATGGCTTTGGTCAAAGTGCTTAGCA
GAGCTGGACTCAGGCAAATGTGCTGA (SEQ ID NO: 144)

5 **AOLFR78 sequences:**

MSPDGNHSSDPTEFVLAGLPNLSARVELFSVFLVYLLNLTGNVLIVGVVRADTRLQTPMYF
FLGNLSCLEILLTSVIIPKMLSNFLSRQHTISFAACTQFYFYFLGASEFLLAVMSADRYLAICH
PLRYPLLMSGAVCFRVALACWVGGLVPVLGPTVAVALLPFCKQGAVVQHFFCDSGPLRLAC
TNTKKLEETDFVLASLVVSSLLITAVSYGLIVLAVLSIPSASGRQKAFSTCTSHLIVVTLFYGSAI
10 FLYVRPSQSGSVDTNWAVTVITTFVTPLNPFYIALRNEQVKEALKDMFRKVAVGLGNLLD
KCLSEKAVK (SEQ ID NO: 145)

ATGAGTCCTGATGGGAACACAGTAGTGATCCAACAGAGTTCGTCCTGGCAGGGCTCCCA
AATCTCAACAGCGCAAGAGTGGAATTATTTTCTGTGTTTCTTCTGTCTATCTCCTGAATCT
15 GACAGGCAATGTGTTGATTGTGGGGGTGGTAAGGGCTGATACTCGACTACAGACCCCTAT
GTACTTCTTTCTGGGTAACCTGTCCTGCCTAGAGATACTGCTCACTTCTGTCATCATTCCAA
AGATGCTGAGCAATTTCTCTCAAGGCAACACACTATTTCTTTGCTGCATGTATCACCCA
ATTCTATTTCTACTTCTTTCTCGGGGCTCCGAGTCTTACTGTTGGCTGTCATGTCTGCGG
ATCGCTACCTGGCCATCTGTCATCCTCTGCGCTACCCCTTGCTCATGAGTGGGGCTGTGTG
20 CTTTCGTGTGGCCTTGGCCTGCTGGGTGGGGGGACTCGTCCCTGTGCTTGGTCCCACAGTG
GCTGTGGCCTTGCTTCTTTCTGTAAGCAGGGTGCTGTGGTACAGCACTTCTTCTGCGACA
GTGGCCCACTGCTCCGCTGGCTTGACCAACACCAAGAAGCTGGAGGAGACTGACTTTGT
CTGGCCTCCCTCGTCATTGTATCTTCTTCTGCTGATCACTGCTGTGTCCTACGGCCTCATTG
TGCTGGCAGTCTGAGCATCCCCTCTGCTTACAGGCCGTCAGAAGGCCTTCTCTACCTGTAC
25 CTCCCACTTGATAGTGGTGACCCTCTTCTATGGAAGTGCCATTTTCTCTATGTGCGGCCAT
CGCAGAGTGGTTCTGTGGACACTAACTGGGCAGTGACAGTAATAACGACATTGTGACAC
CACTGTTGAATCCATTCTATGCTTACGTAATGAGCAAGTCAAGGAAGCTTTGAAGGA
CATGTTTAGGAAGGTAGTGGCAGGCGTTTAGGGAATCTTTACTTGATAAATGTCTCAGT
GAGAAAGCAGTAAAGTAA (SEQ ID NO: 146)

30

AOLFR79 sequences:

MTPGELALASGNHTPVTKFILQGFSNYPDLQELLFGAILLIYAITVVGNLGMMLIFTDSHLQSP
MYFFLNVL SFLDICYSSVTPKLLVNFLVSDKSISFEGCVVQLAFFVHVTAESFLLASMAYDR
FLAICQPLHYGSIMTRGTCLQLVAVSYAFGGANSIAIQTGNVFALPFCGPNQLTHYYCDIPLLH
35 LACANTATARVVLVYVSALVLLPAAVILTSYCLVLVAIGRMRSVAGREKDLSTCASHFLAIAI
FYGTVVFTYVQPHGSTNNTNGQVVSFVYTHIIPMLNPFYISLRNKEVKGALQRKLQVNIFFP
(SEQ ID NO: 147)

ATGACACCTGGAGAACTAGCCCTTGCCAGTGGAACCAACCCCAAGTTCATCT
40 TGCAGGGATTCTCCAATTATCCAGACCTCCAGGAGCTTCTCTTCGGAGCCATCCTGCTCAT
CTATGCCATAACAGTGGTGGGCAACTTGGGAATGATGGCACTCATCTTCACAGACTCCCAT
CTCCAAAGCCCAATGTATTTCTTCTCAATGTCCTCTCGTTTCTTGATATTTGTTACTCTTCT
GTGGTCACACCTAAGCTCTTGGTCAACTTCCCTGGTCTCTGACAAGTCCATCTCTTTTGAGG
GCTGTGTGGTCCAGCTCGCCTTCTTTGTAGTGCAATGTGACAGCTGAGAGCTTCTGCTGGC
45 CTCCATGGCCTATGACCGCTTCTAGCCATCTGTCAACCCCTCCATTATGGTTCTATCATGA
CCAGGGGGACCTGTCTCCAGCTGGTAGCTGTGTCTATGCATTGGTGGAGCCAACTCCGC
TATCCAGACTGGAAATGTCTTTGCCCTGCCTTTCTGTGGGCCCAACAGCTAACACACTAC
TACTGTGACATAACACCCCTTCTCCACCTGGCTTGTGCCAACACAGCCACAGCAAGAGTGG
TCCTCTATGTCTTTCTGCTCTGGTCAACCTTCTGCCTGCTGCAGTCATTCTCACCTCCTACT
50 GCTTGGTCTTGGTGGCCATTGGGAGGATGCGCTCAGTAGCAGGGAGGGAGAAGGACCTCT
CCACTTGTGCCTCCCACTTTCTGGCCATTGCCATTTCTATGGCACTGTGGTTTTACACCTAT
GTTTCAGCCCCATGGATCTACTAACAATACCAATGGCCAAGTAGTGTCCGTCTTCTACACCA
TCATAATTCCCATGCTCAATCCCTTCTATATAGCCTCCGCAACAAGGAGGTGAAGGGCGC
TCTGCAGAGGAAGCTTACAGGTCAACATCTTTCCCGGCTGA (SEQ ID NO: 148)

55

AOLFR80 sequences:

MEGINKTAKMQFFRPFSPDPEVQMLIFVFLMMYLTSLGGNATIAVIVQINHSHTPMYFFLA
 NLAVLEIFYTSITPLALANLLSMGKTPVSITGCGTQMFFVFLGGADCVLLVVMAYDRFIAICH
 PLRYRLMSWSLVCVELLVGSLVLGFLLSLPLTILIFHLFPCHNDEIYHFYCDMPAVMRLACADTR
 5 VHKTALYIISFIVLSIPLSLISISYVFIVAILRIRSAEGRQAYSTCSSHLVLLQYGCTSFTYLSPS
 SSSPEMGRVVSVAYTFTIPILNPLIYSLRNKELKDALRKALRKF (SEQ ID NO: 149)

ATGGAAGGAATAAATAAACTGCAAAGATGCAGTTTTTCTTTCTGTCATTCTCACCTGACC
 CTGAGGTCCAGATGCTGATTTTTGTGGTCTTCCTGATGATGATCTGACCAGCCTCGGTGG
 10 AAATGCTACAATTGCAGTCATTGTTTCAGATCAATCATTCCCTCCACACCCCATGTACTTTT
 TCCTGGCTAATCTGGCAGTTCTAGAAATCTTCTATACATCTTCCATCACCCCATTTGGCCTTG
 GCAAACCTCCTTTCAATGGGCAAAACTCCTGTTTCCATCACGGGATGTGGCACCCAGATGT
 TTTTCTTTGTCTTCTTGGGTGGGGCTGATTGTGTCTGCTGGTAGTCATGGCTTATGACCGG
 TTTATAGCGATCTGTACCCCTCTGCGATACAGGCTCATCATGAGCTGGTCTTGTGTGTGG
 15 AGCTGCTGGTAGGCTCCTTGGTGTGGGGTTCCTGTTGTCACTGCCACTCACCATTTTAATC
 TTCCATCTCCCATTTCTGCCACAATGATGAGATCTACCACTTCTACTGTGACATGCCTGCAGT
 CATGCGCTGGCTTGTGCAGACACACGCGTTCACAAGACTGCTCTGTATATCATCAGCTTC
 ATCGTCCTTAGCATCCCCCTCTCATTGATCTCCATCTCCTATGTCTTCATCGTAGCCAT
 TTTACGGATCCGGTCAGCAGAAGGGCGCCAGCAAGCCTACTCTACCTGCTCTTCTCACATC
 20 TTAGTGGTCCCTCCTGCAATGCTGACCAAGCTTTATATACTTGTCCCCAGTTCCAGCTA
 CTCTCCTGAGATGGGCGGGTGGTATCTGTGGCCTACACATTTATCACTCCCATTTTAAAC
 CCCTTGATCTATAGTTTGAGGAACAAGGAAGTGAAGATGCCCTAAGGAAAGCATTGAGA
 AAATTCTAG (SEQ ID NO: 150)

25 **AOLFR81 sequences:**

MGVKNHSTVTEFLSGLTEQABLQPLFLFLGIYTVTVVGNLSMISIIRLNRLHTPMYYFLSS
 LSFLDFCYSSVITPKMMKLWMESHLIVPETRPSFRMMSNQTLVTEFILQGFSEHPEYRVFLFSCF
 LFLYSGALTGNVLITLAITFNPGLHAPMYFFLLNLATMDIICTSSIMPKALASLVSEESSISYGGC
 MAQLYFLTWAASSELLLLTVMAYDRYAAICHPLHYSSMMSKVFCGLATAVWLLCAVNTAIH
 30 TGLMLRLDFCGPNVHHFCEVPPLLLSCSSTYVNGVMIVLADAFYGIVNFMITIASYGFIVSSI
 LKVKTAWGRQKAFSTCSSHLTVVCMYYTAVFYAYISPVSGYSAGKSKLAGLLYTVLSPTLNPL
 IYTLRNKEVKAALRKLFPFFRN (SEQ ID NO: 151)

ATGAAGCTGTGGATGGAGAGTCACCTGATAGTCCAGAAACCCGTCCCAGCCCAAGGATG
 35 ATGAGTAACCAGACGTTGGTAACCGAGTTCATCCTGCAGGGCTTTTCGGAGCACCCAGAAT
 ACCGGGTGTTCTTATTACAGCTGTTTCTCTTCTACTCTGGGGCCCTCACAGGTAATGTC
 CTCATCACCTTGGCCATCACGTTCAACCCTGGGCTCCACGCTCCTATGTACTTTTTCTTACT
 CAACTTGGCTACTATGGACATTATCTGCACCTCTTCCATCATGCCCAAGGCGTGGCCAGT
 CTGGTGTCCGAAGAGAGCTCCATCTCCTACGGGGGCTGCATGGCCCAGCTCTATTCTCA
 40 CGTGGGCTGCATCCTCAGAGCTGCTGCTCCTCACGGTCATGGCCTATGACCGGTACGCAGC
 CATCTGCCACCCGCTGCATTACAGCAGCATGATGAGCAAGGTGTTCTGCAGCGGGCTGGCC
 ACAGCCGTGTGGCTGCTCTGCGCCGTCAACACGGCCATCCACACGGGGCTGATGCTGCGCT
 TGGATTTCTGTGGCCCCAATGTCAATTATCCATTTCTTCTGCGAGGTCCCTCCCCTGCTGCTT
 CTCTCCTGCAGCTCCACCTACGTCAACGGTGTGATGATTGTCTGGCGGATGCTTTCTACG
 45 GCATAGTGAACCTTCTGATGACCATCGCGTCTATGGCTTCATCGTCTCCAGCATCCTGAA
 GGTGAAGACTGCCTGGGGGAGGCAGAAAGCCTTCTCCACCTGCTCTCCACCTCACCGTG
 GTGTGCATGTATTACACCGCTGTCTTCTACGCCTACATAAGCCCGGTCTCTGGCTACAGCG
 CAGGGAAGAGCAAGTTGGCTGGCCTGCTGTACACTGTGCTGAGTCTACCTCAACCCCT
 CATCTATACTTTGAGAAACAAGGAGGTCAAAGCAGCCCTCAGGAAGCTTTTCCCTTTCTTC
 50 AGAAATTAA (SEQ ID NO: 152)

AOLFR82 sequences:

MQLNNNVTEFILLGLTQDPFWKKIVFVIFLRLYLGTLLGNLLHISVKASQALKNPMMFFLFYLSL
 SDTCLSTSIAPRMIVDALLKKTTSFSECMIQVFSSHVFGCLEIFILITAVDRYVDICKPLHYMTII
 55 SQWVCGVLMMAVAWVGSCVHSLVQIFLALSPLFCGPNVINHCFCDLQPLLKQACSETYVNNLL

VNSNGAICAVSYVMLIFSIVFLHSLRNHSAEVIKKALSTCVSHIIVVILFFGPCIFMYTCPATVFP
MDKMIAVFYTVGTSFLNPVIYTLKNTEVKSAMRKLWSKKLITDDKR (SEQ ID NO: 153)

5 ATGCAACTGAATAATAATGTGACTGAGTTCATTCTGCTTGGATTGACACAGGATCCTTTTT
GGAAGAAAATAGTGTGTTGTTATTTTTTTCGCTCTCTACTTGGGAACACTGTTGGGTAATTT
GCTAATCATTATTAGTGTCAAGGCCAGCCAGGCACTTAAGAACCCAATGTTCTTCTCCTT
TTCTACTTATCTTTATCTGATACTTGCTCTCTACTTCCATAGCCCCCTAGAATGATTGTGGA
TGCCCTTTTGAAGAAGACAACATCTCCTTCAGCGAGTGCATGATCCAAGTCTTTTCATCC
10 CATGTCTTTGGCTGCCTGGAGATCTTCATCCTCATCCTCACGGCTGTTGACCGCTATGTGGA
CATCTGTAAGCCCCCTGCACTACATGACCATCATAAGCCAGTGGGTCTGTGGTGTGTTTGATG
GCTGTGGCCTGGGTGGGATCCTGTGTGCATTCTTTAGTTCAGATTTTTCTTGCCCTGAGTTT
GCCATTCTGTGGCCCCAATGTGATCAATCACTGTTTCTGTGACTTGCAGCCCTTGTGAAA
CAAGCCTGTTCAGAAACCTATGTGGTTAACTACTCCTGGTTTCCAATAGTGGGGCCATTT
GTGCAGTGAGTTATGTCATGCTAATATTCTCCTATGTCATCTTCTTGCAATTCTGTGAGAAAC
15 CACAGTGTGAGTGATAAAGAAAGCACTTCCACATGTGTCTCCACATCATTGTGGGTCA
TCTTGTTCTTTGGACCTTGCAATTTATGTACACATGCCCTGCAACCGTATTCCCCATGGAT
AAGATGATAGCTGTATTTTATACAGTTGGAACATCTTTTCTCAACCTGTGATTTACACGCT
GAAGAATACAGAAGTGAAAAGTGCCATGAGGAAGCTTTGGAGCAAGAAATTGATCACAGA
TGACAAAAGATAA (SEQ ID NO: 154)

20

AOLFR83 sequences:

MGNWTAADVTEFVLLGFSLSREVELLLLVLPTFLLTLGNLLIISTVLSCSRLHTPMYFFLCNL
SILDILFTSVISPKVLANLGSRDKTISFAGCITQCYFYFFLGTVEFLLLTVMYSDRYATICPLRYT
TIMRPSVCIGTVVFSWVGFLSVLFPTILISQLPFCGSNIINHFFCDSPLLALACADTTAIELMDF
25 MLSSMVILCCTVLVAYSYTYILTIVRIPSASGRKKAFTNCASHLTIVIPSIGTVFIYVTPSQKEYL
EINKIPLVLSSVTPFLNPFYTLRNDTVQGVLRDVWVRVRGVFEKRMRAVLRSLSSNKDHQ
GRACSSPPCVYSVKLQC (SEQ ID NO: 155)

30 ATGGGTAAGTGGACTGCAGCGGTGACTGAGTTTGTCTGCTGGGGTTTTCCCTGAGCAGGG
AGGTGGAGCTGCTGCTCCTGGTGCTCCTGCTGCCACGTTCTGCTGACTCTTCTGGGGAA
CCTGCTCATCATCTCCACTGTGCTGCTGCTCCCGCCTCCACACCCCATGTACTTCTTCT
TGTGCAACCTCTCTATCCTGGACATCCTCTTACCTCAGTCATCTCTCCAAAAGTGTGGCC
AACTTAGGATCTAGGGATAAAACCATCTCCTTTGCCGGATGTATCACCCAGTGCTATTTCT
ACTTTTTCTTGGGCACAGTTGAGTTCTCCTGCTGACGGTCATGTCCTATGACCGTTATGCC
35 ACCATCTGCTGCCCCCTGCGGTACACCACCATCATGAGACCTTCTGTCTGCATTGGGACCG
TTGTATTCTCTTGGGTGGGAGGCTTCTGTCTGTGCTCTTTCCAACCATCCTCATCTCCAG
CTGCCCTTCTGTGGCTCCAATATCATTAACCACTTCTTCTGTGACAGTGGACCTTGTGGC
CCTGGCCTGTGCAGACACCACTGCCATCGAGCTGATGGATTTTATGCTTTCTTCCATGGTC
ATCCTCTGCTGCATAGTCTCGTGGCCTATTCTTATACGTACATCATCTTGACCATAGTGCG
40 CATTCTTCTGCAAGTGGAAGGAAGAAGGCCTTTAATACCTGTGCTTCCACCTGACCATA
GTCATCATTCTAGTGGCATCACTGTGTTTATCTATGTGACTCCCTCCCAGAAAGAATATCT
GGAGATCAACAAGATCCCTTTGGTTCTGAGCAGTGTGGTGACTCCATTCTCAACCCCTTT
ATATATACTCTGAGGAATGACACAGTGCAGGGAGTCCCTCAGGGATGTGTGGGTCAGGGTT
CGAGGAGTTTTTGAAGAAGAGGATGAGGGCAGTGTGAGAAGCAGATTATCCTCCAACAAA
45 GACCACCAAGGAAGGCTTGCTCTTCTCCACCATGTGTCTATTCTGTAAAGCTCCAGTGTT
AG (SEQ ID NO: 156)

AOLFR85 sequences:

50 MGAKNNVTEFVLFLGFESREMQHTCFVFFLFHVLTVLGNLLVIITINARKTLKSPMYFFLSQL
SFADICYPSTTIPKMIADTFVEHKIISFNGCMTQLFSAHFFGGTEIFLLTAMAYDRYVAICRPLHY
TAIMDCRKCGLLAGASWLAGFLHSILQTLTVQLPFCGPNEIDNFFCDVHPLLKLACADTYMV
GLIVVANSGMISLASFFILISYVILLNLRQSSED RRKAVSTCGSHVITVLLVLMPPMFMYIRPS
TTLAADKLIILFNIVMPPLNPLIYTLRNNNDVKNAMRKLFVRKSLGEK (SEQ ID NO: 157)

55 ATGGGTGCCAAGAACAATGTGACTGAGTTTGTGTTTATTTGGCCTTTTTGAGAGCAGAGAGA
TGCAGCATACATGCTTTGTGGTATTCTTCTCTTTCATGTGCTCACTGTCCTGGGGAACCTT

CTGGTCATCATCACCATCAATGCTAGAAAGACCCTGAAGTCTCCCATGTATTTCTTCCTGA
 GCCAGTTGTCTTTTGTGACATATGTTATCCATCCACTACCATAACCAAGATGATTGCTGAC
 ACTTTTGTGGAGCATAAGATCATCTCCTTCAATGGCTGCATGACCCAGCTCTTTTCTGCCCA
 CTTCTTTGGTGGCACTGAGATCTTCCTCCTTACAGCCATGGCCTATGACCGCTATGTGGCC
 5 ATCTGTAGGCCCTGCACTACACAGCCATCATGGATTGCCGGAAGTGTGGCCTGCTAGCGG
 GGGCCTCCTGGTTAGCTGGCTTCCTGCATTCCATCCTGCAGACCCTCCTCACGGITCAGCTG
 CCTTTTGTGGGCCCAATGAGATAGACAACITCTTCTGTGATGTTTCATCCCCCTGCTCAAGTT
 GGCCTGTGCAGACACCTACATGGTAGGTCTCATCGTGGTGGCCAACAGCGGTATGATTTCT
 TTAGCATCCTTTTTATCCTTATCATTTCCTATGTTATCATCTTACTGAACCTAAGAAGCCA
 10 GTCATCTGAGGACCGCGTAAGGCTGTCTCCACATGTGGCTCACACGTAATCACTGTCTT
 TTGGTTCTCATGCCCCCATGTTTCATGTACATTCGTCCCTCCACCACCCTGGCTGCTGACAA
 ACTTATCATCCTCTTTAACATTGTGATGCCACCTTTGCTGAACCCTTTGATCTATACACTAA
 GGAACAACGATGTGAAAAATGCCATGAGGAAGCTGTTTAGGGTCAAGAGGAGCTTAGGGG
 AGAAGTGA (SEQ ID NO: 158)

15

AOLFR86 sequences:

MQLVLLLMFLLVFIGNTAPAFSVTLESMDIPQNITEFFMLGLSQNSEVQRVLFVVFLLIYVVTVC
 GNMLIVVTTTSSPTLASPVYFFLANLSFIDTFYSSSMAPKLIADSLYEGRTISYECCMAQLFGAHF
 LGGVEIILLTVMAYDRYVAICKPLHNTTIMTRHLCAMLVGVAWLGGFLHSLVQLLLVLWLPFC
 20 GPNVINHFACDLYPLLEVACTNTYVIGLLVVANSGLICLLNFMMLAASYIVILYSLRSHSADGRC
 KALSTCGAHFIVVALFFVPCIFTYVHPFSTLPIDKNMALFYGILTPMLNPLIYTLRNBVEVKAMR
 KLFTW (SEQ ID NO: 159)

ATGCAATTAGTTCTATTACTTATGTTTCTCCTTGTCTTTATAGGCAATACTGCACCTGCATT
 25 CTCAGTGACCTTGGAACTCTATGGACATACCACAAAATATCACAGAATTTTTCATGCTGGGG
 CTCTCACAGAACTCAGAGGTACAGAGAGTTCTCTTTGTGGTCTTTTGTGATCTATGTGG
 TCACGGTTTGTGGCAACATGCTCATTGTGGTCACTATCACCTCCAGCCCCACGCTGGCTTC
 CCCTGTGTATTTTTCTGGCCAACCTATCCTTTATTGACACCTTTTATTCTTCTTCTATGGC
 TCCTAAACTCATTGCTGACTCATTGTATGAGGGGAGAACCATCTCTTATGAGTGCTGCATG
 30 GCTCAGCTCTTTGGAGCTCATTTTTGGGAGGTGTTGAGATCATTCTGCTCACAGTGATGG
 CTTATGACCGCTATGTGGCCATCTGTAAGCCCCTGCACAATACTACCATCATGACCAAGGCA
 TCTCTGTGCCATGCTTGTAGGGGTGGCTTGGCTTGGGGGCTTCTGCACTTCATTGGTTTCAG
 CTCTCCTGGTCCTTTGGTTGCCCTTCTGTGGGCCCAATGTGATCAATCACTTTGCCTGTGA
 CTTGTACCTTTTGTGGAAGTTGCCTGCACCAATACGTATGTCACTGGTCTGCTGGTGGTT
 35 GCCAACAGTGGTTTAATCTGCCTGTTGAACCTCCTCATGCTGGCTGCCTCCTACATTGTCTAT
 CCTGTACTCCTTGAGGTCCCACAGTGCAGATGGGAGATGCAAAGCCCTCTCCACCTGTGGA
 GCCCCATTCACTGTGTGCTTGTCTTTGTGCCCTGTATATTTACTTATGTGCATCCATT
 TCTACTTTACCTATAGACAAAAATATGGCATTATTTTATGGTATTCTGACACCTATGTTGAA
 TCCACTCATTTATACCCTGAGAAATGAAGAGGTAAAAATGCCATGAGAAAGCTCTTTACA
 40 TGGTAA (SEQ ID NO: 160)

AOLFR87 sequences:

MNNIAQLSLGFDLGIPLVQLKIILTKIILLFKMYVSNCNPCAHRKINYPNTKLDSEQVNNITEFI
 LLGLTQNAEAQKLLFAVFTLIYFLTMVDNLIVVTTTTSPALDSPVYFFLSFFSFIDGCSSTMAP
 45 KMIFDLLTEKKTISFSGCMTQLFVEHFFGGVEIILLVVMAYDCYVAICKPLYLITMNRQVCG
 LVAMAWVGGFLHALIQMLLIVWLPFCGPNVIDHFICDLFPLKLSCTDTHVFGFLVAANSGLM
 CMLIFSILITSYVLILCSQRKALSTCAFHTVVVLFVPCILVYLRPMITFPIDKAVSVFYTVVTPM
 LNPLIYTLRNTVEVKAMKQLWSQIHWGNLDCD (SEQ ID NO: 161)

ATGAATAACATAGCTCAACTTAGTCTTGGGTTTATAGATTTAGGGATTCCATCAGTGTTAC
 AGAAAAATAATCCTGACCAAAATTTTATTGTTCAAAATGTATGTGTCAAATTGCAATCC
 TTGTGCTATTCACAGAAAAATCAATTATCCAAATACCAAACCTGGATTTTCGAGCAAGTGAAC
 AACATAACGGAATTCATCTTGGCTTGGCCTGACACAGAACGCAGAGGCACAGAACTCTTGT
 TTGCTGTGTTTACACTCATCTACTTTCTCACCATGGTAGACAACCTAATCATTGTGGTGACA
 55 ATCACCACCAGCCCAGCCCTGGACTCCCCGTGATTTTTTCTGTCTTTCTTTCTCTCAT
 AGATGGCTGCTCCTCTTCTACCATGGCCCCCAAAATGATATTTGACTTACTCACTGAAAAG

AAAACTATTTCTTCAGTGGGTGCATGACCCAGCTCTTTGTAGAACATTTCTTTGGGGGAG
TTGAGATCATTCTGCTCGTGGTGATGGCCTATGACTGCTATGTGGCCATCTGCAAGCCCCCT
GTACTACCTGATCACAATGAACAGGCAGGTATGTGGCCTCCTGGTGGCCATGGCATGGGTC
GGGGGATTTCTTCACGCTCTGATTCAAATGCTTTTAATAGTCTGGCTGCCCTTCTGTGGCCC
5 CAATGTCAATTGACCATTTTCATCTGTGACCTTTTCCCTCTGCTAAACTCTCCTGCACTGACA
CTCACGTCTTTGGACTCTTTGTTGCCGCCAACAGTGGGCTGATGTGTATGCTCATTTTTTCT
ATTCTTATTACCTCTTACGTCCTAATCCTCTGCTCACAGCGGAAGGCTCTCTTACCTGCGC
CTTCCATATCACTGTAGTCGTCCTATTCTTTGTTCCCTGTATATTGGTGTACCTTCGACCCA
TGATCACCTTCCCTATTGATAAAGCTGTGTCTGTGTTTTATACTGTGGTAACACCCATGTTA
10 AACCTTTAATCTACACCTCAGAAACACAGAGGTGAAAAATGCCATGAAGCAGCTCTGG
AGCCAAATAATCTGGGGTAACAATTTGTGTGATTAG (SEQ ID NO: 162)

AOLFR88 sequences:

MWQKNQTSLADFILEGLFDDSLTHLFLFSLTMVVFLLIAVSGNTLTILLICIDPQLHTPMYFLLSQ
15 LSLMDLMHVSTILKMATNYLSGKKSISFVGCATQHFLYLCLGGAECFLAVMSYDRYVAICH
PLRYAVLMNKKVGLMMAVMSWLGASVNSLIHMAILMHFPFCGPRKVYHFYCEFPVVKLV
GDITVYETTVYISSILLLLPIFLISTSYVFILQSVIQMRSSGSKRNAFATCGSHLTVVSLWFGACIFS
YMRPRSQCTLLQNKVGSVFYSIITPTLNSLIYTLRNKDVAKALRRVLRDVTQCIQRLQLWLP
RV (SEQ ID NO: 163)

20 ATGTGGCAGAAGAATCAGACCTCTCTGGCAGACTTCATCCTTGAGGGGCTCTTCGATGACT
CCCTTACCCACCTTTTCTTTTCTCCTTGACCATGGTGGTCTTCCTTATTGCGGTGAGTGGC
AACACCCTCACCATCTCCTCATCTGCATTGATCCCCAGCTTCATACACCAATGTATTTCT
GCTCAGCCAGCTCTCCCTCATGGATCTGATGCATGTCTCCACAATCATCCTGAAGATGGCT
25 ACCAACTACCTATCTGGCAAGAAATCTATCTCCTTTGTGGGCTGTGCAACCCAGCACTTCC
TCTATTTGTGTCTAGGTGGTGTGAATGTTTTCTCTTAGCTGTCATGTCCTATGACCGCTAT
GTTGCCATCTGTCTCACTGCGCTATGCTGTGCTCATGAACAAGAAGTGGGACTGATGA
TGGCTGTCTGTCTATGGTTGGGGGCATCCGTGAACCTCCCTAATTCACATGGCGATCTTGAT
GCACTTCCCTTTCTGTGGGCCTCGGAAAGTCTACCACTTCTACTGTGAGTTCCAGCTGTTG
30 TGAAGTTGGTATGTGGCGACATCACTGTGTATGAGACCACAGTGTACATCAGCAGCATCTCT
CCTCCTCCTCCCCATCTTCTGATTTCTACATCCTATGTCTTCATCCTTCAAAGTGTCTCA
GATGCGCTCATCTGGGAGCAAGAGAAATGCCTTTGCCACTGTGGCTCCACCTCACGGTG
GTTTCTCTTTGGTTGGTGCCTGCATCTCTCCTACATGAGACCCAGGTCCAGTGCACTCT
ATTGCAGAAACAAAGTTGGTTCTGTGTTCTACAGCATCATTACGCCACATTGAATTCTCTG
35 ATTTATACTCTCCGGAATAAAGATGTAGCTAAGGCTCTGAGAAGAGTGCTGAGGAGAGAT
GTTATCACCCAGTGCAATTCAACGACTGCAATTGTGGTTGCCCCGAGTGTAG (SEQ ID NO:
164)

AOLFR89 sequences:

40 MLDPSSSHLYLHSLFPQGLRKGTMWQKNQTSLADFILEGLFDDSLTHLFLFSLTMVVFLLIAVS
GNTLTILLICIDPQLHTPMYFLLSQLSLMDLMHVSTILKMATNYLSGKKSISFVGCATQHFLYL
CLGGAECFLAVMSYDRYVAICHPLRYAVLMNKKVGLMMAVMSWLGASVNSLIHMAILMHF
PFCGPRKVYHFYCEFPVVKLVCGDITVYETTVYISSILLLLPIFLISTSYVFILQSVIQMRSSGSK
RNAFATCGSHLTVVSLWFGACIFS YMRPRSQCTLLQNKVGSVFYSIITPTLNSLIYTLRNKDVA
45 KALRRVLRDVTQCIQRLQLWLP (SEQ ID NO: 165)

ATGCTGGACCCAGTATTTCCAGTCACACTCTTTATCTCCACTCTCTGTTTCCTCAGGGATT
GAGAAAGGGGACAATGTGGCAGAAGAATCAGACCTCTCTGGCAGACTTCATCCTTGAGGG
GCTCTTCGATGACTCCCTTACCCACCTTTTCTTTTCTCCTTGACCATGGTGGTCTTCCTTAT
50 TGCGGTGAGTGGCAACACCCTCACCATCTCCTCATCTGCATTGATCCCCAGCTTCATACA
CCAATGTATTTCTGCTCAGCCAGCTCTCCCTCATGGATCTGATGCATGTCTCCACAACCAT
CCTGAAGATGGCTACCAACTACCTATCTGGCAAGAAATCTATCTCCTTTGTGGGCTGTGCA
ACCCAGCACTTCTCTATTTGTGTCTAGTGGTGGTGAATGTTTTCTCTTAGCTGTCTGTC
CTATGACCGCTATGTTGCCATCTGTCTATCCACTGCGCTATGCTGTGCTCATGAACAAGAAG
55 GTGGGACTGATGATGGCTGTCTATGGTTGGGGGCATCCGTGAACCTCCCTAATTCACA
TGGCGATCTTGATGCACTTCCCTTTCTGTGGGCCTCGGAAAGTCTACCACTTCTACTGTGA

GTTCCAGCTGTTGTGAAGTTGGTATGTGGCGACATCACTGTGTATGAGACCACAGTGTAC
ATCAGCAGCATTCTCCTCCTCCTCCCATCTTCCTGATTTCTACATCCTATGTCTTCATCCTT
CAAAGTGTCAATTCAGATGCGCTCATCTGGGAGCAAGAGAAATGCCTTTGCCACTTGTGGCT
CCCACCTCACGGTGGTTTCTCTTTGGTTTGGTGCCTGCATCTTCTCCTACATGAGACCCAGG
5 TCCCAGTGCACCTCTATTGCAGAACAAAGTTGGTTCTGTGTTCTACAGCATCATTACGCCCA
CATTGAATTCTCTGATTTATACTCTCCGGAATAAAGATGTAGCTAAGGCTCTGAGAAGAGT
GCTGAGGAGAGATGTTATCACCCAGTGCATTCAACGACTGCAATTGTGGTTGCCCGAGTG
TAG (SEQ ID NO: 166)

10 **AOLFR90 sequences:**

MFSMTTEALNNFALGCTNLLMTMIPQIDLKQIFLCPNCRLYMIPVGAFIFSLGNMQNQSFVTEF
VLLGLSQNPVQEVFVFLFVYIATVGGNMLIVVTILSSPALLVSPMYFFLGFLSFLDACFSSVI
TPKMIVDSLYVTKTISFEGCMMQLFAEHFFAGVEVIVLTAMAYDRYVAICKPLHYSSIMNRRL
CGILMGVAWTGGLLHSMIQLFTFQLPFCGPNVINHFMCPLYLLELACTDTHIFGLMVVINS
15 FICINFSLLVSYAVILLSLRTHSSEGRWKALSTCGSHIAVVILFFVPCIFVYTRPPSAFSLDKMA
AIFYIILNPLNPLIYTFRNKEVKQAMRRIWNRLMVVSDEKENIKL (SEQ ID NO: 167)

ATGTTCTCAATGACAACAGAAGCACTCAATAATTTTGCACCTGGATGTACCAACTTGTTAA
TGACTATGATACCACAAATTGATCTGAAGCAAATTTTCCTTTGTCCTAATTGCAGACTATA
20 CATGATCCCTGTTGGAGCTTTTCATCTTTTCCTTGGGAAACATGCAAAACCAAAGCTTTGTA
ACTGAGTTTGTCTCCTGGGACTTTACAGAATCCAAATGTTGAGGAAATAGTATTTGTTG
TATTTTGTGTTGTCTACATTGCAACTGTTGGGGGCAACATGCTAATTGTAGTAACCATCTC
AGCAGCCCTGCTCTTCTGGTGTCTCCTATGTACTTCTTCTGGGCTTCTGTCTTCTCTGGA
TGCGTGCTTCTCATCTGTCTACCCCAAAGATGATTGTAGACTCCCTCTATGTGACAAAA
25 ACCATCTCTTTTGAAGGCTGCATGATGCAGCTCTTTGCTGAACACTTCTTTGCTGGGGTGG
AGGTGATTGTCTCACAGCCATGGCCTATGATCGTTATGTGGCCATTGCAAGCCCTTGCA
TTACTCTTCTATCATGAACAGGAGGCTCTGTGGCATTCTGATGGGGGTAGCCTGGACAGGG
GGCCTCTTGCAATCCATGATACAAATCTTTTTACTTTCCAGCTTCCCTTTTGTGGCCCCAA
TGTCATCAATCACTTTATGTGTGACTTGTACCCGTTACTGGAGCTTGCCTGCACTGATACTC
30 ACATCTTTGGCCTCATGGTGGTCATCAACAGTGGGTTTATCTGCATCATAAACTTCTCCTTG
TTGCTTGTCTCCTATGCTGTCTCTCTCTGAGAACACACAGTTCTGAAGGGCGCTG
GAAAGCTCTCTCCACCTGTGGATCTCACATTGCTGTTGTGATTTTGTCTTTGTCCCATGCA
TATTTGTATATACAGACCTCCATCTGCTTTTCCCTTGACAAAATGGCGGCAATATTTTAT
ATCATCTTAAATCCCTTGCTCAATCCTTTGATTTACACTTTTCAAGGAATAAGGAAGTAAAC
35 AGGCCATGAGGAGAAATATGGAACAGACTGATGGTGGTTTCTGATGAGAAAGAAATATTA
AACTTTAA (SEQ ID NO: 168)

AOLFR91 sequences:

MGNWSTVTEITLIAFPALLEIRISLFFVVLVVTYTLTATGNTHISLIWIDHRLQTPMYFFLSNLSFL
40 DILYTTVTIPKLLACLLGEEKTISFAGCMQTYFYFFLGTVBFILLAVMSFDRYMAICDPLHYTVI
MNSRACLLVLGCWVGAFSLVLFPTTVVTRLPYCRKEINHFFCDIAPLLQVACINTHLIEKINFL
SALVILSSLAFTTGSYVYIISTILRIPSTQGRQKAFSTCASHITVVSIAHGSNIFVYVRPNQNSSLD
YDKVA AVLITVVTPLNPFYSLRNEKVQEVLRQTVNRIMTLIQRKT (SEQ ID NO: 169)

ATGGGAAACTGGAGCACTGTGACTGAAATCACCTAATTGCCTTCCCAGCTCTCCTGGAGA
TTCGAATATCTCTCTTCGTGGTTCTTGTGGTAACTTACACATTAACAGCAACAGGAAACAT
CACCATCATCTCCCTGATATGGATTGATCATCGCTGCAAACCTCCAATGTACTTCTTCTCTCA
GTAATTTGTCTTTCTGGATATCTTATACACCACTGTCATTACCCCAAAGTTGTTGGCCTGC
CTCCTAGGAGAAGAGAAAACCATATCTTTTGTGGTTGCATGATCCAAACATATTTCTACT
50 TCTTCTGGGGACGGTGGAGTTTATCCTCTTGGCGGTGATGTCCTTTGACCGCTACATGGC
TATCTGCGACCCACTGCACTACACGGTCATCATGAACAGCAGGGCCTGCCTTCTGCTGGTT
CTGGGATGCTGGGTGGGAGCCTTCCCTGTCTGTGTTGTTTCCAACCATGTAGTGACAAGGC
TACCTTACTGTAGGAAAGAAATTAATCATTTCTTCTGTGACATTGCCCTCTTCTTCAGGTG
GCCTGTATAAATACTCACCTCATTGAGAAGATAAACTTTCTCCTCTCTGCCCTTGTCTATCCT
55 GAGCTCCCTGGCATTCACTACTGGGTCTACGTGTACATAATTTCTACCATCCTGCGTATCC
CCTCCACCCAGGGCCGTCAGAAAGCTTTTCTACCTGTGCTTCTCACATCACTGTTGTCTCC

ATTGCCACGGGAGCAACATCTTTGTGTATGTGAGACCCAATCAGAACTCCTCACTGGATT
ATGACAAGGTGGCCGCTGTCTCATCACAGTGGTGACCCCTCTCCTGAACCCCTTTATCTA
CAGCTTGAGGAATGAGAAGGTACAGGAAGTGTGAGAGAGACAGTGAACAGAATCATGAC
CTTGATACAAAGGAAACTTGA (SEQ ID NO: 170)

5

AOLFR92 sequences:

MRNGTVITEFILLGFPVIOGLQTPFLIAIFLTYILTLAGNGLIATVWAEPRLOIPMYFFLCNLSFLE
IWYTTTTVIPKLLGTFVVARVICMSCLLQAFFHFFVGTTEFLILTIMSFDRLTICNPLHHPTIM
TSKLCQLALSSWVVGFTIVFCQTMILLIQLPFCGNNVISHFYCDVGPSLKAACIDTSILELLGVIA
TILVPGSLLFNMSISYTYLSAILRIPSATGHQKTFSTCASHLTVVSLLYGAVLFMYLRPTAHSSFK
INKVSVLNTILTPLLNPFIYTIRNKEVKGALRKAMTCPKTGHAK (SEQ ID NO: 171)

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ATGAGAAATGGCACAGTAATCACAGAATTCATCCTGCTAGGCTTTCCTGTTATCCAAGGCC
TACAAACACCTCTCTTTATTGCAATCTTTCTCACCTACATATTAACCCCTGCAGGCAATGGG
CTTATTATTGCCACTGTGTGGGCTGAGCCAGGCTACAAATCCAATGTACTTCTTCCTTTG
TAACTTGTCTTTCTTAGAAATCTGGTACACCACCACAGTCATCCCCAACTGCTAGGAACC
TTTGTAGTGGCAAGAACAGTAATCTGCATGTCTGCTGCCTGCTGCAGGCCTTCTTCCACT
TCTTCGTGGGCACCAACCGAGTTCCTGATCCTCACTATCATGTCTTTTGACCGCTACCTCACC
ATCTGCAATCCCCTTACCACCCCAACCATCATGACCAGCAAACTCTGCCTGCAGCTGGCCC
TGAGCTCCTGGGTGGTGGGCTTACCATTGTCTTTGTGACAGCATGCTGCTCATCCAGTT
GCCATTCTGTGGCAATAATGTTATCAGTCATTTCTACTGTGATGTTGGGCCAGTTTGA
GCCCGCTGCATAGACACCAGCATTGGAACCTCCTGGGCGTCATAGCAACCATCCTTGTGA
TCCCAGGGTCACTTCTTTAATATGATTTCTTATATCTACATTCTGTCCGCAATCCTACGA
ATTCTTCAGCCACTGGCCACCAAAAGACTTTCTCTACCTGTGCCTCGCACCTGACAGTTGT
CTCCCTGCTCTACGGGGCTGTTCTGTTTCATGTACCTAAGACCCACAGCACACTCCTCCTTA
AGATTAATAAGGTGGTGTCTGTGCTAAATACTATCCTCACCCCTTCTGAATCCCTTTATT
TATACTATTAGAAACAAGGAGGTGAAGGGAGCCTTAAGAAAGGCAATGACTTGCCCAAAG
ACTGGTCATGCAAAGTAA (SEQ ID NO: 172)

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AOLFR93 sequences:

MLMNYSSATEFYLLGFPGSEELHHILFAIFFFFYLVTLMGNTVIIMIVCVDKRLQSPMYFFLGHL
SALEILVTIIVPVMLWGLLLPGMQTYLSACVVQLFLYLAVGTTEFALLGAMAVDRYVAVCN
PLRYNIIMNRHTCNFVVLVSWVFGFLFQIWPVYVMFQLTYCKSNVNNFFCDRGQLLKLSCN
NTLFTEFILFLMAVFVLFGLIPTIVSNAYIISTILKIPSSSGRRKSFSTCASHFTCVVIGYGSCFLFY
VKPKQTQAADYNWVVSMLMSVVTPLNPFIFTLRNDKVIEALRDGVKRCCQLFRN (SEQ ID
NO: 173)

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ATGTTGATGAATTACTCTAGTGCCACTGAATTTTATCTCCTTGGCTTCCCTGGCTCTGAAGA
ACTACATCATATCCTTTTTGCTATATTCTTCTTTTCTACTTGGTGACATTAATGGGAAACA
CAGTCATCATCATGATTGTCTGTGTGGATAAACGTCTGCAGTCCCCCATGTATTTCTTCCTC
GGCCACCTCTCTGCCCTGGAGATCCTGGTCACAACCATAATCGTCCCCGTGATGCTTTGGG
GATTGCTGCTCCCTGGGATGCAGACAATATATTTGTCTGCCTGTGTTGTCCAGCTCTTCTTG
TACCTTGCTGTGGGGACAACAGAGTTCGCATTACTTGGAGCAATGGCTGTGGACCGTTATG
TGGCTGTCTGTAACCCCTCTGAGGTACAACATCATTATGAACAGACACACCTGCAACTTTGT
GGTCTTGTGTGTCATGGGTGTTTGGGTTTCTTTTCAAATCTGGCCGGTCTATGTGATGTTTC
AGCTTACTTACTGCAAAATCAAATGTGGTGAACAATTTTTTTGTGACCGAGGGCAATTGCT
CAAATATCCTGCAATAATACTCTTTTACGGAGTTTATCCTCTTCTTAATGGCTGTTTTTG
TTCTCTTTGGTTCTTTGATCCCTACAATTGTCTCCAACGCCTACATCATCTCCACCATTCTC
AAGATCCCGTCATCCTCTGGCCGGAGGAAATCCTTCTCCACTTGTGCCTCCCACTTCACCTG
TGTTGTGATTGGCTACGGCAGCTGCTTGTCTCTACGTGAAACCCAAGCAAACGCAGGCA
GCTGATTACAATTGGGTAGTTTCCCTGATGGTTTCAGTAGTAACCTCTTCTCAATCCTTT
CATCTTACCCTCCGGAATGATAAAGTCATAGAGGCCCTTCGGGATGGGGTGAAACGCTGC
TGTCAACTATTAGGAATTAG (SEQ ID NO: 174)

AOLFR94 sequences:

METWVNQSYTDGFFLLGIFSHSTADLVLFSSVVMVFTVALCGNVLLIFLIYMDPHLHTPMYFF
LSQLSLMDLMLVCTNVPKMAANFLSGRKSISFVGCIGLQIFVCLVSEGLLLGLMAYDRYVA
ISHPLHYPLMNQVRVCLQITGSSWAFGIIDGLIQMVVVMNFPYCGLRKVNHHFCEMLSLLKLAC
5 VDTSLFEKVIFACCVFMLLFPFSIIVASYAHILGTVLQMHSAQAWKKALATCSSHLTAVTLFYG
AAMFIYLRPRHYRAPSHDKVASIFYTVLTPMLNPLIYSLRNREVMGALRKGLDRCRIGSQH
(SEQ ID NO: 175)

ATGGAGACGTGGGTGAACCAAGTCTACACAGATGGCTTCTTCCTCTTAGGCATCTTCTCCC
10 ACAGTACTGCTGACCTTGTCTCTTCTCCGTGGTTATGGCGGTCTTCACAGTGGCCCTCTGT
GGGAATGTCTCTCATCTTCTCATCTACATGGACCCTCACCTTCACACCCCATGTACTT
CTTCTCAGCCAGCTCTCCCTCATGGACCTCATGTTGGTCTGTACCAATGTGCCAAAGATG
GCAGCCAACTTCTGTCTGTGCAGGAAGTCCATCTCCTTTGTGGGCTGTGGCATACAAATTG
GCCTCTTTGTCTGTCTTGTGGGATCTGAGGGGCTCTTGTCTGGGACTCATGGCTTATGACCG
15 CTATGTGGCCATTAGCCACCCACTTCACTATCCCATCCTCATGAATCAGAGGGTCTGTCTCC
AGATTACTGGGAGCTCCTGGGCCTTTGGGATAATCGATGGCTTGATCCAGATGGTGGTAGT
AATGAATTTCCCTACTGTGGCTTGAGGAAGGTGAACCATTTCTTCTGTGAGATGCTATCC
TTGTTGAAGCTGGCCTGTGTAGACACATCCCTGTTTGAGAAGGTGATATTTGCTTGCTGTG
TCTTCATGCTTCTTCTCCATTCTCCATCATCGTGGCCTCCTATGCTCACATTCTAGGGACT
20 GTGCTGCAATGCACTCTGCTCAGGCCTGGAAAAAGGCCCTGGCCACCTGCTCCTCCCACC
TGACAGCTGTCAACCTCTTCTATGGGGCAGCCATGTTTCTATCTACCTGAGGCCTAGGCACTA
CCGGGCCCCCAGCCATGACAAGGTGGCCTCTATCTTCTACACGGTCTTACTCCCATGCTC
AACCCCTCATTTACAGCTTGAGGAACAGGGAGGTGATGGGGGCACTGAGGAAGGGGCTG
GACCGCTGCAGGATCGGCAGCCAGCACTGA (SEQ ID NO: 176)

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AOLFR95 sequences:

MLGSKPRVHLIYLPASQQVSTMGDRGTSNHSEMTDFILAGFRVRPELHILLFLLFLFVYAMILL
GNVGMMTIIMTDPRLNTPMYFFLGNLSFIDLFYSSVIEPKAMINFWSENKSISFAGCVAQLFLFA
LLIVTEGFLLAAMAYDRFLAICNPILYSVQMSTRCTQLVAGSYFCGCISSVIQTSMTFTLSFCAS
30 RAVDHFYCDRPLQLRLSCSDLFIHRMISFSLSCIILPTIIVIVSYMYTVSTVLKIHSTEGHKKAFST
CSSHLGVVSVLYGAVFFMYLTPDRFPELSKVASLCYSLVTPMLNPLIYSLRNKDVQEALKKFLF
KKNILL (SEQ ID NO: 177)

ATGCTAGGATCCAAACCAAGAGTTCATTTGTATATTTTGCCCTGTGCCTCTCAACAGGTTTC
35 TACCATGGGTGACAGGGGAACAAGCAATCACTCAGAAATGACTGACTTCATTCTTGCAGG
CTTCAGGGTACGCCCAGAGCTCCACATTCTCCTCTTCTGCTATTTTGTGTTTATGCCA
TGATCCTTCTAGGGAATGTTGGGATGATGACCATTAATTATGACTGATCCTCGGCTGAACAC
ACCAATGTATTTTTTCTAGGCAATCTCTCCTTCATTGATCTTTTCTATTCTATCTGTTATTGA
ACCAAGGCTATGATCAACTTCTGGTCTGAAAACAAGTCTATCTCCTTTGCAGGCTGTGTG
40 GCCCAGCTCTTTCTCTTTGCCCTCCTCATTGTGACTGAGGGATTCTCCTGGCGGCCATGGC
TTATGACCGCTTTATTGCCATCTGCAACCTCTGCTCTACTCTGTTCAAATGTCCACACGTC
TGTGTACTCAGTTGGTGGCTGGTTCTATTTTGTGGCTGCATTAGCTCAGTTATTACAGACT
AGCATGACATTTACTTTATCTTTTTGCGCTTCTCGGGCTGTTGACCACTTTTACTGTGATTC
TCGCCCCTTCAGAGACTGTCTTGTCTGATCTCTTTATCCATAGAATGATATCTTTTTCTCT
45 TATCATGTATTATTATCTTGCCTACTATCATAGTCATTATAGTATCTTACATGTATATTGTG
TCCACAGTTCTAAAGATACATTCTACTGAGGGACATAAGAAGGCCTTCTCCACCTGCAGCT
CTCACCTGGGAGTTGTGAGTGTGCTGTATGGTGTCTTTTTTATGTATCTCACTCCTGAC
AGATTTCTGAGCTGAGTAAAGTGGCATCCTTATGTTACTCCCTAGTCACTCCCATGTTGA
ATCCTTTGATTTACTCTCTGAGGAACAAAGATGTCCAAGAGGCTCTAAAAAATTTCTAGA
50 GAAGAAAAATATTATTCTTTGA (SEQ ID NO: 178)

AOLFR96 sequences:

MICENHTRVTEFILLGFTNNPEMQVSLFIFFLAITYTVLLGNFLIVTVTSVDLALQTPMYFFLQN
LSLLEVCFITLVMVPKMLVDLVSPRKIISFVGCQTQMYFFFFGSSECFLLSMMAAYDRFVAICNP
55 LHYSVIMNRSCLLWMAIGSWMSGVPVSMQLQTAWMMALPFCGPNAVDFHFFCDGPPVLKLVTV
DTTMYEMQALASTLLFIMFPFCLILVSYTRIITILRMSSATGRQKAFSTCSSHLIVVSLFYGTASL

TYLRPKSNQSPESKKLVLSYTVITPMLNPITYGLRNNEVKGAVKRTITQKVLQKLDVF (SEQ ID NO: 179)

5 ATGATCTGTGAAAATCACACCAGAGTCACTGAATTTATTCTTCTTGGTTTTACAAACAACC
CCGAGATGCAAGTTTCCCTCTTTATTTTTTTCCTGGCCATTTATACAGTCACTTTGTTGGGC
AACTTTCTTATTGTACAGTTACCAGTGTGGATCTCGCACTTCAAACACCCATGTACTTCTT
TCTTCAAAATCTGTCACTTCTTGAAGTATGTTTACCTTGGTTATGGTGCCAAAAATGCTTG
TAGATCTAGTGTCCCAAGGAAAATTATCTCTTTTGTGGGCTGTGGTACCCAGATGTACTT
10 CTTCTTCTTCTTGGCAGTTCTGAATGTTTCTTCTCTCCATGATGGCTTATGATCGCTTTGT
GGCCATCTGTAACCTCTCCATTATTCAGTCATAATGAACAGGTCCTATGCTTGTGGATG
GCCATAGGCTCTTGGATGTCCGGTGTCTCTGTGTCTATGCTACAGACAGCTTGGATGATGG
CCCTTCTTTCTGTGGACCAAATGCCGTGGACCACTTTTTCTGTGATGGTCCCCAGTGTTA
AAACTAGTCACAGTGGATACAACCATGTATGAAATGCAAGCACTTGCCTCCACACTCCTGT
15 TTATCATGTTTCCCTTTTGTCTCATTTTGGTTTCTACACCCGCATTATCATAACAATTCTG
AGGATGTCCTCTGCCACTGGCCGCCAGAAGGCATTTTCTACTTGTTCCTCACACCTCATTGT
GGTGTCCCTCTTCTACGGAACAGCCAGTCTGACCTACCTGCGGCCAAATCAAACAGTCC
GCTGAGAGCAAGAAGCTAGTGTCAATGTCCTACACTGTCACTCACACCTATGTAAACCCCA
TCATCTACGGCTGAGGAACAATGAAGTAAAGGGGCTGTCAAGAGGACAATCACTCAAA
AAGTCTTACAGAAGTTAGATGTGTTTTGA (SEQ ID NO: 180)

20

AOLFR97 sequences:

MTEFHLQSQMPSIRLIFRRLSLGRIKPSQSPRCSTSMVVPFSIAEHWRMKGANLSQGMFEFL
LGLTDDPQLQRLLFVFLGMYTATLLGNLVMFLLIHVSA TLHTPMYSLKSLSFLDFCYSTTVV
PQTLVNFLAKRKVISYFGCMQMFYAGFATSECYLIAAMA YDRYAAJCNPLLYSTIMSPEVC
25 ASLVGYSYAGFLNLSLIHTGCFSLKFCGAHVVTHFFCDGPPILSLSCVDTS LCELLFIFAGFNLLS
CTLTILISYFLILNTILKMSSAQGRFKAFTCASHLTAICLFFGTTLFMYLRPRSSYSLTQDRTVA
VIYTVVIPVLNPLMYSLRNKDVKKALIKVWGRKTME (SEQ ID NO: 181)

30 ATGACAGAGTTTCATCTGCAAAGCCAAATGCCCTCAATAAGACTCATCTTCAGAAGGCTGT
CCTTAGGCAGAAATTAACCCAGTCAGAGCCCCAGGTGTTCAACCTCATTTATGGTGGTGCC
TTCTTTCTCCATCGCAGAGCACTGGAGAAGGATGAAAGGGGCAAACCTGAGCCAAGGGAT
GGAGTTTGAGCTCTTGGGCCTCACCCTGACCCCACTCCAGAGGCTGCTCTTCGTGGTG
TTCCTGGGCATGTACACAGCCACTCTGCTGGGGAACCTGGTCATGTTCTCCTGATCCATG
TGAGTGCCACCTGCACACACCCATGTACTCCCTCCTGAAGAGCCTCTCCTTCTTGGATTTC
35 TGCTACTCCTCCACGGTTGTGCCCCAGACCCTGGTGAACCTCTTGGCCAAGAGGAAAGTGA
TCTCTTATTTTGGCTGCATGACTCAGATGTTCTTCTATGCGGGTTTTGCCACCACTGAGTGC
TATCTCATCGCTGCCATGGCCTATGACCGCTATGCGGCTATTTGTAACCCCTGCTCTACTC
AACCATCATGTCTCCTGAGGTCTGTGCCTCGCTGATTGTGGGCTCCTACAGTGCAGGATTC
CTCAATTCCTTATCCACACTGGCTGTATCTTGTAGTCTGAAATCTGCGGTGCTCATGTCGT
40 CACTCACTTCTTCTGTGATGGGCAACCCATCCTGCTTGTCTTGTGTAGACACCTCACTGT
GTGAGATCCTGCTCTTCATTTTGTGCTGGTTTCAACCTTTTGTGCTGCACCCCTACCATCTTG
ATCTCCTACTTCTTAATTCTCAACACCATCCTGAAAATGAGCTCGGCCAGGGCAGGTTTA
AGGCATTTTCCACCTGTGCATCCACCTCACTGCCATCTGCCTCTTCTTGGCACAACACTT
TTTATGTACCTGCGCCCCAGGTCCAGCTACTCCTTGACCCAGGACCGCACAGTTGCTGTCA
45 TCTACACAGTGGTGATCCCAGTGCTGAACCCCTCATGTACTCTTTGAGAAACAAGGATGT
GAAGAAAGCTTTAATAAAGGTTTGGGGTAGGAAAACAATGGAATGA (SEQ ID NO: 182)

AOLFR98 sequences:

MRGFNKTTVVQTQFILVGFSSLGELQLLLFVIFLLLYLTILVANVTIMAVIRFSWTLHTPMYGFLEI
50 LSFSESCYTFVIPQLLVHLLSDTKTISFMACATQLFFFLGFACTNCLLIAVMGYDRYVAICHPLR
YTLLINKRLGLELISLSGATGFFIALVATNLICDMRFCGPNRVNHYFCMAPVIKLACTDTHVKE
LALFSLVIMVFPFLLILSYGFIVNTILKIPSAEGKKAFTVCASHLTVVFVHYGCASIYLRPKSK
SASDKDQLVAVTYTVVTPLLNPLVYSLRNKEVKTALKRVLGMPVATKMS (SEQ ID NO: 183)

55 ATGCGAGGTTTCAACAAAACCACTGTGGTTACACAGTTCATCCTGGTGGGTTTCTCCAGCC
TGGGGGAGCTCCAGCTGCTGCTTTTTGTATCTTTCTTCTCCTATACTTGACAATCCTGGTG

GCCAATGTGACCATCATGGCCGTTATTGCTTCAGCTGGACTCTCCACACTCCCATGTATG
 GCTTTCTATTTCATCCTTTTCATTTCTGAGTCCTGCTACACTTTTGTGTCATCATCCCTCAGCTGC
 TGGTCCACCTGCTCTCAGACACCAAGACCATCTCCTTCATGGCCTGTGCCACCCAGCTGTT
 CTTTTCTTGGCTTTGCTTGACCAACTGCCTCCTCATTGCTGTGATGGGATATGATCGCT
 5 ATGTAGCAATTTGTCACCTCTGAGGTACACACTCATCATAAAACAAAAGGCTGGGGTTGGA
 GTTGATTTCTCTCTCAGGAGCCACAGGTTTCTTTATTGCTTTGGTGGCCACCAACCTCATTT
 GTGACATGCGTTTTTGTGGCCCCAACAGGGTTAACCCTATTCTGTGACATGGCACCTGT
 TATCAAGTTAGCCTGCACTGACACCCATGTGAAAGAGCTGGCTTATTTAGCCTCAGCATC
 CTGGTAATTATGGTGCCTTTTCTGTTAATTCTCATATCCTATGGCTTCATAGTTAACACCAT
 10 CCTGAAGATCCCCTCAGCTGAGGGCAAGAAGGCCTTTGTCACCTGTGCCTCACATCTCACT
 GTGGTCTTTGTCCACTATGGCTGTGCCTCTATCATCTATCTGCGGCCCAAGTCCAAGTCTGC
 CTCAGACAAGGATCAGTTGGTGGCAGTGACCTACACAGTGGTTACTCCCTTACTTAATCCT
 CTTGTCTACAGTCTGAGGAACAAAGAGGTAATAAAGTGCATTGAAAAGAGTTCTTGAATG
 CCTGTGGCAACCAAGATGAGCTAA (SEQ ID NO: 184)

15

AOLFR99 sequences:

MERVNETVREVIPLGFSSSLARLQQLLFVIFLLLYLFTLGTNAIISTIVLDRALHIPMYFFLAILSC
 SEICYTFIIVPKMLVDLLSQKKTISFLGCAIQMFSFLFLGCSHSFLLAVMGYDRYIAICNPLRYSV
 LMGHGVCMGLVAAACACGFTVAQIITSLVFHLPFYSSNLHFFCDIAPVLKLASHHNFHSQIV
 20 IFMLCTLVLAIPLLLILVSYVHLSAILQFPSTLGRCKAFSTCVSHLIIVTVHYGCASFYLRPQSNY
 SSSQDALISVSYTIITPLFNPMIYSLRNKEFKSALCKIVRRTISLL (SEQ ID NO: 185)

ATGGAGCGGGTCAATGAGACTGTGGTGAGAGAGGTTCATCTTCCTCGGCTTCTCATCCCTGG
 CCAGGCTGCAGCAGCTGCTCTTTGTTATCTTCCTGCTCCTCTACCTGTTCACTCTGGGCACC
 25 AATGCAATCATCATTTCCACCATTGTCTGGACAGGGCCCTTCATATCCCCATGTACTTCTT
 CCTTGCCATCCTCTCTTGCTCTGAGATTTGCTACACCTTCATCATTGTACCCAAGATGCTGG
 TTGACCTGCTGTCCAGAAGAAGACCATTTCTTTCCTGGGCTGTGCCATCCAAATGTTTTC
 TTCCTCTTCCTTGGCTGCTCTCACTCCTTTCTGCTGGCAGTCATGGGTTATGATCGTTACAT
 AGCCATCTGTAACCCACTGCGCTACTCAGTGCTAATGGGACATGGGGTGTGTATGGGACTA
 30 GTGGCTGCTGCCTGTGCCTGTGGCTTCACTGTGTCACAGATCATCACATCCTTGGTATTTC
 CCTGCCTTTTTATTCTCCAATCAACTACATCACTTCTTCTGTGACATTGCTCCTGTCTCA
 AGCTGGCATCTCACCATAACCCTTTAGTCAGATTGTCATCTTCATGCTCTGTACATTGGTC
 CTGGCTATCCCCCTTATTGTTGATCTTGGTGTCTATGTTTCACATCCTCTCTGCCATACTTCA
 GTTTCCTTCCACACTGGGTAGGTGCAAAGCTTTTTCTACCTGTGTATCTCACCTCATTATTG
 35 TCACTGTCCACTATGGCTGTGCCTCCTTTATCTACTTAAGGCCTCAGTCCAATACTCCTCA
 AGCCAGGATGCTCTAATATCAGTATCCTACACTATTATAACTCCATTGTTCAACCCAATGA
 TTTATAGCTTGAGAAATAAAGAGTTCAAATCAGCTCTTTGTAAATTTGTGAGAAGAACAAT
 TTCCCTGTTGTAA (SEQ ID NO: 186)

40

AOLFR101 sequences:

MDTGNWSQVAEFILGFPHLQGVQIYLFLLLLLIYLMTVLGNLLIFLVVCLDSRLHTPMYHFVSI
 LSFSELGYTAATIPKMLANLLSEKKTISFSGCLLQIYFFHSLGATECYLLTAMAYDRYLAICRPL
 HYPITLMTPTLCAEIAIGCWLGGLAGPVVEISLISRLPFCGPNRIQHVFCDFPPVLSLACTDTSINV
 LVDFVINSCKILATFLILCSYVQIICTVLRIPSAAGKRKAISTCASHFTVVLIFYGSILSMYVQLK
 45 KSYSLDYDQALAVVYSVLTPLNPFYISLRNKEIKEAVRRQLKRIGILA (SEQ ID NO: 187)

ATGGACACAGGGAAGTGGAGCCAGGTAGCAGAATTCATCATCTTGGGCTTCCCCCATCTCC
 AGGGTGTCCAGATTTATCTCTTCCTCTTGTGCTTCTCATTTACCTCATGACTGTGTTGGGA
 AACCTGCTGATATTCCTGGTGGTCTGCCTGGACTCCCGGCTTCACACACCCATGTACCACT
 50 TTGTGACATTTCTCCTTCTCAGAGCTTGCTATACAGCTGCCACCATCCCTAAGATGCTG
 GCAAACTTGCTCAGTGAGAAAAAGACCAATTTTCATTCTCTGGGTGTCTCCTGCAGATCTATT
 TCTTTCACTCCCTTGGAGCGACTGAGTGCTATCTCCTGACAGCTATGGCCTACGATAGGTA
 TTTAGCCATCTGCCGGCCCCCTCCACTACCCAACCCTCATGACCCCAACACTTTGTGCAGAG
 ATTGCCATTGGCTGTTGGTTGGGAGGCTTGGCTGGGCCAGTAGTTGAAATTTCTTGTGATTT
 55 CACGCTCCCATTTCTGTGGCCCCAATCGCATTACAGCACGTCTTTTGTGACTTCCCTCCTGTG
 CTGAGTTTGGCTTGCATGATACGTCTATAAATGTCCTAGTAGATTTTGTATAAATTCCTG

CAAGATCCTAGCCACCTTCCTGCTGATCCTCTGCTCCTATGTGCAGATCATCTGCACAGTGC
TCAGAAATCCCTCAGCTGCCGCAAGAGGAAGGCCATCTCCACGTGTGCCTCCCACTTCAC
TGTGGTTCTCATCTTCTATGGGAGCATCCTTTCCATGTATGTGCAGCTGAAGAAGAGCTAC
TCACTGGACTATGACCAGGCCCTGGCAGTGGTCTACTCAGTGCTCACACCCTTCCTCAACC
5 CCTTCATCTACAGCTTGCACAACAAGGAGATCAAGGAGGCTGTGAGGAGGCAGCTAAAGA
GAATTGGGATATTGGCATGA (SEQ ID NO: 188)

AOLFR102 sequences:

MPVGLVFNQSEPTFVFRAFTTATEFQVLLFLLFLLYLMILCGNTAIWVVCVTHSTLRTPMYF
10 FLSNLSFLELCYTTVVVPLMLSNILGAQKPISLAGCGAQMFFVTLGSTDCFLLAIMAYDRYVAI
CHPLHYTLIMTRELCTQMLGGALGLALFPSLQLTALIFTLPFCGHHQEINHFLCDVPPVLRACA
DIRVHQAVLYVVSILVLTIPFLICVSYVFITCAILSIRSAEGRRRAFSTCSFHLTVVLLQYGCCSL
VYLRPRSSTSEDEDSQIALVYTFVTPLNPLLYSLRNKDKGALRSAIRKAASDAN (SEQ ID
NO: 189)

15 ATGCCTGTGGGGAAACTTGTCTTCAACCAGTCTGAGCCCACTGAGTTTGTGTTCCGTGCGT
TCACCACAGCCACTGAATCCAGGTTCTTCTCTCTCCTCTCTCCTCCTCTACTTGATG
ATCCTCTGTGGCAACACAGCCATCATCTGGGTGGTGTGCACACACAGCACCCCTCCGACCC
CGATGTATTTCTTCTGTCCAACCTGTCTTTCTGGAACCTCTGCTACACCACCGTGGTAGTA
20 CCCTTGATGCTTTCCAACATTTTGGGGGCCAGAAAGCCATTTCTGTTGGCTGGATGTGGGG
CCCAAATGTTCTTCTTTGTCAACCTCGGCAGCACGGACTGTTTCTCTTGGCGATCATGGCC
TATGACCGCTATGTGGCTATCTGCCACCGCTGCACTACACCCTCATCATGACCCGCGAGC
TGTGCACGCAGATGCTGGGTGGGGCCCTGGGCCCTGGCCCTCTTCCCCTCCCTGCAGCTCAC
CGCCTTAATCTTCAACCTGCCCTTTTGGGCCACCACCAGGAAATCAACCACTTCTCTGCG
25 ATGTGCCTCCCGTCTGCGCTGGCCTGCGCTGACATCCGCGTGCACCAGGCTGTCTCTA
TGTCGTGAGCATCCTCGTGCTGACCATCCCTTCTCTGCTCATCTGCGTCTCCTACGTGTTCA
TCACCTGTGCCATCCTGAGCATCCGTTCTGCCGAGGGCCGCGCCGGGCCCTTCTCCACCTG
CTCCTTCCACCTCACCGTGGTCTGCTGCAGTATGGCTGCTGCAGCCTCGTGTAACCTGCGTC
CTCGGTCCAGCACCTCAGAGGATGAGGACAGCCAAATCGCGTTGGTCTACACCTTTGTCA
30 CCCCTTACTCAACCTTTGCTTTACAGCCTTAGGAACAAGGATGTCAAAGGTGCTCTGAGG
AGTGCCATTATCCGTAAAGCAGCCTCTGACGCCAACTGA (SEQ ID NO: 190)

AOLFR103 sequences:

MAEMNLTLVTEFLLIATFEYPEWALPLFLLLLFMYLITVLGNLEMILILMDHQLHAPMYFLLSH
35 LAFMDVCYSSITVPQMLAVLLEHGAALS YTRCAAQFFLFTFFGSIDCYLLALMAYDRYLAVCQ
PLLYVTILTQARLSLVAGAYVAGLISALVRTVSAFTLSFCGTSEIDFIFCDLPPLLKLTGCESYT
QEVLIIMFAIFVIPASMVVILVSYLFIIIVAIMGIPAGSQAFTSTCTSHLTA VSLFFGTLIFMYLRG
NSDQSSEKNRVSVLYTEVIPMLNPLIYSLRNKEVKEALRKILNRAKLS (SEQ ID NO: 191)

40 ATGGCAGAGATGAACCTCACCTTGGTGACCGAGTTCCTCCTTATTGCATTCACTGAATATC
CTGAATGGGCACTCCCTCTCTTCTCTTGTATTATTTATGTATCTCATCACCGTATTGGGG
AACTTAGAGATGATTATTCTGATCCTCATGGATCACCAGCTCCACGCTCCAATGTATTTCCT
TCTGAGTCACCTCGCTTTCATGGACGTCTGCTACTCATCTATCACTGTCCCCCAGATGCTGG
CAGTGTCTGCTGGAGCATGGGGCAGCTTTATCTTACACACGCTGTGCTGCTCAGTTCTTTCT
45 GTTCACCTTCTTTGGTTCCATCGACTGCTACCTCTTGGCCCTCATGGCCTATGACCGTACT
TGGCTGTGTGCCAGCCCTGCTTTATGTACCATCCTGACACAGCAGGCCCGCTTGAGTCT
TGTGGCTGGGGCTTACGTTGCTGGTCTCATCAGTGCCTTGGTGCGGACAGTCTCAGCCTTC
ACTCTCTCCTTCTGTGGAACCAAGTGAGATTGACTTTATTTTCTGTGACCTCCCTCCTCTGTT
AAAGTTGACCTGTGGGGAGAGCTACACTCAAGAAGTGCTGATTATTATGTTTGCCATTTTT
50 GTCATCCCTGCTTCCATGGTGGTGATCTTGGTGCTTACCTGTTTATCATCGTGGCCATCAT
GGGGATCCCTGCTGGAAGCCAGGCCAAGACCTTCTCCACCTGCACCTCCACCTCACTGCT
GTGTCACCTCTTCTTGGTACCCTCATCTTCATGTACTTGAGAGGTAACTCAGATCAGTCTTC
GGAGAAGAATCGGGTAGTGTCTGTGCTTTACACAGAGGTATCCCCATGTTGAATCCCCCTC
ATCTACAGCCTGAGGAACAAGGAAGTGAAGGAGGCCCTGAGAAAAATTCTCAATAGAGCC
55 AAGTTGTCCTAA (SEQ ID NO: 192)

AOLFR105 sequences:

MQGLNHTSVSEFILVGFSAPHLQLMLFLLFLLMYLFTLLGNLLIMATVWSERSLHMPMYLFLC
 ALSITEILYTVAIIPRMLADLLSTQRSIAFLACASQMFFSFGFTHSFLLTVMGYDRYVAICHPL
 RYNVLM SLRGCTCRVGC SWAGGLVMGMVVTSAIFHLAFCGHKEIHFFCHVPPLLKLACGDD
 5 VL VVAKGVGLVCITALLGCFLILLSYAFIVAAILKIPSAEGRNKAFTSCASHLTVVVVHYGFAS
 VIYLPKGPQSPGDTLMGITVTVLTPFLSPIIFSLRNKELKVAMKKTCTFKLPQNC (SEQ ID
 NO: 193)

ATGCAGGGGCTAAACCACACCTCCGTGTCTGAATTCATCCTCGTTGGCTTCTCTGCCCTTCCC
 10 CCACCTCCAGCTGATGCTCTTCCTGCTGTTCTGCTGATGTACCTGTTACGCTGCTGGGCA
 ACCTGCTCATCATGGCCACTGTCTGGAGCGAGCGCAGCCTCCACATGCCCATGTACCTCTT
 CCTGTGTGCCCTCTCCATCACCAGATCCTCTACACCGTGGCCATCATCCC GCGCATGCTG
 GCCGACCTGCTGTCCACCCAGCGCTCCATCGCCTTCCTGGCCTGTGCCAGTCAGATGTTCTT
 CTCCTTCAGCTTCGGGTTCACCCACTCCTTCCTGCTCACTGTCATGGGGCTACGACCGCTACG
 15 TGGCCATCTGCCACCCCTGCGTTACAACGTGCTCATGAGCCTGCGGGGCTGCACCTGCCG
 GGTGGGCTGCTCCTGGGCTGGTGGCTTGGTCATGGGGATGGTGGTGACCTCGGCCATTTTC
 CACCTCGCCTTCTGTGGACACAAGGAGATCCACCATTCTTCTGCCACGTGCCACCTCTGTT
 GAAGTTGGCCTGTGGAGATGATGTGCTGGTGGTGGCCAAAGGCGTGGGCTTGGTGTGTAT
 CACGGCCCTGTGGGCTGTTTTCTCCTCATCCTCCTCTCCTATGCCCTCATCGTGGCCGCCA
 20 TCTTGAAGATCCCTTCTGCTGAAGGTCGGAACAAGGCCTTCTCCACCTGTGCCTCTCACCT
 CACTGTGGTGGTCTGCTGCACTATGGCTTTGCCTCCGTCATTTACCTGAAGCCCAAAGTCCC
 CAGTCTCCGGAAGGAGACACCTTGATGGGCATCACCTACACGGTCTCACACCTTCTCTCA
 GCCCCATCATCTTCAGCCTCAGGAACAAGGAGCTGAAGGTCGCCATGAAGAAGACTTGCTT
 CACCAAACCTCTTCCACAGAAGTCTGTA (SEQ ID NO: 194)

25

AOLFR106 sequences:

METANYTKVTEFVLTLGLSQTPEVQLVLFVIFLSFYLFILPGNLIICTISLDPHLTSPMYLLANLA
 FLDIWYSSITAPEMLIDFFVERKIISFDGCIQLFFLHFAGASEMFLLTVMAFDLYTAICRPLHYA
 TIMNQRLCCILVALSWRGGFIHSIIQVALVRLPFCGPNELDSYFCDITQVVRACANTFPEELVM
 30 ICSSGLISVVCLIALMSYAFLLALFKKLSGSGENTNRAMSTCYSHITIVLMFGPSIYTYARPF
 SFLDKVVSFVNTLIFPLRNPIYTLRNKEVKAAMRKLVTKYLCCKE (SEQ ID NO: 195)

ATGGAACTGCAAATTACACCAAGGTGACAGAATTTGTTCTCACTGGCCTATCCCAGACTC
 35 CAGAGGTCCAAGTAGTCCTATTTGTTATATTTCTATCCTTCTATTTGTTTCATCCTACCAGGA
 AATATCCTTATCATTTGCACCATCAGTCTAGACCCTCATCTGACCTCTCCTATGTATTTCT
 GTTGGCTAATCTGGCCTTCCTTGATATTTGGTACTCTTCCATTACAGCCCCTGAAATGCTCA
 TAGACTTCTTTGTGGAGAGGAAGATAATTTCTTTTGATGGATGCATTGCACAGCTCTTCTT
 CTTACACTTTGCTGGGCTTCGGAGATGTTCTTGTCTCACAGTGATGGCCTTTGACCTCTACA
 CTGCTATCTGCCGACCCCTCCACTATGCTACCATCATGAATCAACGTCTCTGCTGTATCCTG
 40 GTGGCTCTCTCCTGGAGGGGGGCTTCATTCTATCATACAGGTGGCTCTCATTGTTT
 GACTTCTTTCTGTGGGCCCAATGAGTTAGACAGTTACTTCTGTGACATCACACAGTTGT
 CCGGATTGCCTGTGCCAACACCTTCCCAGAGGAGTTAGTGATGATCTGTAGTAGTGGTCTG
 ATCTCTGTGGTGTGTTGATTGCTCTGTTAATGTCCTATGCCTTCCTTCTGGCCTTGTTCAA
 GAAACTTTCAGGCTCAGGTGAGAATACCAACAGGGCCATGTCCACCTGCTATTCCCACATT
 45 ACCATTGTGGTGCTAATGTTTGGGCCATCCATCTACATTTATGCTCGCCATTGACTCGTT
 TTCCCTAGATAAAGTGGTGTCTGTGTTCAATACTTTAATATTCCCTTTACGTAATCCCATTA
 TTTACACATTGAGAAACAAGGAAGTAAAGGCAGCCATGAGGAAGTTGGTCACCAAATATA
 TTTTGTGTAAAGAGAAGTGA (SEQ ID NO: 196)

AOLFR107 sequences:

MELWNFTLGSFILVGLNDGSPPELLCATITILYLLALISNGLLLAITMEARLHMPMYLLLGQ
 LSLMDLLFTSVVTPKALADFLRRENTISFGGALQMFLALTMGGAEDLLAFMAYDRYVAICH
 PLTYMTLMSRACWLMVATSWILASLSALIYTVYTMHYPCRAQEIRHLLCEPHLLKVACAD
 TSTRYELMVYVMGVTFILPSLAAILASYTQILLTVLHMPNSNEGRKKALVTCSSHLTVVGMFYGA
 55 ATFMVYLPSSFHSTRQDNIIISVFYITVTPALNPLIYSLRNKEVMRALRRVLGKYMLPAHSTL
 (SEQ ID NO: 197)

5 ATGGAGCTCTGGAACCTCACCTTGGGAAGTGGCTTCATTTTGGTGGGGATTCTGAATGACA
 GTGGGTCTCCTGAACTGCTCTGTGCTACAATTACAATCCTATACTTGTGGCCCTGATCAG
 CAATGGCCTACTGCTCCTGGCTATCACCATTGGAAGCCCGGCTCCACATGCCCATGTACCTC
 10 CTGCTTGGGCAGCTCTCTCTCATGGACCTCCTGTTTACATCTGTTGTCACCTCCCAAGGCCCT
 TGGCGGACTTTCTGCGCAGAGAAAACACCATCTCCTTTGGAGGCTGTGCCCTTCAGATGTTT
 CTGGCACTGACAATGGGTGGTGTGAGGACCTCCTACTGGCCTTCATGGCCTATGACAGGT
 ATGTGGCCATTTGTCTATCCTCTGACATACATGACCCTCATGAGCTCAAGAGCCTGCTGGCT
 CATGGTGGCCACGTCTCGATCCTGGCATCCCTAAGTGCCCTAATATATAACCGTGATACC
 15 ATGCACTATCCCTTCTGCAGGGCCAGGAGATCAGGCATCTTCTCTGTGAGATCCCACT
 TGCTGAAGGTGGCTGTGCTGATACCTCCAGATATGAGCTCATGGTATATGTGATGGGTGT
 GACCTTCTGATTCCCTCTCTTGTGCTATACTGGCCTCCTATACACAAATCTACTCAGT
 TGCTCCATATGCCATCAAATGAGGGGAGGAAGAAAGCCCTTGTACCTGCTCTTCCCACCT
 GACTGTGGTTGGGATGTTCTATGGAGCTGCCACATTATGTATGTCTTGGCCAGTTCTCTCC
 20 ACAGCACCAGACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAA
 TCCACTCATCTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCTGGG
 AAAATACATGCTGCCAGCACACTCCACGCTCTAG (SEQ ID NO: 198)

AOLFR108 sequences:

20 MCSFFLCQTGKQAKISMGEENQTFVSKFIFLGLSDDLQTLILLFILFLITYLLTVLGNQLIILIFLD
 SRLHTPMYFFLRNLSFADLCFSTSIVPQVLVHFLVKRKTISFYGCMTQIIVFLLVGTECALLAV
 MSYDRYVAVCKPLYSTIMTQRVCLWLSFRSWASGALVSLVDTSTFHLPHYWGQNIINHYFCE
 PPALLKLASIDTYSTEMAIFSMGVVILLAPVSLILGSYWNIIISTVIQMOSGEGRLKAFSTCGSHLI
 25 VVVLFGSGIFTYMRPNSKTTKELDKMISVFYTAITPMLNPIIYSLRNKDVKGALRKLVRKRC
 FSHRQ (SEQ ID NO: 199)

30 ATGTGTTCTTTTTTCTTGTGCCAAACAGGTAAACAGGCAAAAATATCAATGGGAGAAGAAA
 ACCAAACCTTTGTGTCCAAGTTTATCTTCTGGGTCTTTCACAGGACTTGCAGACCCAGAT
 CCTGCTATTTATCCTTTTCTCATCTTTATCTGCTGACCGTGCTTGGAAACCAGCTCATCA
 TCATTCTCATCTTCTGGATTCTCGCCTTCACACTCCCATGTATTTTTTTCTTAGAAATCTCT
 CCTTTCAGATCTCTGTTTCTCTACTAGCATTGTCCCTCAAGTGTGGTTCACCTCTTGGTA
 AAGAGGAAAACCATTTCTTTTTATGGGTGTATGACACAGATAATTGTCTTCTTCTGGTTG
 GGTGTACAGAGTGTGCGCTGCTGGCAGTGATGTCTATGACCGGTATGTGGCTGTCTGCAA
 35 GCCCCTGTACTACTCTACCATCATGACACAACGGGTGTGTCTCTGGCTGTCTTCAGGTCTT
 GGGCCAGTGGGGCACTAGTGTCTTTAGTAGATAACCAGCTTTACTTTCCATCTTCCCTACTG
 GGGACAGAATATAATCAATCACTACTTTTGTGAACCTCCTGCCCTCCTGAAGCTGGCTTCC
 ATAGACACTTACAGCACAGAAATGGCCATCTTTTCAATGGGCGTGGTAATCCTCCTGGCCC
 CTGTCTCCCTGATTCTTGGTTCTTATTGGAATATTATCTCCACTGTTATCCAGATGCAGTCT
 GGGGAAGGGAGACTCAAGGCTTTTTCCACCTGTGGCTCCCATCTTATTGTTGTTGTCCTCTT
 40 CTATGGGTGAGGAATATTCACCTACATGCGACCAAACCTCCAAGACTACAAAAGAACTGGA
 TAAAATGATATCTGTGTTCTATACAGCGGTGACTCCAATGTTGAACCCCATATTTATAGC
 TTGAGGAACAAAGATGTCAAAGGGGCTCTCAGGAACTAGTTGGGAGAAAGTGCTTCTCT
 CATAGGCAGTGA (SEQ ID NO: 200)

AOLFR109 sequences:

45 MLRNGSIVTEFILVGFQSSSTSTRALLFALFLALYSLTAMNGLIIFITSWTDPKLNSPMYFFLG
 HLSLLDVCFTTTTIPQMLIHLVVRDHVSVFCCMTQMYFVFCVGVAEICILLAFMAYDRYVAICY
 PLNYVPISQKVCVRLVGTAWFFGLINGIFLEYISFREPFRRDNHIESFFCEAPIVIGLSCGDPQFSL
 WAIFADAIIVILSPMVLTVTSYVHILATILSKASSSGRGKTFSTCASHLTVVIFLYTSAMFSYMN
 50 PHSTHGPDKDKPFSLLYTIITPMCNPIIYSFRNKEIKEAMVRALGRTRLAQPQSV (SEQ ID NO:
 201)

55 ATGCTAAGGAATGGCAGCATAGTGACGGAATTTATCCTCGTGGGCTTTCAGCAGAGCTCCA
 CTTCCACACGAGCATTGCTCTTTGCCCTCTTCTTGGCCCTCTACAGCCTCACCATGGCCATG
 AATGGCCTCATCATCTTTATCACCTCCTGGACAGACCCCAAGCTCAACAGCCCCATGTACT
 TCTTCTCGGCCATCTGTCTCTCCTGGATGTCTGCTTCATCACCCTACCATCCACAGATG

TTGATCCACCTCGTGGTCAGGGACCACATTGTCTCCTTTGTATGTTGCATGACCCAGATGT
 ACTTTGTCTTCTGTGTTGGTGTGGCCGAGTGCATCCTCTTGGCTTTCATGGCCTATGACCGT
 TATGTTGCTATCTGCTACCCACTTAACTATGTCCCGATCATAAGCCAGAAGGTCTGTGTCA
 GGCTTGTGGGAAGTGCCTGGTCTTTGGGCTGATCAATGGCATCTTTCTCGAGTATATTTC
 5 ATTCCGAGAGCCCTTCCGAGAGACAACCACATAGAAAGCTTCTTCTGTGAGGCCCCCATA
 GTGATTGGCCTCTCTTGTGGGGACCCCTCAGTTTGTCTGTGGGCAATCTTTGCCGATGCCA
 TCGTGGTAATTCTCAGCCCCATGGTGCTCACTGTCACTTCCTATGTGCACATCCTGGCCACC
 ATCCTCAGCAAAGCCTCCTCCTCAGGTGCGGGGAAGACTTCTCTACTTGTGCCTCTCACC
 TGACTGTGGTCATCTTTCTCTACACTTCAGCTATGTTCTCTTACATGAACCCCCACAGCACA
 10 CATGGGCCTGACAAAGACAAACCTTTCTCCCTCCTGTACACCATCATTACCCCCATGTGCA
 ACCCCATCATTATAGTTTCCGCAACAAGGAAATTAAGGAGGCCATGGTGAGGGCACTTG
 GAAGAACCAGGCTGGCCCAGCCACAGTCTGTCTAG (SEQ ID NO: 202)

AOLFR110 sequences:

15 MKIANNTVVTEFILLGLTQSQDIQLLVFVLILIFYLILPGNFLIIFIRSDPGLTAPLYLFLGNLAFL
 DASYSFIVAPRMLVDFLSEKKVISYRGCTQLFFLHFLGGEGLLLVVMAFDRYIAICRPLHCST
 VMNPRACYAMMLALWLGGFVHSIIQVVLRLPFCGPNQLDNFFCDVRQVIKLA CTDMFVVEL
 LMVFNSGLMTLLCFLGLLASAYAVILCHVRRASEGKNKAMSTCTTRVIIIIMFGPAIFYMCPF
 20 RALPADKMSVSLFHTVIFPLMNPMTIYLRNQEVKTSMKRLLSRHVVCQVDFIIRN (SEQ ID NO:
 203)

ATGAAGATAGCAAACAACACAGTAGTGACAGAATTTATCCTCCTTGGTCTGACTCAGTCTC
 AAGATATTCAGCTCTTGGTCTTTGTGCTGATCTTAATTTTCTACCTTATCATCCTCCCTGGA
 AATTTTCTCATTATTTTACCATAAAGGTCAGACCCTGGGCTCACAGCCCCCTCTATTTATT
 25 TCTGGGCAACTTGGCCTTCTGGATGCATCCTACTCCTTCATTGTGGCTCCCAGGATGTTG
 TGGACTTCTCTCTGAGAAAAAGGTAATCTCCTACAGAGGCTGCATCACTCAGCTCTTTTT
 CTTGCACCTTCTTGGAGGAGGGGAGGGATTACTCCTTGTGTGATGGCCTTTGACCGCTAC
 ATCGCCATCTGCCGGCCTCTGCACTGTTCAACTGTCATGAACCCTAGAGCCTGCTATGCAA
 TGATGTTGGCTCTGTGGCTTGGGGGTTTTGTCCACTCCATTATCCAGGTGGTCTCATCCTC
 30 CGCTTGCTTTTTGTGGCCCAAACAGCTGGACAACCTTCTTCTGTGATGTCCGACAGGTCA
 TCAAGCTGGCTTGCACCGACATGTTTGTGGTGGAGCTTCTAATGGTCTTCAACAGTGGCCT
 GATGACACTCCTGTGCTTTCTGGGGCTTCTGGCTTCTATGCAGTCATCCTCTGCCATGTTT
 GTAGGGCAGCTTCTGAAGGGAAGAACAAGGCCATGTCCACGTGCACCACTCGTGTCTTAT
 TTATACTTCTTATGTTTGGACCTGCTATCTTCACTACATGTGCCCTTTCAGGGCCTTACCA
 35 GCTGACAAAGATGGTTTCTCTCTTTCACACAGTGATCTTTCCATTGATGAATCCTATGATTTA
 TACCCTTCGCAACCAGGAAGTGAAAACCTCCATGAAGAGGTTATTGAGTCGACATGTAGTC
 TGTCAAGTGGATTTTATAATAAGAACTGA (SEQ ID NO: 204)

AOLFR111 sequences:

40 MCYTYLIFKEWTLIFYFSLLLFLQITPAIMANLTIVTEFILMGFSTNKNMCLHSILFLLIYLCALM
 GNVLIIMITTLDHHLHTPVYFELKNLSFLDLCLISVTAPKSIANSLIHNNSISFLGCVSQVFLLS
 ASAEULLLTVMSFDRTAICHPLHYDVIMDRSTCVQRATVSWLYGGLIAVMHTAGTFSLSYCG
 SNMVHQFFCDIPQLLAISCENLIREIALILINVLDFFCFIVIIIYVHVSTVKKIPSTEGQSKAY
 45 SICLPHELLVFLSTGFIAYLKPASESPSILDAVISVFYTMLPPTFNPITYSLRNKAIKVALGMLIKG
 KLTKK (SEQ ID NO: 205)

ATGTGTTATATATATTTAATATTTAAAGAGTGGACATTGATATTTTACTTCAGTCTTCTCCT
 TTTCTGCAATTACTCCTGCAATAATGGCAAATCTCACAATCGTGACTGAATTTATCCTTA
 TGGGGTTTTCTACCAATAAAAATATGTGCATTTTGCATTGCGATTCTTCTTGTGATTAT
 50 TTGTGTGCCCTGATGGGGAATGTCCTCATTATCATGATCACAACCTTTGGACCATCATCTCC
 ACACCCCCGTGATTTCTTCTTGAAGAATCTATCTTTCTTGGATCTCTGCCTTATTTAGTC
 ACGGCTCCCAAATCTATCGCCAATCTTTGATACACAACAACCTCCATTTCACTTCTTGGCTG
 TGTTTCCCAGGTCTTTTGTGCTTTCTTCACTCTGCAGAGCTGCTCCTCCTCAGGGTGA
 TGTCTTTGACCGCTATACTGCTATATGTCACCTCTGCACTATGATGTCATCATCGACAGG
 55 AGCACTGTGTCCAAAGAGCCACTGTGTCTTGGCTGTATGGGGGTCTGATTGCTGTGATGC
 ACACAGCTGGCACCTTCTCCTTATCCTACTGTGGGTCCAACATGGTCCATCAGTTCTTCTGT

GACATTCCCCAGTTATTAGCTATTTCTTGCTCAGAAAATTTAATAAGAGAAATTGCACTCA
 TCCTTATTAATGTAGTTTTGGATTTCTGCTGTTTTATTGTCATCATCATTACCTATGTCCAC
 GTCTTCTCTACAGTCAAGAAGATCCCTTCCACAGAAGGCCAGTCAAAAGCCTACTCTATTT
 GCCTTCCACACTTGCTGGTTGTGTTATTTCTTTCCACTGGATTCAATTGCTTATCTGAAGCCA
 5 GCTTCAGAGTCTCCTTCTATTTTGGATGCTGTAATTTCTGTGTTCTACACTATGCTGCCCCC
 AACCTTTAATCCATTATATACAGTTTGAGAAACAAGGCCATAAAGGTGGCTCTGGGGATG
 TTGATAAAGGGAAAGCTCACCAAAAAGTAA (SEQ ID NO: 206)

AOLFR113 sequences:

10 MKFWHGFSSHLNPMFSSFLYLSPWINTTIQAWLNLCSLALPVWAMSGAGFLSCCYWHTCSP
 SVVTCSSSQSSDWMQLCTHLCTTSLVFFPSWSCGILPLSLRCLIFSRRKPFLLQDASFRPTSS
 TPWGACECYLLTAMAYDRYLAICRPLHYPIIMTTTLCAKMAAACWTCGFLCPISEVILASQLPF
 CAYNEIQHIFCDFPPLSLACKDTSANILVDFAINAFIILITFFIMISYARIIGAVLKIKTASGRKK
 AFSTCASHLA VVLIFFGSIFMYVRLKKSYSLTLDRTLAI VYSVLT PMVNPPIYSLRNKEIKAIKR
 15 TIFQKGDKASLAHL (SEQ ID NO: 207)

ATGTGTCAACAAATCTTACGGGATTGCATTCTTCTCATACATCATTTTGTGCATTAACAGGA
 AAAAAGTCTCACTTGTGATGCTGGGTCCAGCTTATAACCACACAATGGAAACCCCTGCCTC
 CTTCCTCCTTGTGGGTATCCCAGGACTGCAATCTTCACATCTTTGGCTGGCTATCTCACTGA
 20 GTGCCATGTACATCATAGCCCTGTTAGGAAACACCATCATCGTGAAGTCAATCTGGATGGA
 TTCCACTCGGCATGAGCCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATGTGA
 TGGCCTCCTCGGTGGTACCCAAGATGGTGAGCATCTTCTGCTCAGGAGACAGCTCAATCAG
 CTTTAGTGCTTGTTCCTCACTCAGATGTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGG
 CTGCTGCTGACCATGGCTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGA
 25 GAATTCTCAGCCTCAAGTGATGCTGGGAATGAGTATGGCCATCACCATCAGAGCTATCAT
 AGCCATAACTCCACTGAGTTGGATGGTGAGTCATCTACCTTTCTGTGGCTCCAATGTGGTT
 GTCCACTCCTACTGTGAGCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCCA
 GCAGTCTCTACAGTCTGATTGGTTCCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCT
 GCCTCCTATATCTTAATTCTCAAGGCAGTATTTGGTCTCTCCTCAAAGACTGCTCAGTTGAA
 30 AGCATTAAAGCACATGTGGCTCCCATGTGGGGGTTATGGCTTTGTAATCTACCTGGGATG
 GCATCCATCTATGCGGCCCTGGTTGGGGCAGGATGTAGTGCCCTTGACACCCCAAGTCCCTGC
 TAGCTGACCTGTACGTGATCATCCCAGCCACCTTAAATCCCATCATCTATGGCATGAGGAC
 CAAACAACCTGCGGGAGAGAATATGGAGTTATCTGATGCATGTCCTCTTTGACCATTCCAAC
 CTGGGTTTCATGA (SEQ ID NO: 208)

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AOLFR114 sequences:

MERINHTSSVSEFILLGLSSRPEDQKTLFVLFLIVYLVTITGNLLIILAIRFNPHLQTPMYFFLSFLS
 LTDICFTTSVVPKMLMNFLEKKTISYAGCLTQMYFLYALGNSDSCLLAVMAFDYRVAVCDPF
 HYVTTMSHHHCVLLVAFSCSFPHLHSLHTLLNRLTFCDNSNVHHLCDLSPVLKLSCSSIFVN
 40 EIVQMTEAPIVLVTRFLCIAFSYIRILTVLKIPSTSGKRKAFSTCGFYLTVVTLFYGSIFCVYLQP
 PSTYAVKDHVATTIVYTVLSSMLNPFYISLRNKDLKQGLRKLMSKRS (SEQ ID NO: 209)

ATGGAAAGAATCAACCACACCAGCAGTGTCTCCGAGTTTATCCTCCTGGGACTCTCCTCCC
 GGCCTGAGGACCAAAGACACTCTTTGTTCTCTTCTCATCGTGACCTGGTCACCATAAC
 45 AGGGAACCTGCTCATCATCCTGGCCATTGCTTCAACCCCCATCTTACAGACCCCTATGTATT
 TCTTCTTGAGTTTTCTGTCTCTCACTGATATTTGCTTTACAACAAGCGTTGTCCCCAAGATG
 CTGATGAACTTCTGTCAGAAAAGAAGACCATCTCCTATGCTGGGTGTCTGACACAGATGT
 ATTTTCTCTATGCCTTGGGCAACAGTGACAGCTGCCTTCTGGCAGTCATGGCCTTTGACCG
 CTATGTGGCCGTCTGTGACCCCTTTCCACTATGTCACCACCATGAGCCACCACCACTGTGTCC
 50 TGCTGGTGGCCTTCTCCTGCTCATTTCCTCACCTCCACTCACTCCTGCACACACTTCTGCTG
 AATCGTCTCACCTTCTGTGACTCCAATGTTATCCACCCTTTCTCTGTGACCTCAGCCCTGT
 GCTGAAATTGTCTGCTCTTCCATATTTGTCAATGAAATTGTGCAGATGACAGAAGCACCT
 ATTGTTTGGTGACTCGTCTTCTCTGTCATTTCTCTTATATACGAATCCTCACTACAGT
 TCTCAAGATTCCCTCTACTTCTGGGAAACGCAAAGCCTTCTCCACCTGTGGTTTTTACCTCA
 55 CCGTGGTGACGCTCTTTTATGGAAGCATCTTCTGTGTCTATTTACAGCCCCCATCCACCTAC
 GCTGTCAAGGACCACGTGGCAACAATTGTTTACACAGTTTGTGTCATCCATGCTCAATCCTT

TTATCTACAGCCTGAGAAACAAAGACCTGAAACAGGGCCTGAGGAAGCTTATGAGCAAGA
GATCCTAG (SEQ ID NO: 210)

AOLFR115 sequences:

5 MEGFYLRRSHELQGMGKPGRVNQTTVSDFLLGLSEWPPEQPLLFGIFLGMYLVTMVGNNLLI
LAISSDPHLHTPMYFFLANLSLTDACFTSASIPKMLANIHTQSQIISYSGCLAQLYFLLMFGGLD
NCLLAVMAYDRYVAICQPLHYSTSMSPQLCALMLGVCWVLTNCPALMHTLLLTRVAFCAQK
AIPHFYCDPSALLKLACSDTHVNELMIITMGLLFLTVPLLLVFSYVRIFWAVFVISSPGGRWKA
FSTCGSHLTVVLLFYGSLMGVYLLPPSTYSTERESRAAVLYMVIIPTLNPFTYSLRNRDMKEALG
10 KLFVSGKTFFL (SEQ ID NO: 211)

ATGGAAGGTTTTTATCTGCGCAGATCACACGAACTACAAGGGATGGGAAAACCAGGCAGA
GTGAACCAAACTGTTTCAGACTTCCTCCTTCTAGGACTCTCTGAGTGGCCAGAGGAGC
AGCCTCTTCTGTTTGGCATCTTCCTTGGCATGTACCTGGTCACCATGGTGGGGAACCTGCTC
15 ATTATCCTGGCCATCAGCTCTGACCCACACCTCCATACTCCCATGTACTTCTTTCTGGCCAA
CCTGTCAATTAAGTATGCCTGTTTCACTTCTGCCTCCATCCCCAAAATGCTGGCCAAACATTC
ATACCCAGAGTCAGATCATCTCGTATTCTGGGTGTCTTGCACAGCTATATTTCTCCTTATG
TTTGGTGGCCTTGACAACTGCCTGCTGGCTGTGATGGCATATGACCGCTATGTGGCCATCT
GCCAACCCTCCATTACAGCACATCTATGAGTCCCCAGCTCTGTGCACTAATGCTGGGTGT
20 GTGCTGGGTGCTAACCAACTGTCCTGCCCTGATGCACACACTGTTGCTGACCCGCGTGGCT
TTCTGTGCCAGAAAGCCATCCCTCATTTCTATTGTGATCCTAGTGCTCTCCTGAAGCTTGC
CTGCTCAGATACCCATGTAAACGAGCTGATGATCATACCATGGGCTTGCTGTTCTCCTACT
GTTCCCCTCCTGCTGATCGTCTTCTCCTATGTCCGATTTTCTGGGCTGTGTTTGTCTACTC
ATCTCCTGGAGGAGATGGAAGGCCTTCTCTACCTGTGGTCTCATCTCACGGTGGTTCTG
25 CTCTTCTATGGGTCTCTTATGGGTGTGATTACTTCTCCATCAACTTACTCTACAGAGAG
GGAAAGTAGGGCTGCTGTTCTCTATATGGTGATTATTTCCACGCTAAACCCATTCAATTTAT
AGCTTGAGGAACAGAGACATGAAGGAGGCTTTGGGTAACTTTTTGTGAGTGAAAAACA
TTCTTTTTATGA (SEQ ID NO: 212)

AOLFR116 sequences:

30 MDEANHSVSEFVFLGLSDSRKIQLLLFLFFSVFYVSSLMGNLLIVLTVTSDPRLQSPMYFFLAN
LSIINLVFCSSTAPKMIYDLFRKHKTISFGGCVVQIFFIHAVGGTEMVLLIAMAFDRYVAICKPLH
YLTIMNPQRCLFLVISWIIHHSVIQLAFVVDLLFCGPNELDSFFCDLPRFIKLACIETYTLGFMV
TANSGFISLASFLILISYIFILVTQKKSSGGIFKAFLSAHVIVVVLVFGPLIFFYIFPPTSHLD
35 KFLAIFDAVITPVLNPVIYTFRNKEMMVAMRRRCSQFVNYSKIF (SEQ ID NO: 213)

ATGGATGAAGCCAATCACTCTGTGGTCTCTGAGTTTGTGTTCTCTGGGACTCTCTGACTCGC
GGAAGATCCAGCTCCTCCTCTTCTCTTTTTCTCAGTGTTCTATGTATCAAGCCTGATGGGA
AATCTCCTCATTTGTGCTAACTGTGACCTCTGACCTCGTTTACAGTCCCCCATGTACTTCT
40 GCTGGCCAACTTTCCATCATCAATTTGGTATTTTGTTCCTCCACAGCTCCCAAGATGATT
ATGACCTTTTCAGGAAGCACAAGACCATCTCTTTTGGGGGCTGTGTAGTTCAGATCTTCTT
TATCCATGCAGTTGGGGGAAGTGAAGTGGTGTGCTCATAGCCATGGCTTTTGACCGATAT
GTGGCCATATGTAAGCCTCTCCACTACCTGACCATCATGAACCCACAAAGGTGCATTTTGT
TTTTAGTCATTTCTGGATTATAGGTATTATTACTCAGTGATTGAGTTGGCTTTTGTGTA
45 GACCTGTGTTCTGTGGCCCTAATGAATTAGATAGTTTCTTTTGTGATCTTCTCGATTTAT
CAAAGTGGCTTGATAGAGACCTACACATTGGGATTGATGGTTACTGCCAATAGTGGATTT
ATTTCTCTGGCTCTTTTTTAATTCTCATAATCTCTTACATCTTTATTTTGGTGACTGTTGAG
AAAAAATCTTCAGGTGGTATATTCAAGGCTTTCTCTATGCTGTGAGCTCATGTGATTGTTG
TGTTTTTGGTCTTTGGGCCATTAATCTTTTTCTATATTTTCCATTTCCACATCACATCTTG
50 ATAAATTCCTTGCCATCTTTGATGCAGTTATCACTCCCGTTTTGAATCCAGTCATCTATACT
TTTAGAAATAAAGAGATGATGGTGGCAATGAGAAGACGATGCTCTCAGTTTGTGAATTAC
AGTAAATCTTTTAA (SEQ ID NO: 214)

AOLFR117 sequences:

55 MNNTIVFVIKIQIEKSDLKYRAISLQEISKISLLFWVLLLVISRLLAMTLGNSTEVTEFYLLGFGA
QHEFWCILFIVFLLIYVTSIMGNSGILLINTDSRFQTLTYFFLQHLAFVDICYTSAITPKMLQSF

EEKNLILFQGCVIQFLVYATFATSDCYLLAMMAVDPYVAICKPLHYTVIMSRTVCIRLVAGSYI
MGSINASVQTGFTCSLSFCKSNSINHHFFCDVPPILALSCSNVDINIMLLVVFVGSNLIFTGLVVIFS
YTYMATILKMSSSAGRKKSFSSTCASHLTAVTIFYGTLSTYMYLQSHSNNSQENMKVAFIFYGTVI
PMLNPLIYSLRNKEVKEALKVIGKKLF (SEQ ID NO: 215).

5

ATGAATAACACTATTGTATTTGTCATAAAAAATACAAATAGAAAAAAGTGACTTGAAATATA
GAGCCATTTTCATTGCAAGAAATCTCAAAGATTTCCCTTCTTTTCTGGGTCTTCTCTTGGTC
ATTTCTAGACTTTTACTAGCCATGACACTAGGAAACAGCACTGAAGTCACTGAATTCTATC
TTCTGGGATTTGGTGCCAGCATGAGTTTTGGTGTATCCTCTTCATTGTATTCTTCTCATC
10 TATGTGACCTCCATAATGGGTAATAGTGGAATAATCTTACTCATCAACACAGATTCCAGAT
TTCAAACACTCACGTACTTTTTCTACAACATTTGGCTTTTGTGTATATCTGTTACACTTCT
GCTATCACTCCCAAGATGCTCCAAAGCTTCACAGAAGAAAAGAATTTGATATTATTTTCAGG
GCTGTGTGATACAAATCTTAGTTTATGCAACATTTGCAACCAGTGACTGTTATCTCCTGGCT
ATGATGGCAGTGGATCCTTATGTTGCCATCTGTAAGCCCCTTCACTATACTGTAATCATGT
15 CCCGAACAGTCTGCATCCGTTTGGTAGCTGGTTCATACATCATGGGCTCAATAAATGCCTC
TGACAAAACAGGTTTTACATGTTCACTGTCCTTCTGCAAGTCCAATAGCATCAATCACTTTT
TCTGTGATGTTCCCCCTATTCTTGTCTTTTCATGCTCCAATGTTGACATCAACATCATGCTA
CTTGTGTCTTTGTGGGATCTAACTTGATATTCAGTGGGTTGGTTCATCTTTTCTACAT
CTACATCATGGCCACCATCCTGAAAATGTCTTCTAGTGCAGGAAGGAAAAAATCCTTCTCA
20 ACATGTGCTTCCACCTGACCGCAGTCACCATTTTCTATGGGACACTCTCTTACATGTATTT
GCAGTCTCATTCTAATAATTCCCAGGAAAATATGAAAGTGGCCTTTATATTTTATGGCACA
GTTATTCCCATGTTAAATCCTTAACTATAGCTTGAGAAATAAGGAAGTAAAGAAGCTT
TAAAAGTGATAGGGAAAAAGTTATTTTAA (SEQ ID NO: 216)

25 **AOLFR118 sequences:**

MNHMSASLKISNSSKFQVSEFILLGFPGIHSWQHWLSLPLALLYLSALAANTLILIIWQNPSLQQ
PMYIFLGILCMVDMGLATTIIPKILAFWFDKVISLPECFAQIYAIHFFVGMESGILLCMAFDRIY
VAICHPLRYPISIVTSSLILKATLFMVLNRGLFVTPVPVLAQRDYCSKNEIEHCLCSNLGVTSLA
CDDRRPNSICQLVLAWLGMGSDLILILSYILILYSVLRNLNSAEAAAKALSTCSSHLTLILFFYTTV
30 VVISVTHLTEMKATLIPVLLNVLHNIIPPSLNPTVYALQTKELRAAFQKVLFAITKEIRS (SEQ ID
NO: 217)

ATGAATCATATGTCTGCATCTCTCAAAATCTCCAATAGCTCCAAATCCAGGTCTCTGAGTT
CATCCTGCTGGGATTCCCGGGCATTACAGCTGGCAACACTGGCTATCTCTGCCCCTGGCA
35 CTACTGTATCTCTCAGCACTTGCTGCAAACACCCTCATCCTCATCATCTGGCAGAACCC
TTCTTTACAGCAGCCCATGTATATTTTCTTGGCATCCTCTGTATGGTAGACATGGGTCTGG
CCACTACTATCATCCCTAAGATCCTGGCCATCTTCTGGTTTGATGCCAAGGTTATTAGCCTC
CCTGAGTGCCTTTGCTCAGATTTATGCCATTCACTTCTTTGTGGGCATGGAGTCTGGTATCCT
ACTCTGCATGGCTTTTGATAGATATGTGGCTATTTGTACCCCTCTTCGCTATCCATCAATTG
40 TCACCAGTTCCTTAATCTTAAAAGCTACCCTGTTTCATGGTGCTGAGAAATGGCTTATTTGTC
ACTCCAGTGCCTGTGCTTGCAGCACAGCGTGATTATTGCTCCAAGAATGAAATTGAACACT
GCCTGTGCTCTAACCTTGGGGTCACAAGCCTGGCTTGTGATGACAGGAGGCCAAACAGCAT
TTGCCAGTTGGTTCTGGCATGGCTTGGGAATGGGGAGTGATCTAAGTCTTATTATACTGTCA
TATATTTTGATTCTGTACTCTGTACTTAGACTGAACTCAGCTGAAGCTGCAGCCAAGGCC
45 TGAGCACTTGATGTTACATCTCACCCCTCATCCTTTTCTTTTACACTATTGTTGTAGTGATT
TCAGTGACTCATCTGACAGAGATGAAGGCTACTTTGATTCCAGTTCTACTTAATGTGTTGC
ACAACATCATCCCCCTTCCCTCAACCCTACAGTTTATGCACTTCAGACCAAAGAAGCTTAG
GGCAGCCTTCCAAAAGGTGCTGTTTGCCCTTACAAAAGAAATAAGATCTTAG (SEQ ID NO:
218)

50

AOLFR119 sequences:

MPLFNSLCWFPTIHVTPPSFILNGIPGLERVHVWISLPLCTMYIIFLVGNLGLVYLIYYEESLHHP
MYFFFGHALSLIDLLTCTTLPNALCIFWFSLEKINFNACLAQMFFVHGFTGVESGVLMLMALD
RYIAICYPLRYATTLTNPIAKAELATFLRGVLLMIPFPFLVKRLPFCQSNISHTYCDHMSVVKL
55 SCASIKVNVITYGLMVALLIGVFDICISLSYTLILKAAISLSSSDARQKAFSTCTAHISAMITYVPA

FFTFFAHRFGGHTTPPSLHIIVANLYLLLPPTLNPVYGVKTKQIRKSVIKFFQGDKGAG (SEQ ID NO: 219)

5 ATGCCTCTATTTAATTCATTATGCTGGTTTCCAACAATTCATGTGACTCCTCCATCTTTTAT
TCTTAATGGAATACCTGGTCTGGAAAGAGTACATGTATGGATCTCCCTCCCACTCTGCACA
ATGTACATCATCTTCTTGTGGGGAATCTTGGTCTTGTGTACCTCATTTATTATGAGGAGTC
CTTACATCATCCGATGTATTTTTTTTTTGGCCATGCTCTCTCCCTCATTGACCTCCTTACCTG
CACCACCACTCTACCCAATGCACTCTGCATCTTCTGGTTCAGTCTCAAAGAAATTAACCTCA
10 ATGCTTGCTTGGCCCAGATGTTCTTTGTTTCATGGGTTACAGGTGTGGAGTCTGGGGTGCT
CATGCTCATGGCTCTAGACCGCTATATAGCCATTTGCTACCTTTGCGTTATGCTACCACAC
TCACCAACCTATCATTGCCAAGGCTGAGCTTGCCACCTTCTGAGGGGTGTATTGCTGAT
GATTCCTTTCCCATTTCTTGGTTAAGCGTTTGCCTTCTGCCAAAGCAATATTATCTCCATA
CGTACTGCGACCACATGTCTGTAGTAAAGCTATCTTGTGCCAGCATCAAGGTCAATGTAAT
CTATGGTCTAATGGTTGCTCTCCTGATTGGAGTGTGTTGACATTTGTTGTATATCTTTGTCTT
15 ACACCTTTGATCCTCAAGGCAGCGATCAGCCTCTCTTCATCAGATGCTCGGCAGAAGGCTTT
CAGCACTGCACCTGCCCATATATCTGCCATCATCACCTATGTTCCAGCATTTCTTCACTT
TCTTTGCCACCGTTTTTGGGGGACACACAATTCCCCCTTCTCTTACATCATTGTGGCTAAT
CTTTATCTTCTTCTCCCCCACTCTAAACCTATTGTTTATGGAGTAAAGACAAAACAGAT
ACGCAAGAGTGTCTATAAAGTTCTTCCAGGGTGATAAGGGTGCAGGTTGA (SEQ ID NO: 220)

20

AOLFR120 sequences:

MQPYTKNWTQVTEFVMMGFAGIHEAHLFFILFLTMLYFTLVENLAAILVVGLDHLRLRRPMYF
FLTHLSCLIEWYTSVTPKMLAGFIGVDGKKNISYAGCLSQLFIFTFLGATECFLLAAMAYDRY
VAICMPLHYGAFVSWGT CIRLAAACWLVGFLTPILPIYLLSQLTCGPNVIDHFSCDASPLLALS
25 CSDVTWKETVDFLVSLAVLLASSMVIASVGNIVWTLHLIRSAERWKAFTCAHLTVVSLF
YGTLLFFMYVQTKVTSSINFNKVVSVFYSVVTPLNPLIYSLRNKEVKALGRVFSLNFWKGQ
(SEQ ID NO: 221)

30 ATGCAACCATATACCAAAAACTGGACCCAGGTAAGTGAATTTGTCATGATGGGCTTTGCTG
GCATCCATGAAGCACACCTCCTCTTCTTCATACTCTCCTCACCATGTACCTGTTACCTTG
GTGGAGAATTTGGCCATCATTTTAGTGGTGGGTTTGGACCACCGACTACGGAGACCCATGT
ATTTCTTCCTGACACACTTGTCTGCCTTGAAATCTGGTACACTTCTGTTACAGTGCCCAAG
ATGCTGGCTGGTTTTATTGGGGTGGATGGTGGCAAGAATATCTCTTATGCTGGTTGCCTAT
CCCAGCTCTTCATCTTCACCTTTCTTGGGGCAACTGAGTGTTTCCTACTGGCTGCCATGGCC
35 TATGATCGTTATGTGGCCATTTGTATGCCTCTCCACTATGGGGCTTTTGTGTCTGGGGCAC
CTGCATCCGCTCTGGCAGCTGCCTGTGGCTGGTAGGTTTCTTCACCCCATCTTGCCAACTCT
ACCTCTTGTCTCAGCTAACATTTTGTGGCCAAATGTCAATTGACCATTTCTCCTGTGATGCC
TCACCTTGCTAGCCTTGTCTGCTCAGATGTCACTTGAAGGAGACTGTGGATTTCTCTGG
TGTCTCTGGCTGTGCTACTGGCCTCCTCTATGGTCATTGCTGTGTCTATGGCAACATCGTC
40 TGGACACTGCTGCACATCCGCTCAGCTGCTGAGCGCTGGAAGGCCTTCTTACCTGTGCAG
CTCACCTGACTGTGGTGAGCCTCTTCTATGGCACTCTTTTCTTTATGTATGTCCAGACCAAG
GTGACCTCCTCCATCAACTTCAACAAGGTGGTATCTGTCTTCTACTCTGTTGTACGCCCAT
GCTCAATCCTCTCATCTACAGTCTTAGGAACAAGGAAGTGAAGGGAGCTCTGGGTGCGAGTC
TTTTCTCTCAACTTTTGAAGGGACAGTGA (SEQ ID NO: 222)

45

AOLFR121 sequences:

MKRKNFTEVSEFIFLGFSSFGKHQITLFFVFLTVYILTLVANIIIVTHCIDHHLHTPMYFFLSMLA
SSETVYTLVIVPRMLLSLIFHNQPISLAGCATQMFFVILATNNCFLLTAMGYDRYVAICRPLRY
TVIMSKGLCAQLVCGSFGIGLTMAVLHVTAMFNLPFCGTVVDHFFCDIYPVMKLSCIDTTINEII
50 NYGVSSFVIFVPIGLIFISYVLVISSILQIASAEGRKKTFATCVSHLTVVIVHCGCASIAYLKPKSES
SIEKDLVLSVYTIITPLNPNVYSLRNKEVKDALCRVVGGRNIS (SEQ ID NO: 223)

55 ATGAAGAGAAAGAACTTCACAGAAGTGTCAGAATTCATTTTCTTGGGATTTTCTAGCTTTG
GAAAGCATCAGATAACCCTCTTTGTGGTTTTCTAACTGTCTACATTTTAACTCTGGTTGCT
AACATCATCATTTGTGACTATCATCTGCATTGACCATCATCTCCACACTCCCATGTATTCTT
CCTAAGCATGCTGGCTAGTTCAGAGACGGTGTACACACTGGTCATTGTGCCACGAATGCTT

TTGAGCCTCATTTTTTCATAACCAACCTATCTCCTTGGCAGGCTGTGCTACACAAATGTTCTT
 TTTTGTATCTTGGCCACTAATAATTGCTTCTGCTTACTGCAATGGGGTATGACCGCTATG
 TGGCCATCTGCAGACCCCTGAGATACACTGTCATCATGAGCAAGGGACTATGTGCCACGCT
 GGTGTGTGGGTCCTTTGGCATTGGTCTGACTATGGCAGTTCTCCATGTGACAGCCATGTTT
 5 AATTTGCCGTTCTGTGGCACAGTGGTAGACCACTTCTTTTGTGACATTTACCCAGTCATGA
 AACTTTCTTGCATTGATACCACTATCAATGAGATAATAAATTATGGTGTAAAGTTCAATTTGT
 GATTTTTGTGCCCATAGGCCTGATATTTATCTCCTATGTCCTTGTCTCTCTCCATCCTTC
 AAATTGCCTCAGCTGAGGGCCGGAAGAAGACCTTTGCCACCTGTGTCTCCACCTCACTGT
 GGTATTGTCCACTGTGGCTGTGCCTCCATTGCCTACCTCAAGCCGAAGTCAGAAAGTTCA
 10 ATAGAAAAAGACCTTGTCTCTCAGTGACGTACACCATCATCACTCCCTTGTGAAACCTGT
 TTGTTTACAGTCTGAGAAACAAGGAGGTAAAGGATGCCCTATGCAGAGTTGTGGGCAGAA
 ATATTTCTTAA (SEQ ID NO: 224)

AOLFR122 sequences:

15 MEWENQTLVEFFLKGHVHPRLLELFFVLIFIMYVILLGNGTLILISILDPHLHTPMYFFLGNL
 SFLDICYTTSIPSTLVSFSLSERKTISFSGCAVQMFLGLAMGTTECVLLGMMAFDRYVAICNPLR
 YPIIMSKNAYVPMVAVGSWFAGIVNSAVQTTFFVQLPFCRKNVINHFSCIELAVMKLACADISGN
 EFLMLVATILFTLMPLLLIVISYSLIISILKIHSSSEGRSKAFSTCSAHLTVVIFGYTILFMYMKPKS
 KETLNSDDL DATDKIISMFYGVMTMPMMNPLIYSLRNKDVK EAVKHLNRRFFSK (SEQ ID NO:
 20 225)

ATGGAATGGGAAAACCAACCAATTCTGGTGGAATTTTTCTGAAGGGACATTCTGTTTACC
 CAAGGCTTGAGTTACTCTTTTTGTGCTAATCTTCATAATGTATGTGGTCATCCTTCTGGGG
 AATGGTACTCTCATTTTAATCAGCATCTTGGACCCCTCACCTTCACACCCCTATGTACTTCTT
 25 TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCACCTCTATTCCCTCCACACTAG
 TGAGCTTCTTTTCAAGAAAGAAAGACCAATTTCTTTTCTGGCTGTGCAGTGCAGATGTTCTT
 GGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCATGATGGCCTTTGACCGCTATG
 TGGCTATCTGCAACCCCTGAGATATCCCATCATCATGAGCAAGAAATGCCTATGTACCCAT
 GGCTGTTGGGTCCTGGTTTGCAGGGATTGTCAACTCTGCAGTACAACTACATTTGTAGTA
 30 CAATTGCCTTTCTGCAGGAAGAATGTCATCAATCATTTCTCATGTGAAATTCTAGCTGTCTAT
 GAAGTTGGCCTGTGCTGACATCTCAGGCAATGAGTTCCTCATGCTTGTGGCCACAATATTG
 TTCATTGATGCCACTGCTCTTGATAGTTATCTCTTACTCATTAATCATTTCAGCATCCT
 CAAGATTCACTCCTCTGAGGGGAGAAGCAAGCTTTCTCTACCTGCTCAGCCCATCTGACT
 GTGGTCATAATATTCTATGGGACCATCCTCTTCATGTATATGAAGCCCAAGTCTAAAGAGA
 35 CACTTAATTGAGATGACTTGGATGCTACCGACAAAATTATATCCATGTTCTATGGGGTGAT
 GACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAAGAGGCAGT
 AAAACACCTACCGAACAGAAGGTTCTTTAGCAAGTGA (SEQ ID NO: 226)

AOLFR123 sequences:

40 MYRFTDFDVSNSIYLNHVLFYTTQQAGDLEHMETRNYSAMTEFFLVGLSQYPELQLFLFLCL
 IMYMIILLGNSLLIITILDSRLHTPMYFFLGNSLFLDICYTSSSIPMLIIFMSERKSISFIGCALQM
 VVSLGLSTECVLLAVMAYDHYVAICNPLRYSIIMNGVLVYQMAAWSWIIGCLTSLQTVLT
 MMLPFCGNVIDHITCEILALLKLVCSBITINVLIMTVTNIVSLVILLLLIFISYVFLSSILRINCAE
 GRKKAFTSCSAHSIVVILFYGSALFMYMKPKSKNTNTSDEHGLSYGVVSPMLNPIIYSLRNKEV
 45 KEAVKKVLSRHLHLLKM (SEQ ID NO: 227)

ATGTACAGATTTACAGATTTTGATGTATCAAACATTTCAATTTACCTGAATCATGTCCTTTT
 CTATACTACCCAGCAGGCAGGTGACCTAGAACACATGGAGACAAGAAATTACTCTGCCAT
 GACTGAATTTCTTCTGGTGGGGCTTTCCCAATATCCAGAGCTCCAGCTTTTTCTGTTCTCTGC
 50 TCTGCCTCATCATGTACATGATAATCCTCCTGGGAAATAGCCTCCTCATTATCATCAACATC
 TTGGATTCTCGCCTCCATACTCCCATGTATTTCTTTCTTGGAAACCTCTCATTCTTGGACAT
 CTGTTACACATCCTCATCCATTCTCCCAATGCTTATTATATTTATGTCTGAGAGAAAATCCA
 TCTCCTTCATGGCTGTGCTCTGCAGATGGTTGTGTCCCTTGGCTTGGGCTCCAGTGT
 GTCCTCCTGGCTGTGATGGCCTATGACCACTATGTGGCCATCTGCAACCCACTGAGGTACT
 55 CCATCATCATGAACGGAGTGCTGTATGTGCAATGGCTGCATGGTCTGGATCATAGGCTG
 TCTGACCTCCCTATTGCAACAGTTCTGACAATGATGTTGCCTTTCTGTGGGAATAATGTC

ATTGATCATATTACCTGTGAAATTTTGGCCCTTCTAAAACTTGTTTGTTTCAGATATCACCAT
 CAATGTGCTTATCATGACAGTGACAAATATTGTTTCACTGGTGATTCTTCTACTGTTAATTT
 TCATCTCCTATGTGTTTATTCTCTCTTCCATCCTGAGAATTAATTGTGCTGAGGGAAGAAAG
 AAAGCCTTCTCTACCTGTTTCAGCGCACTCGATTGTGGTCATCTTATTCTACGGTTCAGCCCT
 5 TTTTATGTACATGAAACCCAAGTCAAAGAACTAATAACATCTGATGAGATTATTGGGCTG
 TCTTATGGAGTGGTAAGCCCAATGTTAAATCCCATCATCTATAGCCTCAGGAATAAAGAGG
 TCAAAGAGGCTGTAAAGAAAGTCTGAGCAGACATCTGCATTTATTGAAAATGTGA (SEQ
 ID NO: 228)

10 **AOLFR124 sequences:**

MNHSVVFTEFILLGLTKPELQGIIFLFFLIVYLVAFLGNMLIIIAKIYNNLHTPMYVFLTLAVV
 DIICTTIIPKMLGTMLTSENTISYAGCMSQLFLFTWSLGAEMVLFTTMAYDRYVAICFPLHYST
 VMNHHMVCALLSMVMAIAVTNSWVHTALIMRLTFCGPNTIDHFFCEIPLLALS CSPVRINEV
 MVYVADITLAIGDFILTCISYGFIIIVAILRIRTVGKRFKAFSTCSSHLTVVTLYYSPVIYTYRPA
 15 YTFERDKVVAALYTLVPTLNPVVSFQNRMQAGIRKVFAFLKH (SEQ ID NO: 229)

ATGAATCACAGCGTTGTAAGTGAAGTTCATTATTCTGGGCCTCACCAAAAAGCCTGAACTCC
 AGGGAATTATCTTCCTCTTTTTCTCATTTGTCTATCTTGTGGCTTTTCTCGGCAACATGCTC
 ATCATCATTGCCAAAATCTATAACAACACCTTGATACGCCCATGTATGTTTTCTTCTGAC
 20 ACTGGCTGTTGTGGACATCATCTGCACAACAAGCATCATACCGAAGATGCTGGGGACCAT
 GCTAACATCAGAAAATACCATTTTATATGCAGGCTGCATGTCCAGCTCTTCTTGTTCACA
 TGGTCTCTGGGAGCTGAGATGGTTCTCTTACCACCATGGCCTATGACCGCTATGTGGCCA
 TTTGTTTCCCTCTTATTACAGTACTGTTATGAACCACCATATGTGTGTAGCCTTGCTCAGC
 ATGGTCATGGCTATTGCAGTCACCAATTCCTGGGTGCACACAGCTCTTATCATGAGGTTGA
 25 CTTTCTGTGGGCCAAACACCATGACCACTTCTTCTGTGAGATAACCCCATGCTGGCTTTG
 TCCTGTAGCCCTGTAAGAATCAATGAGGTGATGGTGTATGTTGCTGATATTACCTGGCCA
 TAGGGGACTTTATTCTTACCTGCATCTCCTATGGTTTTATCATTGTTGCTATTCTCCGTATC
 CGCACAGTAGAAGGCAAGAGGAAGGCCTTCTCAACATGCTCATCTCATCTCACAGTGGTG
 ACCCTTTACTATTCTCCTGTAATCTACACCTATATCCGCCCTGCTTCCAGCTATACATTTGA
 30 AAGAGACAAGGTGGTAGCTGCACTCTATACTCTTGTGACTCCACATTAAACCCGATGGTG
 TACAGCTTCCAGAATAGGGAGATGCAGGCAGGAATTAGGAAGGTGTTTGCATTTCTGAAA
 CACTAG (SEQ ID NO: 230)

AOLFR125 sequences:

MTNQTQMMEFLLVRFTENWVLLRLHALLFSLIYLTAVLMNLVIIIIMILDHRLHMAMYFFLRH
 LSFLDLCLISATVPKSLNSVASTDSISFLGCVLQLFLVLLAGSEIGILTAMSYDRYAAICCPHLC
 EAVMSRGLCVQLMALSWLNRGALGLLYTAGTFSLNPHYGSDELHQFFCDVPALLKLTCSKEHAI
 ISVSVAIGVCYAFSCLVCIVVSYVYIFSAVLRISQRQRQSKAFSNCVPHLIVVTVFLVTGAVAYL
 KPGSDAPSILDLLVSVFYSVAPPTLNPVIYCLKNKDIKSALS KVLWNVRSSGVMKDD (SEQ ID
 40 NO: 231)

ATGACCAATCAGACACAGATGATGGAATTCTTGCTTGTGAGATTTACTGAGAATTGGGTGC
 TCCTGAGGCTGCATGCTTTGCTCTTCTCACTGATCTACCTCACGGCTGTGCTGATGAATTTA
 GTCATCATTTCTCCTCATGATTCTGGACCATCGTCTCCACATGGCAATGTACTTTTCTCCTCCG
 45 ACATTTGTCCTTCTTAGACCTGTGTCTCATTTCTGCCACAGTCCCCAAATCCATCCTCAACT
 CTGTGCGCTCCACTGACTCCATCTCCTTCTGGGGTGTGTGTTGCAGCTCTTCTTGGTGGTA
 CTGCTGGCTGGATCAGAGATTGGCATCCTTACTGCCATGTCCTATGACCGCTATGCTGCCA
 TCTGCTGCCCCCTACACTGTGAGGCTGTCATGAGCAGAGGGCTCTGTGTCCAGTTGATGGC
 TCTGTCTGGCTCAACAGAGGGGCTTGGGACTCTTGTACACAGCTGGAACATTCTCTCTG
 50 AATTTTTATGGCTCTGATGAGCTACATCAGTTCTTCTGCGATGTCCCTGCCCTACTAAAGCT
 CACTTGTCTTAAAGAACATGCCATCATTAGTGTGAGTGTGGCCATTGGGGTCTGTTATGCA
 TTTTCATGTTTAGTTTGCATTGTAGTTTCTTATGTGTACATTTTCTCTGCTGTGTTAAGGAT
 ATCAGAGACAGAGACAATCCAAAGCCTTTTCCAAGTGTGTGCTCACCTCATCTTGTGTC
 ACTGTGTTTCTTGTAAACAGGTGCTGTTGCTTATTTAAAGCCAGGGTCTGATGCACCTTCTAT
 55 TCTAGACTTGCTGGTGTCTGTGTTCTATTCTGTGCGACCTCCAACCTTGAACCTGTTATCT

ACTGTCTGAAGAACAAGGACATTAAATCCGCTCTGAGTAAAGTCCTGTGGAATGTTAGAA
GCAGTGGGGTAATGAAAGATGACTAA (SEQ ID NO: 232)

AOLFR126 sequences:

5 MFLYLCFIFQRTCSEEMBEENATLLTEFVLTGFLHQPDKIPLFLAFLVIYELITIMGNLGLIVLIW
KDPHLHIPMYLFLGSLAFVDASLSSTVTPKMLINFLAKSKMISLSECMVQFFSLVTTVTTECFLL
ATMAYDRYVAICKALLYPVIMTNELCIQLLVLSFIGGILLHALIHEAFSRLTFCNSNIQHIFYCDII
PLLKISCTDSSINFLMVFIAGSVQVFTIGTILISYTIILFTILEKKSIKIRKAVSTCGAHLSSVSLY
10 YGPLTFKYLGSASPQADDQDMMESLFYTVIVPLLNPMIYSLRNKQVIASFTKMFKSNV (SEQ ID
NO: 233)

ATGTTCCCTTTACCTTTGCTTCATTTTTTCAGAGGACATGCAGTGAGGAGATGGAAGAGGAAA
ATGCAACATTGCTGACAGAGTTTGTCTCACAGGATTTTTACATCAACCTGACTGTAAAAT
ACCGCTCTTCCTGGCATTCTTGGTAATATATCTCATCACCATCATGGGGAATCTTGGTCTAA
15 TTGTTCTCATCTGGAAGACCCCTCACCTTCATATCCCAATGTACTTATTCCTTGGGAGTTTA
GCCTTTGTGGATGCTTCGTTATCATCCACAGTGAAGGACTCCGAAGATGCTGATCAACTTCTTAG
CTAAGAGTAAGATGATATCTCTCTGAATGCATGGTACAATTTTTTCCCTTGTAACCACT
GTAACCACAGAAATGTTTTCTCTTGGCAACAATGGCATATGATCGCTATGTAGCCATTGCA
AAGCTTTACTTTATCCAGTCATTATGACCAATGAACTATGCATTGAGCTATTAGTCTTGTC
20 TTTATAGGTGGCCTTCTTCATGCTTTAATCCATGAAGCTTTTTTCATTGAGTTAACCTTCTG
TAATTCCAACATAATACAACACTTTTACTGTGACATTATCCATTGTTAAAGATTTCTGTA
CTGATTCCTCTATTAACCTTTCTAATGGTTTTTATTTTCGAGGTTCTGTTCAAGTTTTTACCA
TTGGAACATTCTTATATCTTATACAATATCCTCTTTACAATCTTAGAAAAGAAGTCTATC
AAAGGGATACGAAAAGCTGTCTCCACCTGTGGGGCTCATCTCTTATCTGTATCTTTATACT
25 ATGGCCCCCTCACCTTCAAATATCTGGGCTCTGCATCTCCGCAAGCAGATGACCAAGATAT
GATGGAGTCTCTATTTTACACTGTCATAGTTCCCTTTATTAATCCCATGATCTACAGCCTGA
GAAACAAGCAAGTAATAGCTTCATTCACAAAAATGTTCAAAAGCAATGTTTAG (SEQ ID
NO: 234)

30 **AOLFR127 sequences:**

MSNEDMEQDNTLLTEFVLTGLTYQPEWKMPFLVFLVIYELITIVWNLGLIALIWNDPQLHIPM
YFFLGSLAFVDAWISSTVTPKMLVNFLAKNRMISLSECMIQFFSFAGGTTECFLLATMAYDRY
VAICKPLLYPVIMNNSLCIRLLAFSLGGFLHALIHEVLIFRLTFCNSNIUHHIFYCDIIPLMISCTD
PSINFLMVFILSGSIQVFTIVTVLNSYTFALFTILKKKSVRGVRKAFSTCGAHLSSVSLYGGPLIF
35 MYLRPASQADDQDMIDSVFYTIIPLLNPIIYSLRNKQVIDSFTKMKVKNV (SEQ ID NO: 235)

ATGTCGAATGAGGACATGGAACAGGATAATACAACATTGCTGACAGAGTTTGTCTCACA
GGACTTACATATCAGCCAGAGTGGAATAATGCCCTGTCTTGGTGTTCTTGGTGATCTATC
TCATCACTATTGTGTGGAACCTTGGTCTGATTGCTCTTATCTGGAATGACCCACAACCTCAC
40 ATCCCCATGTACTTTTTTCTTGGGAGTTTAGCCTTTGTTGATGCTTGGATATCTTCCACAGT
AACTCCCAAAATGTTGGTTAATTTCTTGGCCAAAAACAGGATGATATCTCTGTCTGAATGC
ATGATTCAATTTTTTCTTTGCAATTTGGTGGAACACTACAGAATGTTTTCTTGGCAACAAT
GGCATATGATCGCTATGTAGCCATATGCAACCTTTACTATATCCAGTGATTATGAACAAT
TCACTATGCATACGGCTGTTAGCCTTCTCATTTTTAGGTGGCTTCCTCCATGCCTTAATTCA
45 TGAAGTCCTTATATTGAGATTAACCTTCTGCAATTCTAACATAATACATCATTTTTTACTGTG
ATATTATACCACTGTTTATGATTTCTGTACTGACCCTTCTATTAATTTTCTAATGGTTTTTA
TTTTGTCTGGCTCAATTCAGGTATTCACCATTTGTGACAGTTCTTAATTTCTTACACATTTGCT
CTTTTACAATCCTAAAAAAGAAGTCTGTTAGAGGCGTAAGGAAAGCCTTTTCCACCTGTG
GAGCCCATCTCTTATCTGTCTCTTTATATTATGGCCCACTTATCTTCATGTATTTGCGCCCT
50 GCATCTCCACAAGCAGATGACCAAGATATGATAGACTCTGTCTTTTATACAATCATAATTC
CTTTGCTAAATCCCATTATCTACAGTCTGAGAAATAAACAAGTAATAGATTCATTCACAAA
AATGGTAAAAAGAAATGTTTAG (SEQ ID NO: 236)

AOLFR128 sequences:

55 METQNLTVVTEFILLGLTQSQDAQLLVFVLVLFYLIILPGNFLIIFTIKSDPGLTAPLYFFLGNL
LLDASYSFIVVPRMLVDFLSEKKVISYRSCITQLFFLHFLGAGEMFLLVVMADFRIYIAICRPLHY

STIMNPRACYALSLVLWLGGFIHSIVQVALILHLPFCGPNQLDNFFCDVPQVIKLACTNTFVVEL
LMVSNSSGLLSLLCFLGLLASYAVILCRIREHSSEKSKAISTCTTHIIIFLMFGPAIFIYTCPFQAFP
ADKVVSLFHTVIFPLMNPVIYTLRNQEVKASMRKLLSQHMFC (SEQ ID NO: 237)

- 5 ATGGAACACAGAACCTCACAGTGGTGACAGAATTCATTCTTCTTGGTCTGACCCAGTCTC
AAGATGCTCAACTTCTGGTCTTTGTGCTAGTCTTAATTTTCTACCTTATCATCCTCCCTGGA
AATTTCTCATCATTTTACCATAAAGTCAGACCCTGGGCTCACAGCCCCCTCTATTCTT
TCTGGGCAACTTGGCCTTACTGGATGCATCCTACTCCTTCATTGTGGTTCCAGGATGTTG
GTGGACTTCTCTCTGAGAAGAAGGTAATCTCCTATAGAAGCTGCATCACTCAGCTCTTTT
10 TCTTGCATTTTCTTGGAGCGGGAGAGATGTTCTCCTCGTTGTGATGGCCTTTGACCGCTAC
ATCGCCATCTGCCGGCCTTTACACTATTCAACCATCATGAACCCTAGAGCCTGCTATGCAT
TATCGTTGGTTCTGTGGCTTGGGGGCTTTATCCATTCCATTGTACAAGTAGCCCTTATCCTG
CACTTGCCTTTCTGTGGCCCAACCAGCTCGATAACTTCTTCTGTGATGTTCCACAGGTCAT
CAAGCTGGCCTGCACCAATACCTTTGTGGTGGAGCTTCTGATGGTCTCCAACAGTGGCCTG
15 CTCAGCCTCCTGTGCTTCTTGGCCTTCTGGCCTCCTATGCAGTCATCCTCTGTCTGATAAG
GGAGCACTCCTCTGAAGGAAAGAGCAAGGCTATTTCCACATGCACCACCCATATTATCATT
ATATTTCTCATGTTTGGACCTGCTATTTCTACATCTACACTTGGCCCTTCCAGGCTTTCCGAGC
TGACAAGGTAGTTTCTCTTTTCCATACTGTCATCTTTCCTTTGATGAACCCTGTTATTTATA
CGCTTCGCAACCAGGAGGTGAAAGCTTCCATGAGGAAGTTGTTAAGTCAACATATGTTTTG
20 CTGA (SEQ ID NO: 238)

AOLFR129 sequences:

- MALYFSLHLHGMSDLFFLSTGHPRASCRMEAMKLLNQSQVSEFILLGLTSSQDVEFLLFALFSVI
YVVTVLGNLLIIVTFNTPNLNTPMYFLLGNLSFVDMTLASFATPKVILNLLKKQKVISFAGCFT
25 QIFLLHLLGGVEMVLLVSMADRYVAICKPLHYMTIMNKKVCVLLVVTSWLLGLLHSGFQIPF
AVNLPFCGPNVVDISIFCDLPLVTKLACIDIYFVQVVIVANSGLSCFIILLISYSLILITIKNHSPT
GQSKARSTLTAHITVVILFFGPCIFIYIWPFGNHSVDKFLAVFYTIITPILNPIIYTLRNKEMKISMK
KLWRAVNSREDT (SEQ ID NO: 239)
- 30 ATGGCTCTTTATTTTCACTCATACTCCATGGTATGAGTGATCTTTTCTTTCTCTCTACAGG
TCATCCAAGAGCGAGCTGTAGGATGGAGGCCATGAACTATTAAATCAATCTCAAGTGTC
AGAATTCATTTTGTCTGGGACTGACCAGCTCCAGGATGTAGAGTTTCTTCTCTTTGCCCTCT
TCTCGGTTATCTATGTGGTCACAGTTTTGGGTAACCTTCTTATTATAGTCACAGTGTTTAAAC
ACCCCTAACCTGAATACTCCCATGTATTTTCTCCTTGGTAATCTCTCTTTTGTAGATATGAC
35 CCTTGCTTCTTTTGCCACCCCTAAGGTGATTCTGAACCTTGTTAAAAAAGCAGAAGGTAATT
TCTTTTGTCTGGGTGCTTCACTCAGATAATTTCTCCTTCACTTACTGGGTGGGGTTGAAATGGT
ACTGTTGGTCTCCATGGCTTTTGACAGATATGTGGCCATTTGTAAGCCCCTACACTACATG
ACCATCATGAACAAGAAGGTATGTGTTTGTCTGTAGTGACCTCATGGCTCTTGGGTCTCC
TTCACTCAGGGTTTCAGATACCATTGTGCTGTAACCTTGGCCTTTTGTGGTCCCAATGTGGTA
40 GACAGCATTTTTTGTGACCTCCCTTTGGTTACTAAGCTTGCCTGTATAGACATATATTTGT
ACAGGTAGTCATTGTTGCCAACAGTGGCATAATCTCCCTGAGCTGTTTCATTATTTTGCTTA
TCTCCTACAGTCTGATCCTCATAACCATTAAAGAACCCTCTCCTACTGGGCAATCTAAAGC
CCGTTCCACTTTGACTGCTCACATCACAGTGGTGATTCTCTTCTTTGGCCCATGCATCTTTA
TCTACATTTGGCCCTTCGGCAACCCTCTGTAGATAAGTTCCCTTGCTGTGTTTTATACCATC
45 ATCACTCCTATCTTGAATCCAATTATCTATACTCTGAGAAACAAAGAAATGAAGATATCCA
TGAAAAAAGCTCTGGAGAGCTTTTGTGAATTCTAGAGAAGATACTTAG (SEQ ID NO: 240)

AOLFR131 sequences:

- MASTSNVTELIPTGLFQDPAVQSVCFVFLPVYLATVVGNGLIVLTVSISKSLDSPMYFFLSCLS
50 LVEISYSTIAPKFIIDLLAKIKTISLEGCLTQIFFHFFGVAEILLIVVMA YDCYVAICKPLHYMNI
ISRQLCHLLVAGSWLGGFCHSIIQILVIIQLPFCGPNVIDHYFCDLQPLFKLACTDTFMEGVIVLA
NSGLFSVFSFLILVSSYIVILVNLNRNHSABGRHKALSTCASHITVVILFFGPAIFLYMRPSTFTED
KLAVAFYTVITPMLNPIIYTLRNAEVKIAIRRLWSKKENPGRE (SEQ ID NO: 241)
- 55 ATGGCCAGTACAAGTAATGTGACTGAGTTGATTTTCACTGGCCTTTTCCAGGATCCAGCTG
TGCAGAGTGATGCTTTGTGGTGTCTTCTCCCGTGTACCTTGCCACGGTGGTGGGCAATGG

CCTCATCGTTCTGACGGTCAGTATCAGCAAGAGTCTGGATTCTCCCATGTACTTCTTCCCTTA
GCTGCCTGTCTTGGTGGAGATCAGTTATTCCTCCACTATCGCCCCTAAATTCATCATAGAC
TACTTGCCAAGATTAAAACCATCTCTCTGGAAGGCTGTCTGACTCAGATATTCTTCTTCCA
CTTCTTTGGGGTTGCTGAGATCCTTTTGATTGTGGTGATGGCCTATGATTGCTACGTGGCC
5 ATTTGCAAGCCTCTTCATTATATGAACATTATCAGTCGTCAACTGTGTACCTTCTGGTGGC
TGGTTCCTGGCTGGGGGGCTTTTGTCACTCCATAAATTCAGATTCTCGTTATCATCCAATTGC
CCTTCTGTGGTCCCAATGTGATTGACCACTATTTCTGTGACCTCCAGCCTTTATTCAAGCTT
GCCTGCACTGACACCTTCATGGAGGGGGTTATTGTGTTGGCCAACAGTGGATTATTCTCTG
TCTTCTCCTTCCCTCATCTTGGTGTCTCTTATATTGTCAATTCTGGTCAACTTGAGGAACCAT
10 TCTGCAGAGGGGAGGCACAAAGCCCTCTCCACCTGTGCTTCTCACATCACAGTGGTCATCT
TGTTTTTTGGACCTGCTATCTTCTCTACATGCGACCTTCTTCCACTTTCAGTGAAGATAAA
CTTGTGGCTGTATTCTACACGGTCATCACCCCATGCTGAACCCCATCATTTACACACTCAG
GAATGCAGAGGTGAAAATCGCCATAAGAAGATTGTGGAGCAAAAAGGAGAATCCAGGA
GGGAGTGA (SEQ ID NO: 242)

15

AOLFR132 sequences:

MVATNNVTEIFVGFSPQNWSQRVISVMFLMYTAVVLGNGLIVVTILASKVLTSPLYFFLSYL
SFVEICYCSVMAPKLIFDSFIKRVISLKGCLTQMFSLHFFGGTEAFLMVMAYDRYVAICKPL
HYMAIMNQRMCGLLVRIAWGGGLLSVGQTFLIFQLPFCGPNIMDHYFCDVHPVLELACADT
20 FFISLLITNGGSISVVSFFVLMASYLILHLRSHNLEGQHKALSTCASHVTVDLFFIPCSLVYIR
PCVTLPADKIVAVFYTVVTPLLNPVIYSFRNAEVKNAMRRFIGGKVI (SEQ ID NO: 243)

ATGGTTGCTACAAACAATGTGACTGAAATAATTTTCGTGGGATTTTCCCAGAATTGGAGTG
AGCAGAGGGTCATTTCTGTGATGTTTCTCCTCATGTACACAGCTGTTGTGCTGGGCAATGG
25 CCTCATTGTGGTGACCATCCTGGCCAGCAAAGTGCTCACCTCCCCATGTATTTCTTTCTCA
GCTACTTATCCTTTGTGGAGATCTGCTACTGTTCTGTCTATGGCCCCCAAGCTTATCTTTGAC
TCCTTTATCAAGAGGAAAGTCATTTCTCTCAAGGGCTGCCTCACACAGATGTTTTCCCTCC
ATTTCTTTGGTGGCACTGAGGCCTTTCTCCTGATGGTGATGGCCTATGACCGCTATGTGGC
CATCTGCAAGCCCTTGCACTACATGGCCATCATGAACCAGCGAATGTGTGGTCTCCTCGTG
30 AGGATAGCATGGGGCGGGGGCCTGCTGCATTCTGTTGGGCAAACCTTCTGATTTTCCAGC
TCCCGTTCTGTGGCCCCAACATCATGGACCACTACTTCTGTGATGTCCACCCAGTGCTGGA
GCTGGCCTGCGCAGACACCTTCTTCATTAGCCCTGCTGATCATCACCAATGGCGGCTCCATC
TCCGTAGTCAGTTTCTTCGTGCTGATGGCTTCTACCTGATCATCCTGCACTTCTTGAGAAG
CCACAACCTTGAGGGGGCAGCACAAGGCCCTCTCCACCTGTGCCTCTCATGTACAGTTGTC
35 GACCTGTTCTTCATACCTTGCTCCTTGGTCTATATTAGGCCCTGTGTACCCCTCCCTGCAGA
CAAGATAGTTGCTGTATTTTATACAGTGGTCACACCTCTCTTAAACCCTGTGATTTACTCCT
TCAGGAATGCTGAAGTGAAAAATGCCATGAGGAGATTTATTGGGGGAAAAGTAATTTGA
(SEQ ID NO: 244)

40 **AOLFR133 sequences:**

MTEFIFLVLSNPQEVQRVCFVIFLYTAIVLGNFLIVLTVMTSRSLGSPMYFFLSYLSFMEICYS
SATAPKLISDLLAERKVISWWGCMAQLFLHFFGGTEIFLLTVMAYDHYVAICKPLSYTTIMN
WQVCTVLVGIAWVGGMHSFAQILLIFHLLFCGPNVINHYFCDLVPLLKLACSDTFLIGLLIVAN
GGTILSVISFGVLLASYMVILLHLRTWSSEGWCKALSTCGSHFAVVILFFGPCVFNSLRPSTTLPI
45 DKMVAVFYTVITAILNPVIYSLRNAEMRKAMKRLWIRTLRLNEK (SEQ ID NO: 245)

ATGACTGAATTCATTTTTCTGGTACTTTCTCCCAACCAGGAGGTGCAGAGGGTTTGCTTTG
TGATATTTCTGTTCTTGTACACAGCAATTGTGCTGGGGAATTTCTCATTGTGCTCACTGTC
50 ATGACCAGCAGAAGCCTTGGTTCCCCCATGTACTTCTTCTCAGCTACCTCTCCTTCATGGA
GATCTGCTACTCCTCCGCTACAGCCCCCAAATCATCTCAGATCTGCTGGCTGAAAGGAAA
GTCATATCTTGGTGGGGCTGCATGGCACAGCTTTTCTTCTTGCACTTCTTTGGTGGCACTGA
GATTTTCTGCTCACTGTGATGGCCTATGACCACTATGTGGCCATCTGCAAGCCCCCTCAGC
TACACCACCATCACTGAACCTGGCAGGTGTGTACTGTCTTGTAGGAATAGCATGGGTGGGA
GGCTTCATGCATTCTTTGCACAAATCCTTCTCATCTTCCACCTGCTCTTCTGTGGCCCCAA
55 TGTGATCAATCACTATTTCTGTGACCTAGTTCCCCTTCTCAAACCTGCCTGCTCTGACACCT
TCCTCATTGGTCTGCTGATTGTTGCCAATGGAGGCACCCTGTCTGTGATCAGTTTTGGGGT

CCTCTTAGCATCCTATATGGTCATCTTGCTCCATCTGAGAACCTGGAGCTCTGAAGGGTGG
TGCAAAGCCCTCTCCACCTGTGGGTCCCATTTTCGCTGTGGTTATCTTGTTCTTTGGGCCCTG
CGTCTTCAACTCTCTGAGGCCTTCTACCACTCTGCCCCATAGACAAGATGGTGGCTGTGTTCT
ACACAGTGATAACCGCGATCCTGAACCCTGTCATCTACTCTCTGAGAAATGCTGAAATGAG
5 GAAGGCCATGAAGAGGCTGTGGATTAGGACATTGAGACTAAATGAGAAATAG (SEQ ID
NO: 246)

AOLFR134 sequences:

MTTILEVDNHTVTTRFILLGFPTPAFQLLFFSIFLATYLLTLENLLILAIHSDGQLHKPMYFFL
10 SHLSFLEMWYVTVISPKMLVDFLSHDKSISFNGCMTQLYFFVTFVCTEYILLAIMAFDRYVAIC
NPLRYPVIMTNQLCGTLAGGCWFCGLMTAMIKMVFLAQLHYCGMPQINHYFCDISPLLNVSCE
DASQAEMVDFFLALMVIAIPLCVVVASYAAILATILRIPSAQGRQKAFSTCASHLTVVILFYSMT
LFTYARPKLMYAYNSNKVSVLYTVIVPLLNPIIYCLRNHEVKAALRKTIHCRGSGPQNGAFS
S (SEQ ID NO: 247)
15
ATGACCACCATAATTCTGGAAGTAGATAATCATACAGTGACAACACGTTTCATTCTTCTGG
GGTTTCCAACACGACCAGCCTTCCAGCTTCTCTTTTTCTCCATTTTCCTGGCAACCTATCTG
CTGACACTGCTGGAGAATCTTCTTATCATCTTAGCTATCCACAGTGATGGGCAGCTGCATA
AGCCCATGTACTTCTTCTTGAGCCACCTCTCCTTCTGGAGATGTGGTATGTACAGTCATC
20 AGCCCCAAGATGCTTGTGACTTCCTCAGTCATGACAAGAGTATTTCCCTCAATGGCTGCA
TGACTCAACTTTACTTTTTGTGACCTTTGTCTGCACTGAGTACATCCTTCTTGCTATCATG
GCCTTTGACCGCTATGTAGCCATTTGTAATCCACTACGCTACCCAGTCATCATGACCAACC
AGCTCTGTGGCACACTGGCTGGAGGATGCTGGTTCTGTGGACTCATGACTGCCATGATTAA
GATGGTTTTTATAGCACAACTTCACTACTGTGGCATGCCTCAGATCAATCACTACTTTTGTG
25 ATATCTCTCCACTCCTTAACGTCTCCTGTGAGGATGCCTCACAGGCTGAGATGGTGGACTT
CTTCTTGGCCCTCATGGTCATTGCTATTCTCTTTGTGTTGTGGTGGCATCCTACGCTGCTA
TCCTTGCCACCATCCTCAGGATCCCTTCTGCTCAGGGCCGCCAAAAGGCATTCTCCACCTG
TGCTCCCACCTGACCGTCGTAATTCTCTTCTATTCCATGACACTTTTCACCTATGCCCGTC
CCAAACTCATGTATGCCTACAATTCCAACAAAGTGGIATCTGTCTCTACACTGTCAATTGTT
30 CCACTCCTCAACCCCATCATTTACTGTCTGAGGAACCATGAAGTAAAGGCAGCCCTCAGAA
AGACCATACATTGCAGAGGAAGTGGGCCCCAGGGAATGGGGCTTTCAGTAGTTAA (SEQ
ID NO: 248)

AOLFR135 sequences:

MIFPSHDSQAFTSVDMEVGNCTILTEFILLGFSADSQWQPILFGVFLMLYLITLSGNMTLVILRT
35 DSHLHTPMYFFIGNLSFLDFWYTSVYTPKILASCVSEDKRISLAGCGAQLFFSCVVAYTECYLL
AAMAYDRHAAICNPLLYSGTMTALCTGLVAGSYGGFLNAIAHTANTFRLHFCGKNIDHFFC
DAPPLVKMSCTNTRVYEKVLGTVGFTVLSSILAILISYVNILLAILRIHSASGRHKAFSTCASHL
ISVMLFYGSLLFMYSRPSSTYSLERDKVAALFYTVINPLNPLIYSLRNKDIKEAFRKATQTIQPQ
40 T (SEQ ID NO: 249)

ATGATTTTCCCTTCTCATGATAGTCAGGCTTTCACCTCCGTGGACATGGAAGTGGGAAATT
GCACCATCCTGACTGAATTCATCTTGTGGGTTTCTCAGCAGATTCCAGTGGCAGCCGAT
TCTATTTGGAGTGTTTCTGATGCTCTATTTGATAACCTTGTCAGGAAACATGACCTTGGTTA
45 TCTTAATCCGAACCTGATTCCCACTTGCATACCTATGTACTTTTTTATTGGCAATCTGTCT
TTTTTGGATTCTGGTATACCTCTGTGTATACCCCAAAATCCTGGCCAGTTGTGTCTCAGA
AGATAAGCGCATTTCTTGGCTGGATGTGGGGCTCAGCTGTTTTTTCTGTGTGTAGCCT
ACACTGAATGCTATCTCCTGGCAGCCATGGCATATGACCGCCATGCAGCAATTTGTAACCC
ATTGCTTTATTACAGGTACCATGTCCACCGCCCTCTGTACTGGGCTTGTGTGCTGCTCCTACA
50 TAGGAGGATTTTTGAATGCCATAGCCCATACTGCCAATACATTCCGCCTGCATTTTTGTGG
TAAAAATATCATTGACCACITTTTCTGTGTATGACCACCATTGGTAAAAATGTCTGTACA
AACACAGGGTCTACGAAAAAGTCTGTGCTTGGTGTGGTGGGCTTCACAGTACTCTCCAGCA
TTCTTGCTATCCTGATTTCTATGTCAACATCCTCCTGGCTATCCTGAGAATCCCACTCAGCT
TCAGGAAGACACAAGGCATTCTCCACCTGTGCTTCCACCTCATCTCAGTCATGCTCTTCTA
55 TGGATCATTGTTGTTTATGTATTCAAGGCCTAGTTCACCTACTCCCTAGAGAGGGACAAA
GTAGCTGCTCTGTTCTACACCGTGATCAACCCACTGCTCAACCCTCTCATCTATAGCCTGAG

AAACAAAGATATCAAAGAGGCCTTCAGGAAAGCAACACAGACTATACAACCACAAACATG
A (SEQ ID NO: 250)

AOLFR136 sequences:

5 MTMENYSMAAQFVLDGLTQQAELQLPLFLLFLGIYVVTVVGNLGMILLIAVSPLLHTPMYYFL
SSLSFVDFCYSSVITPKMLVNFLGKKNILYSECMVQLFFFVVFVVAEGYLLTAMAYDRYVAIC
SPLLYNAIMSSWVCSLLVLAFFLGLFSLALHTSMMKLSFCKSHIINHYFCDVLPILLNLSCSNT
HLNELLFFIAGFNTLVPTLAVAVSYAFILYSILHIRSSEGRSKAFGTCSHLMVAVIFFGSITFMY
FKPPSSNSLDQEKVSSVFYTTVIPMLNPLIYSLRNKDVKKALRKVLVGK (SEQ ID NO: 251)

10 ATGACCATGGAAAATTATCTATGGCAGCTCAGTTTGTCTTAGATGGTTTAACACAGCAAG
CAGAGCTCCAGCTGCCCTCTTCTCCTGTTCTGGAATCTATGTGGTCACAGTAGTGGG
CAACCTGGGCATGATTCTCCTGATTGCAGTCAGCCCTCTACTTCACACCCCCATGTACTATT
TCCTCAGCAGCTTGTCTTCGTCGATTTCTGCTATTCTCTGTCTATTACTCCAAAATGCTG
15 GTGAACCTCCTAGGAAAGAAGAATACAATCCTTTACTCTGAGTGCATGGTCCAGCTCTTTT
TCTTTGTGGTCTTTGTGGTGGCTGAGGGTTACCTCCTGACTGCCATGGCATATGATCGCTA
TGTTGCCATCTGTAGCCCACTGCTTTATAATGCGATCATGTCTCATGGGTCTGCTCACTGC
TAGTGCTGGGTGCTTCTTCTTGGGCTTTCTCTGCTTGAATCATACAAGTGCCATGATG
AAACTGTCCTTTTGCAAATCCACATTATCAACCATTACTTCTGTGATGTTCTTCCCTCCT
20 CAATCTCTCCTGCTCCACACACACCTCAATGAGCTTCTACTTTTATCATTGCGGGGTTTA
ACACCTTGGTGCCCACTAGCTGTGTGCTGCTCTCTATGCTTCATCCTCTACAGCATCCTT
CACATCCGCTCCTCAGAGGGCCGGTCCAAAGCTTTTGAACATGCAGCTCTCATCTCATGG
CTGTGGTGATCTTCTTTGGGTCCATTACCTTCATGTATTTCAAGCCCCCTTCAAGTAACTCC
CTGGACCAGGAGAAGGTGTCCTCTGTGTTCTACACCACGGTGATCCCCATGCTGAACCCTT
25 TAATATACAGTCTGAGGAATAAGGATGTGAAGAAAGCATTAAAGGAAGGTCTTAGTAGGAA
AATGA (SEQ ID NO: 252)

AOLFR137 sequences:

30 MSPENQSSVSEFLLLGLPIRPEQQA VFFALFLGMYLTTVLGNLLIMLLIQLDShLHTPMYFFLSH
LALTDISFSSVTPKMLNMQTQHLAVFYKGCISQTYFFIFFADLDSFLITSMAYDRYVAICHPL
HYATIMTQSQCVMVLVAGSWVIACALLHTLLLAQLSFCADHIIPHYFCDLGALLKLSCSDTSL
NQLAIFTAALTAIMLPFLCILVSYGHIGVTILQIPSTKGICKALSTCGSHLSVVITYYRTIIGLYFLP
PSSNTNDKNILASVIYTA VTPMLNPFYISLRNKDIKALRKLLSRSGAVAHACNLSTLGG (SEQ
ID NO: 253)

35 ATGAGCCCTGAGAACCAGAGCAGCGTGTCCGAGTTCCTCCTCCTGGGCCTCCCCATCCGGC
CAGAGCAGCAGGCCGTGTTCTTCGCCCTGTTCCTGGGCATGTACCTGACCACGGTGCTGGG
GAACCTGCTCATCATGCTGCTCATCCAGCTAGACTCTCACCTTCACACCCCCATGTACTTCT
TCCTTAGCCACTTGGCCCTCACTGACATCTCCTTTTTCATCTGTCACTGTCCCTAAGATGCTG
40 ATGAACATGCAGACTCAGCACCTAGCCGCTTTTACAAGGGATGCATTTACAGACATATT
TTTTCATATTTTTTGTGACTTAGACAGTTTCTTATCACTTCAATGGCATATGACAGGTAT
GTGGCCATCTGTATCCTCTACATTATGCCACCATCATGACTCAGAGCCAGTGTGTATGC
TGGTGGCTGGGTCTGGGTGCTGCTTGTGCGTGTGCTCTTTTGCATACCCTCCTCCTGGCC
CAGCTTTCTTCTGTGCTGACCACATCATCCCTCACTACTTCTGTGACCTTGGTGCCCTGCT
45 CAAGTTGTCTGCTCAGACACCTCCCTCAATCAGTTAGCAATCTTTACAGCAGCATTGACA
GCCATTATGCTTCCATTCCCTGTGCATCCTGGTTTCTTATGGTCACATTGGGGTCACCATCCT
CCAGATTCCCTCTACCAAGGGCATATGCAAAGCCTTGTCCACTTGTGGATCCCACCTCTCA
GTGGTGACTATCTATTATCGGACAATTATTGGTCTCTATTTTCTTCCCCCATCCAGCAACAC
CAATGACAAGAACATAATTGCTTCAGTGATATACACAGCAGTCACTCCCATGTTGAACCCA
50 TTCATTTACAGTCTGAGAAATAAAGACATTAAAGGAGCCCTAAGAAAACCTCTTGAGTAGG
TCAGGCGCAGTGGCTCATGCCTGTAATCTCAGCACTTTGGGAGGCTGA (SEQ ID NO: 254)

AOLFR138 sequences:

55 MLNFTDVFTEFILLGLTSRREWQVLFFIVFLVYIITVVGNIGMMLLIKVSPQLNSPMYFFLSHLS
FVDVWFSSNVTTPKMLENLFSDDKKTISYADCLAQCFFIALVHVEIFILAAIAFDRYTVIGNPLLY
GSKMSRGVCIRLITFPYIYGFLTSLTATLWTYGLYFCGKIEINHFCADPPLIKMACAGTFVKEY

TMLILAGINFTYSLTVIIISYLFILIAILRMRSABGRQKAFSTCGSHPTAVIIFYGTLIFMYLRRPTE
ESVEQGMVAVFYTTVIPMLNPMIYSLRNKDVKKAMMKVISRSC (SEQ ID NO: 255)

5 ATGCTCAATTTACCGATGTGACAGAGTTCAATCTTTTGGGGCTAACGAGCCGTCGGGAAT
GGCAAGTCTCTTCTTTCATCGTTTTCTTGTGGTCTACATTATCACCGTGGTGGGCAATATC
GGCATGATGTTGTTAATCAAGGTCAGTCTCAGCTTAACAGCCCCATGTACTTTTTCTCTCA
GTCACCTGTCAATTTGTTGATGTGTGGTTTTCTTCCAATGTCACCCCTAAAATGTTGGaAAAT
CTGTTATCAGATAAAAAACAATTTCTTATGCTGGCTGTTTAGCACAGTGTTCCTTCTTCAT
TGCTCTTGTCCATGTGGAAATTTTTATTCTTGTGCGATTGCCTTTGATAGATACACAGTGA
10 TTGGAAATCCTTTGCTTTATGGCAGCAAAATGTCAAGGGATGTCTGTATTGACTGATTAC
TTTCCCTTACATTTATGGTTTTCTGACGAGTCTGACAGCAACATTATGGACTTATGGCTTGT
ACTTCTGTGGAAAAATGAGATCAACCATTTCTACTGTGCAGATCCACCTCTCATCAAAAT
GGCCTGTGCCGGGACCTTTGTAAAAGAATATACAATGCTCATACTTGCCGGCATCAACTTC
ACATATTCCTGACTGTAATTATCATCTCTTACTTATTCATCCTCATTGCCATTCTGCGAAT
15 GCGCTCAGCAGAAGGAAGGCAGAAGGCCTTTTCCACATGTGGGTCCCATCTGACAGCTGT
CATCATATTTCTATGGTACTCTGATCTTTCATGTATCTCAGACGTCCACAGAGGAGTCTGTG
GAGCAGGGGAAGATGGTGGCTGTGTTCTATACCACAGTGATCCCCATGTTGAATCCCATGA
TCTACAGTCTGAGGAACAAGGATGTGAAAAAGGCCATGATGAAAGTGATCAGCAGATCAT
GTAA (SEQ ID NO: 256)

20

AOLFR139 sequences:

MGFPGIHSWQHWSLPLALLYLLALSANILILIINKEAALHQPMMYYFLGILAMADIGLATTIMP
KILAILWFNAKTISLLECFQAQMYAIHCFVAMESSTFVCMADRYVAICRPLRYPSTITESFVKAN
GFMALRNSLCLISVPLLAQRHYCSQNQIEHCLCSNLGVTSLSCDDRRINSINQVLLAWTLMGS
25 DLGLIILSYALILYSVLKLSPEAASKALSTCTSHLILILFFYTVIIVISITRSTGMRVPLIPVLLNVL
HNVIPPALNPMVYALKNKELRQGLYKVLRLGVKGT (SEQ ID NO: 257)

30 ATGGGATTCCCTGGCATTACAGTTGGCAGCACTGGCTCTCCCTGCCCTGGCTCTGCTCT
ACCTCTTAGCTCTCAGTGCCAACATCCTTATCCTGATCATCATCAACAAAGAGGCAGCACT
GCACCAGCCTATGTACTATTTCTGGGCATCTTGGCTATGGCAGACATAGGCCTGGCTACC
ACCATCATGCCTAAGATTTTGGCCATCTTATGGTTCAATGCTAAGACCATCAGTCTCCTGG
AGTGCTTTGCTCAGATGTATGCCATACATTGCTTTGTGGCCATGGAATCAAGTACCTTTGT
CTGCATGGCTATTGATAGATATGTAGCCATTTGTGACCGCTACGATATCCATCAATCATC
ACTGAATCTTTTGTTCAAAGCAAATGGGTTTCATGGCACTGAGAAACAGCCTGTGTCTCA
35 TCTCAGTGCCTCTGTTGGCTGCCAGAGGCATTACTGCTCCAGAATCAAATTGAGCACTG
TCTTTGTTCTAACCTTGGAGTCACTAGCCTATCTTGTGATGATCGAAGAATCAATAGCATT
AACCAGGTCTTTTGGCTTGGACACTCATGGGAAGTGACCTGGGTTTGATTATTTTATCAT
ATGCTCTAATACTTTACTCTGTCTGAAGCTGAAGTCTCCAGAAGCTGCATCCAAGGCCTT
AAGTACCTGCACCTCCACCTCATCTTAATCCTTTTCTTCTACACAGTCATCATTGTGATTT
40 CCATTACTCGTAGTACAGGAATGAGAGTTCCCCTTATCCAGTTCTACTTAATGTGCTACA
CAATGTCATTCCCCCTGCCCTGAACCCCATGGTATATGCACTCAAGAACAAGGAAGTCAAG
CAAGGCTTATACAAGGTACTTAGACTGGGAGTGAAGGGCACCTGA (SEQ ID NO: 258)

AOLFR140 sequences:

45 MLTLNKTDLIPASFILNGVPGLEDTQLWISFPFCSMYVVMVGNCGLLYLIHYEDALHKPMYY
FLAMLSFTDLVMCSSTIPKALCIFWFHLKDIFDECLVQMFFIHTFTGMESGVLMLMALDRYV
AICYPLRYSTILNTPVIKVGATFLRGVLLIIPFTFLTKRLPYCRGNILPHTYCDHMSVAKLSCG
NVKVNATYGLMVALLIGGFDILCITISYTMILRAVVSLSADARQAFNTCTAHICATVFSYTPAF
FSFFSHRFGEHIIPPSCHIIIVANIYLLLPPTMNPIVYGKTKQIRDCVIRILSGSKDTKSYSM (SEQ
50 ID NO: 259)

55 ATGCTAACACTGAATAAAACAGACCTAATACCAGCTTCATTTATTCTGAATGGAGTCCAG
GACTGGAAGACACAACTCTGGATTTCCTTCCCATCTGCTCTATGTATGTTGTGGCTAT
GGTAGGGAATTGTGGACTCCTCTACCTCATCTACTATGAGGATGCCCTGCACAAACCCATG
TACTACTTCTTGGCCATGCTTTCCTTACTGACCTTGTATGTGCTCTAGTACAATCCCTAA
AGCCCTCTGCATCTTCTGGTTTCATCTCAAGGACATTGGATTGATGAATGCCTTGTCAG

ATGTTCTTCATCCACACCTTCACAGGGATGGAGTCTGGGGTGCTTATGCTTATGGCCCTGG
 ATCGCTATGTGGCCATCTGCTACCCCTTACGCTATTCAACTATCCTCACCAATCCTGTAATT
 GCAAAGGTTGGGACTGCCACCTTCCTGAGAGGGGTATTACTCATTATTCCTTTACTTTTCCT
 CACCAAGCGCCTGCCCTACTGCAGAGGCAATATACTTCCCCATACCTACTGTGACCACATG
 5 TCTGTAGCCAAATTGTCTGTGGTAATGTCAAGGTCAATGCCATCTATGGTCTGATGGTTG
 CCCTCCTGATTGGGGGCTTTGACATACTGTGTATCACCATCTCCTATAACCATGATTCTCCGG
 GCAGTGGTCAGCCTCTCCTCAGCAGATGCTCGGCAGAAAGGCCTTTAATACCTGCACTGCCC
 ACATTTGTGCCATTGTTTTCTCCTATACTCCAGCTTTCTTCTCCTTTCTTTCCACCGCTTTG
 10 GGGAAACACATAATCCCCCTTCTTGCCACATCATTGTAGCCAATATTTATCTGCTCCTACCA
 CCCACTATGAACCTATTGTCTATGGGGTGAAAACCAAACAGATACGAGACTGTGTCATAA
 GGATCCTTTCAGGTTCTAAGGATACCAAATCCTACAGCATGTGA (SEQ ID NO: 260)

AOLFR141 sequences:

MSSTLGHNMESPNTDVPDSVFLLGIPGLEQFHLWLSLPVCGLTATVGNITILVVVATEPVL
 15 HKPVYLFCLMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAQMFFIHAFMMESTVLLAM
 AFDRYVAICHPLRYATILDTIAHIGVAAVVRGSLMLPCPFLIGRLNFCQSHVILHTYCEHMA
 VVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALSAQAVLRLSSHEARSKALGTCGSHVC
 VILISYTPALFSFFTHRFHGHVPHIHILLANVYLLPPLNPNVVGKTKQIRKRVVRVFSQG
 GMGIKASE (SEQ ID NO: 261)

ATGTCCAGCACTCTTGGCCACAACATGGAATCTCCTAATCACACTGATGTTGACCCCTCTG
 TCTTCTTCTCCTGGGCATCCCAGGTCTGGAACAATTTCAATTTGTGGCTCTCACTCCCTGTG
 TGTGGCTTAGGCACAGCCACAATTGTGGGCAATATAACTATTCTGGTTGTTGTTGCCACTG
 AACCAAGTCTTGACACAAGCCTGTGTACCTTTTTCTGTGCATGCTCTCAACCATCGACTTGGCT
 25 GCCTCTGTCTCCACAGTTCCCAAGCTACTGGCTATCTTCTGGTGTGGAGCCGGACATATAT
 CTGCCTCTGCCTGCCTGGCACAGATGTTCTTCATTTCATGCCTTCTGCATGATGGAGTCCACT
 GTGCTACTGGCCATGGCCTTTGATCGCTACGTGGCCATCTGCCACCCACTCCGCTATGCCA
 CAATCCTCACTGACACCATCATTGCCACATAGGGGTGGCAGCTGTAGTGCGAGGCTCCCT
 GCTCATGCTCCCATGTCCCTTCTTATTGGGCGTTTGAACCTCTGCCAAAGCCATGTGATCC
 30 TACACACGTAAGTGAGCAGATGGCTGTGGTGAAGCTGGCCTGTGGAGACACCAGGCCTA
 ACCGTGTGTATGGGCTGACAGCTGCACTGTTGGTCATTGGGGTTGACTTGTTTTGCAATTGG
 TCTCTCCTATGCCCTAAGTGACAAAGCTGTCTTTCGCTCTCATCCCATGAAGCTCGGTCCA
 AGGCCCTAGGGACCTGTGGTTCCCATGTCTGTGTCATCCTCATCTCTTATACACAGGCCCTC
 TTCTCCTTTTTTACACACCGCTTTGGCCATCACGTTCCAGTCCATATTCACATTCTTTTGGC
 35 CAATGTTTATCTGCTTTTGCCACCTGCTCTTAATCTGTGGTATATGGAGTTAAGACCAAAC
 AGATCCGTAAGAGAGTTGTGAGGGGTGTTTCAAAGTGGGCAGGGAATGGGCATCAAGGCAT
 CTGAGTGA (SEQ ID NO: 262)

AOLFR143 sequences:

MLGLNGTPFPATLQLTGIPGIQTGLTWVALIFCILYMISIVGNLSILTLVFWEPALHQPMMYYFL
 40 SMLALNDLGVFSSTLPTVISTFCFNYNHVAFNACLVMFFIHTFSFMESGILLAMSLDRFVAICY
 PLRYVTVLTHNRILAMGLILTKSFTTLFPFPFVVKRLPFCKGNVLHHSYCLHPDLMKVACGDI
 HVNNIYGLLVIFTYGMDSFILLSYALILRAMLVISQEQRLKALNTCMISHICAVLAFYVPIAVS
 MIHRFWKSAPPVVHVMMSNVYLFVPPMLNPIIYSVKTKERKILKFFHKSQA (SEQ ID NO:
 45 263)

ATGCTGGGTCTCAATGGCACCCCTTCCAGCCAGCAACACTCCAGCTGACAGGCATTCTCTG
 GGATACAAACAGGCCTCACCTGGGTTGCCCTGATTTTCTGCATCCTCTACATGATCTCCATT
 GTAGGTAACCTCAGCATTCTCACTCTGGTGTGTTTGGGAGCCTGCTCTGCATCAGCCCATGT
 50 ACTACTTCTCTCTATGCTCGCTCTCAATGATCTGGGAGTGTCCTTTTCTACACTTCCCACT
 GTGATTTCTACTTTCTGCTTCAACTACAACCATGTTGCGTTTAATGCTTGCCTGGTCCAGAT
 GTTCTTCATCCACACTTTCTCCTTCATGGAGTCAGGCATACTGCTGGCCATGAGCTTGGATC
 GCTTTGTGGCTATTTGTTATCCATTACGCTATGTCACTGTGCTCACTCACAACCGTATATTG
 GCTATGGGTCTGGGCATCCTTACCAAGAGTTTCACCACTCTCTTCCCTTTCCCTTTTGTGGT
 55 GAAACGACTGCCCTTCTGCAAAGGCAATGTTTTGCATCACTCCTACTGTCTCCATCCAGAT
 CTCATGAAAGTAGCATGTGGAGACATCCATGTTAACAACATTTATGGGCTCTTGGTGATCA

TTTTTACCTATGGTATGGACTCAACTTTTCATCCTGCTTTCCTACGCATTGATCCTGAGAGCC
ATGCTGGTCATCATATCCCAGGAACAGCGGCTCAAGGCACTCAACACCTGCATGTACACA
TCTGTGCAGTGCTGGCCTTTTATGTGCCATAATTGCTGTCTCCATGATTCACCGCTTCTGG
AAAAGTGCTCCACCTGTTGTTTCATGTTCATGTCCAATGTCTACCTGTTTGTACCAACCAT
5 GCTCAACCCTATCATCTACAGTGTGAAAACCAAGGAGATCCGCAAAGGGATTCTCAAGTTC
TTCCATAAATCCCAGGCCTGA (SEQ ID NO: 264)

AOLFR144 sequences:

10 MGLFNVTHPAFFLLTGIPGLESSHWSLGPCLVVMYAVALGGNTVILQAVRVEPSLHEPMYYFL
SMLSFSDDVAISMATLPTVLRFTCLNARNITFDACLIQMFLIHFFSMMESGILLAMSFDTRYVAICD
PLRYATVLTTEVIAAMGLGAAARSFTTLFPLPFLIKRLPICRSNVLSHSYCLHPDMMRLACADISI
NSIYGLFVLVSTFGMDLFFIFLSYVLLRSVMATASREERLKALNTCVSHILAVLAFYVPMIGVS
TVHRFGKHVPCYIHLMSNVYLFVPPVLNPLIYSAKTKEIRRAIFRMFHIIKI (SEQ ID NO: 265)

15 ATGGGGTTGTCAATGTCACCTCACCTGCATTCTTCCTCCTGACTGGTATCCCTGGTCTGGA
GAGCTCTCACTCCTGGCTGTCAGGGCCCCCTCTGCGTGATGTATGCTGTGGCCCTTGGGGGA
AATACAGTGATCCTGCAGGCTGTGCGAGTGAGGCCAGCCTCCATGAGCCCATGTACTACT
TCCTGTCCATGTTGTCTTCAGTGATGTGGCCATATCCATGGCCACACTGCCCACTGTACTC
CGAACCTTCTGCCTCAATGCCCCGAACATCACTTTTGATGCCTGTCTAATTGAGATGTTTCT
20 TATTCACCTTCTTCTCCATGATGGAATCAGGTATTCTGCTGGCCATGAGTTTTGACCGCTATG
TGGCCATTTGTGACCCCTTGCGCTATGCAACTGTGCTCACCCTGAAGTCATTGCTGCAAT
GGGTTTAGGTGCAGCTGCTCGAAGCTTCATCACCTTTTCCCTCTTCCCTTTCTTATTAAGA
GGCTGCCTATCTGCAGATCCAATGTTCTTCTCACTCCTACTGCCTGCACCCAGACATGATG
AGGCTTGCCTGTGCTGATATCAGTATCAACAGCATCTATGGACTCTTTGTTCTTGTATCCAC
25 CTTTGGCATGGACCTGTTTTTATCTTCTCTCCTATGTGCTCATTCTGCGTTCTGTCATGG
CCACTGCTTCCCGTGAGGAACGCCTCAAAGCTCTCAACACATGTGTGTCACATATCCTGGC
TGTACTTGCAATTTATGTGCCAATGATTGGGGTCTCCACAGTGCACCGCTTTGGGAAGCAT
GTCCCATGCTACATACATGTCTCATGTCAAATGTGTACCTATTTGTGCCTCCTGTGCTCAA
CCCTCTCATTTATAGCGCCAAGACAAAGGAAATCCGCCGAGCCATTTTCCGCATGTTTCAC
30 CACATCAAAATATGA (SEQ ID NO: 266)

AOLFR145 sequences:

MSVQYSLSPQFMLLSNITQFSPIFYLTSPFGLGKHWIFIPFFMYMVAISGNCFILIIKTNPRLH
TPMYLLSLLALDGLCVSTLPTTMGIFWFNSQSIYFGACQIQMFCIHSFSFMESSVLLMMSFD
35 RFVAICHPLRYSVITGQQVVRAGLIVFRGPVATIPVLLLKAFPYCGSVVLSHSFCLHQEVIQLA
CTDITTFNNLYGLMVVFTVMLDLVLIALSYGLLHTVAGLASQEEQRRAFQTCTAHLCAVLVF
FVPMMLGLSLVHRFGKHAPPAIHLMLANVYLFVPPMLNPIYSIKTKEIHRAIILKLLGLKKASK
(SEQ ID NO: 267)

40 ATGTCAGTCCAATATTCGCTCAGTCCTCAATTCATGCTGCTATCCAACATTACTCAGTTTAG
CCCCATATTCTATCTCACCAGCTTTCTCGGATTGGAAGGCATCAAACACTGGATTTTCATCC
CCTTTTTCTTTATGTACATGGTTGCCATCTCAGGCAATTGTTTCATTCTGATCATTATTAAG
ACCAACCCCTCGTCTGCACACACCCATGTACTATCTACTATCCTTGCTGGCCCTCACTGACCT
GGGGCTGTGTGTGTCCACGTTGCCACCACTATGGGGATCTTCTGGTTTAACTCCCAGAGT
45 ATCTACTTTGGAGCGTGTCAAATCCAGATGTTCTGCATCCACTCTTTTCTTTCATGGAGTC
CTCAGTGCTCCTCATGATGTCCTTTGACCGCTTTGTGGCCATCTGCCACCCTCTGAGGTATT
CGGTCATTATCACTGGCCAGCAAGTGGTCAGAGCAGGCCTAATTGTCATCTTCCGGGGACC
TGTGGCCACTATCCCTATTGTCCTCCTCCTGAAGGCTTTTCCCTACTGTGGATCTGTGGTCC
TCTCCCACTCATTTTGCCTGCACCAGGAAGTGATACAGCTGGCCTGCACAGATACCACCTT
50 CAATAATCTGTATGGACTGATGGTGGTAGTTTTCACTGTGATGCTGGACCTGGTGCTCATC
GCATGTCTATGGACTCATCTGCACACAGTAGCAGGCCTGGCCTCCCAAGAGGAGCAGC
GCCGTGCCTTTCAGACATGCACCGCTCATCTGTGCTGTGCTAGTATTCTTTGTGCCCATG
ATGGGGCTGTCCCTGGTGACCGTTTGGGAAGCATGCCCCACCTGCTATTCTCTTCTTAT
GGCCAATGTCTACCTTTTGTGCCTCCCATGCTTAACCCAATCATATACAGCATTAAGACC
55 AAGGAGATCCACCGTGCCATTATCAAACCTCTAGGTCTTAAAAAGGCCAGTAAATGA (SEQ
ID NO: 268)

AOLFR146 sequences:

- MSQVTNTTQEGIFYILTDPGFESHIIWISIPVCCLYTISIMGNITILTVIRTEPSVHQRMVFLSM
 LALTDLGLTLTLPVLMQLLWFNVRRISSEACFAQFFFLHGFSESSVLLAMSVDCYVAICCP
 5 LHYASILTNEVIGRTGLAIICCCVLAVLPSLFLKRLPFCHSHLLSRSYCLHQDMIRLVCADIRLN
 SWYGFALALLIIVDPLLVISYTLILKNILGTATWAERLRALNNCLSHILAVLVLYIPMVGVSMT
 HRFKASPLVHVIMANTYLLAPPVMNPITYSVKNKQIQWGMNLNLSLKNMHSR (SEQ ID NO:
 269)
- 10 ATGTCCCAGGTGACTAACACCACACAAGAAGGCATCTACTTCATCCTCACGGACATCCCTG
 GATTTGAGGCCTCCACATCTGGATCTCCATCCCCGTCTGCTGTCTCTACACCATCTCCATC
 ATGGGCAATACCACCATCCTCACTGTCATTGCGACAGAGCCATCTGTCCACCAGCGCATGT
 ATCTGTTTCTCTCCATGCTGGCCCTGACGGACCTGGGTCTCACCTCACCACCCTACCCACA
 GTCATGCAGCTTCTCTGGTTCAACGTTTCGTAGAATCAGCTCTGAGGCCTGTTTTGCTCAGTT
 15 TTCTTCCTTCATGGATTCTCCTTATGGAGTCTTCTGTCCTCCTGGCTATGTCCGTTGACT
 GCTATGTGGCCATCTGCTGTCCCTCCATTATGCCTCCATCCTCACCAATGAAGTCATTGGT
 AGAACTGGGTTAGCCATCATTTGCTGCTGTGTTCTGGCGGTTCTTCCCTCCCTTTTCTTACT
 CAAGCGACTGCCTTTCTGCCACTCCCACCTTCTCTCTCGCTCCTATTGCCTCCACCAGGATA
 TGATCCGCTGGTCTGTGCTGACATCAGGCTCAACAGCTGGTATGGATTGTCTTGCCTT
 20 GCTCATTATTATCGTGGATCCTCTGCTCATTGTGATCTCCTATACACTATTCTGAAAAATA
 TCTTGGGCACAGCCACCTGGGCTGAGCGACTCCGTGCCCTCAATAACTGCCTGTCCACAT
 TCTAGCTGTCTGGTCTCTACATTCCCATGGTTGGTGTATCTATGACTCATCGCTTTGCCA
 AGCATGCCTCTCCACTGGTCCATGTTATCATGGCCAATATCTACCTGCTGGCACCCCCGGT
 GATGAACCCCATCATTTACAGTGTAAGAACAAGCAGATCCAATGGGGAATGTAAATTC
 25 CTTCCCTCAAAAATATGCATTCAAGATGA (SEQ ID NO: 270)

AOLFR147 sequences:

- MPSASAMIIFNLSSYNPGFVLVGPGLQFHVWIGIPFCIIYTVAVVGNCLLYLIVVEHSLHEPMPF
 FFLSMLAMTDLILSTAGVPKALSIFWLGAIRETFPGCLTQMFFLHYNFVLDLSAILMAMAFDHYV
 30 AICSPLRYTTILTPKTIKSAMGISFRSFCILPDVFLLTCLPFCRTRIPHTYCEHIGVAQLACADISI
 NFWYGFCVPIMTVISDVILIAVSYAHILCAVFGFLPSQDACQKALGTCGSHVCVILMFYTPAFFSI
 LAHRFHGHNVSRTHFIMFANLYIVIPPALNPMVYGVKTKQIRDKVILLFSKGTG (SEQ ID NO:
 271)
- 35 ATGCCATCTGCCTCTGCCATGATCATTTTTCAACCTGAGCAGTTACAATCCAGGACCCCTTCAT
 TCTGGTAGGGATCCCAGGCCTGGAGCAATTCCATGTGTGGATTGGAATCCCTTCTGTATC
 ATCTACATTGTAGCTGTTGTGGGAAACTGCATCCTTCTCTACCTCATTGTGGTGGAGCATA
 GTCTTCATGAACCCATGTTCTTCTTCTCTCCATGCTGGCCATGACTGACCTCATCTTGTCC
 ACAGCTGGTGTGCCTAAAGCACTCAGTATCTTTGGCTAGGGGCTCGCGAAATCACATTCC
 40 CAGGATGCCTTACACAAATGTTCTTCTTCACTATAACTTTGTCTGGATTGAGCCATTCTG
 ATGGCCATGGCATTGATCACTATGTAGCTATCTGTTCTCCCTTGAGATATAACCACCATCTT
 GACTCCCAAGACCATCATCAAGAGTGCTATGGGCATCTCCTTTGGAAGCTTCTGCATCATC
 CTGCCAGATGTATTCTTGCTGACATGCCTGCCTTTCTGCAGGACACGCATCATACCCACA
 CATACTGTGAGCATATAGGTGTTGCCAGCTCGCCTGTGCTGATATCTCCATCAACTTCTG
 45 GTATGGCTTTTGTGTTCCCATCATGACGGTCATCTCAGATGTGATTCTCATTGCTGTTTCTT
 ACGCACACATCCTCTGTGCTGTCTTTGGCCTTCCCTCCCAAGATGCCTGCCAGAAAGCCCT
 CGGCACCTTGTTGTTCTCATGTCTGTGTCATCCTCATGTTTTATACACCTGCCTTTTCTCCA
 TCCTCGCCCATCGCTTTGGACACAATGTCTCTCGACCTTCCACATCATGTTTGCCAATCTC
 TACATTGTTATCCACCTGCACTCAACCCCATGGTTTACGGAGTGAAGACCAAGCAGATCA
 50 GAGATAAGGTTATACTTTGTTTTCTAAGGGTACAGGATGA (SEQ ID NO: 272)

AOLFR148 sequences:

- MPTVNHSGTSHTVFHLLGIPGLQDQHMWISIPFFISYVTALLGNSLLIFILTKRSLHEPMYFLC
 MLAGADIVLSTCTIPQALAIWFWRAGDISLDRCTQLFFIHSTFISESGILLVMAFDHYIAICYPLR
 55 YTTLTNALIKKICVTVSLRSYGTIFPIIFLLKRLTFCQNNIIPHTFCEHIGLAKYACNDIRINWYG

FSILMSTVVLDDVVLIFISYMLILHAVFHMPSPDACHKALNTFGSHVCIILFYGSGIFTILTQRFRGR
HPPCIHIPLANVCILAPPMLNPIIYGKTKQIQEQVVQFLFIKQKITLV (SEQ ID NO: 273)

5 ATGCCTACTGTAAACCACAGTGGCACTAGCCACACAGTCTTCCACTTGCTGGGCATCCCTG
GCCTACAGGACCAGCACATGTGGATTCTATCCCATTCTTCATTTCCTATGTACCCGCCCTT
CTTGGGAACAGCCTGCTCATCTTCATTATCCTCACAAAGCGCAGCCTCCATGAACCCATGT
ACCTCTTCTCTGCATGCTGGCTGGAGCAGACATTGTCTCTCCACGTGCACCATTCCTCAG
GCCTTAGCTATCTTCTGGTTCCGTGCTGGGGACATCTCCCTGGATCGTTGCATCACTCAGCT
10 CTTCTTCATCCATTCCACCTTCATCTCTGAGTCAGGGATCTTGCTGGTGATGGCCTTTGACC
ACTATATTGCCATATGCTACCCACTGAGGTACACCACCATTCCTACAAATGCTCTGATCAA
GAAAATTTGTGTGACTGTCTCTCTGAGAAGTTATGGTACAATTTCCCTATCATATTTCTTT
TAAAAAGATTGACTTTCTGCCAGAATAATATTATCCACACACCTTTTGTAACACATTGG
CCTAGCCAAATATGCATGTAATGACATTGCAATAAACATTTGGTATGGGTTTTCCATTCTA
15 ATGTCGACGGTGGTCTTAGATGTTGTACTAATTTTTATTTCTATATGCTGATTCTCCATGC
TGTCTTCCACATGCCTTCTCCAGATGCTTGCCACAAAGCTCTCAACACATTTGGCTCCCATG
TCTGCATCATCATCCTCTTTTATGGGTCTGGCATCTTCACAATCCTTACCCAGAGGTTTGA
CGCCACATTCCACCTTGTATCCACATCCCGTTGGCTAATGTCTGCATTCTGGCTCCACCTAT
GCTGAATCCCATTATTTATGGGATCAAAACCAAGCAAATCCAGGAACAGGTGGTTCAGTTT
20 TTGTTTATAAAACAGAAAATAACTTTGGTTTAA (SEQ ID NO: 274)

AOLFR149 sequences:

MSNASLLTAFILMGLPHAPALDAPLFGVFLVYVVLTVLGNLLILLVIRVDSHLHTTMYFYFLTNL
SFIDMWFSTVTVPKLLMTLVFPSGRAISFHSMAQLYFFHFLGGTECFLYRVMSCDRYLAISSYP
LRYTSMMTGRSCTLLATSTWLSGSLHSAVQAILTFHLPYCGPNWQHYLCDAPPILKLACADTS
25 AIETVIFVTVGIVASGCFVLIVLSYVSIVCSILRIRTSEKHFRAFQTCASHCIVVLCFFGPGFLFIYLR
PGSRKAVDGVVAVFYTVLPLLNPPVYTLRNKEVKKALLKLKDKVAHSQSK (SEQ ID NO:
275)

30 ATGTCCAACGCCAGCCTACTGACAGCGTTTCATCCTCATGGGCCTTCCCCATGCCCCAGCGC
TGGACGCCCCCTCTTTGGAGTCTTCTGCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCACCATGTACTACTTCTCTCA
CCAACCTGTCGTTTCATTGACATGTGGTTCTCCACTGTCACGGTGCCCAAATTGCTGATGAC
TTTGGTGTTCCCAAGTGGCAGGGCTATCTCCTTCCACAGCTGCATGGCTCAGCTCTATTCTT
TTCACTTCTAGGGGGCACCAGTGTTCCTCTACAGGGTCATGTCCTGTGATCGCTACCT
35 GGCCATCAGTTACCCGCTCAGGTACACCAGCATGATGACTGGGCGCTCGTGTACTCTTCTG
GCCACCAGCATTTGGCTCAGTGGCTCTCTGCACCTCTGCTGTCCAGGCCATATTGACTTTCC
ATTTGCCCTACTGTGGACCCAACTGGATCCAGCACTATTTGTGTGATGCACCGCCCATCCT
GAAACTGGCCTGTGCAGACACCTCAGCCATAGAGACTGTCAATTTTGTGACTGTTGGAATA
GTGGCCTCGGGCTGCTTTGTCCTGATAGTGTCTCTATGTGTCCATCGTCTGTTCCATCCT
40 GCGGATCCGCACCTCAGAGGGGAAGCACAGAGCCTTTCAGACCTGTGCCTCCCACTGTATC
GTGGTCTTTGCTTCTTTGGCCCTGGTCTTTTCATTTACCTGAGGCCAGGCTCCAGGAAAGC
TGTGGATGGAGTTGTGGCCGTTTTCTACACTGTGCTGACGCCCTTCTCAACCCTGTTGTGT
ACACCCTGAGGAACAAGGAGGTGAAGAAAGCTCTGTTGAAGCTGAAAGACAAAGTAGCAC
45 ATTCTCAGAGCAAATAG (SEQ ID NO: 276)

AOLFR150 sequences:

MELGNVTRVKEIFLGLTQSQDQSLVFLFLCLVYMTTLLGNLLIMVTVCESRLHTPMYFLLR
NLAILDICFSSTTAPKVLLDLLSKKKTISYTSMTQIFLHLLGGADIFSLSVMAFDCYMAISKPL
HYVTIMSRGQCTALISASWMGGFVHSIVQISLLPLPFCGPNVLDTFYCDVPQVLKLTCTDTFA
50 LEFLMISNNGLVTTLWFIFLLVSYTVILMTLRSQAGGGRRKAISTCTSPHHCGBPFCALHCLC
PALHCPPHRKGHLCCHLHCHLPSAEPFDLHSEBPGNEVSHEKTEBKTRAF (SEQ ID NO: 277)

ATGGAGTTGGGAAATGTCACCAGAGTAAAAGAATTTATATTTCTGGGACTTACTCAATCCC
AAGACCAGAGTTTGGTCTTGTCTTTTATATGCTTGTGTACATGACGACTCTGCTGGGA
55 AACCTCCTCATGTTGTCACCGTGACCTGTGAGTCTCGCCTTACACCCCCATGTACTTCT
GCTCCGCAATCTAGCCATCCTTGACATCTGCTTCTCCTCCACAACTGCTCCTAAAGTCTTGC

TGGACCTTCTGTCAAAGAAAAAGACCATATCCTATACAAGCTGCATGACACAGATATTTCT
 CTTCCACCTCCTTGGTGGGGCAGACATTTTTCTCTCTGTGATGGCGTTTGACTGCTACA
 TGGCCATCTCCAAGCCCTGCACTATGTGACCATCATGAGTAGAGGGCAATGCACTGCCCT
 CATCTCTGCCCTCTTGGATGGGGGGCTTTGTCCACTCCATCGTGCAGATCTCCCTGTTGCTGC
 5 CTCTCCCTTTCTGTGGACCCAATGTTCTTGACACTTTCTACTGCGATGTCCCCCAGGTCCTC
 AAACCTCACTTGCACTGACACTTTTGCTCTTGAGTTCTTGATGATTTCCAACAATGGCCTGGT
 CACTACCCTGTGGTTTATCTTCCTGCTTGTGTCTACACAGTCATCCTAATGACGCTGAGGT
 CTCAGGCAGGAGGGGGCAGGAGGAAAGCCATCTCCACTTGCACTCCCCACATCACTGTG
 GTGACCCTGCATTTTGTGCCCTGCATCTATGTCTATGCCCCGGCCCTTCACTGCCCTCCCCAC
 10 AGAAAAGGCCATCTCTGTCACTTCACTGTCTATCTCCCTCTGCTGAACCCTTTGATCTACA
 CTCTGAGGAACCAAGAAATGAAGTCAGCCATGAGAAGACTGAAGAGAAGACTCGTGCCTT
 CTGA (SEQ ID NO: 278)

AOLFR151 sequences:

15 MFSPNHTIVTEFILLGLTDDPVLEKILFGVFLAIYLITLAGNLCMILLRTNSHLQTPMYFFLGHLS
 FVDICYSSNVTPNMLHNFLSEQKTISYAGCFTQCLLFIALVITEFYILASMALDRYVAICSPHYS
 SRMSKNICVCLVTIPYMYGFLSGFSQSLTFHLSFCGSLEINHFYCADPPLIMLACSDTRVKKMA
 MFVVAGFNLSSSLFILLSYLFIFAAIFRIRSAEGRHKAFSTCASHLTIVTLFYGTLFCMYVRPPE
 KSVEESKITA VFYTF LSPMLNPLIYSLRNTDVILAMQQMIRGKSFHKIAV (SEQ ID NO: 279)

20 ATGTTCTCCCCAAACCACACCATAGTGACAGAATTCATTCTCTTGGGACTGACAGACGACC
 CAGTGCTAGAGAAGATCCTGTTTGGGGTATTCTTGCGATCTACCTAATCACACTGGCAGG
 CAACCTGTGCATGATCCTGCTGATCAGGACCAATCCACCTGCAAAACACCATGTATTTCT
 TTCCTTGGCCACCTCTCCTTTGTAGACATTTGCTATTCTTCCAATGTTACTCCAAATATGCT
 25 GCACAATTTCTCTCAGAACAGAAAGACCATCTCCTACGCTGGATGCTTACACAGTGTCTT
 CTCTTCATCGCCCTGGTGATCACTGAGTTTACATCCTTGCTTCAATGGCATTGGATCGCTA
 TGTAGCCATTTGCAGCCCTTTGCATTACAGTTCCAGGATGTCCAAGAACATCTGTGTCTGT
 CTGGTCACTATCCCTTACATGTATGGGTTTCTTAGTGGGTTCTCTCAGTCACTGCTAACCTT
 TCACCTATCCTTCTGTGGCTCCCTTGAAATCAATCATTTCTACTGCGCTGATCCTCCTCTTA
 30 TCATGCTGGCCTGCTCTGACACCCGTGTCAAAAGATGGCAATGTTTGTAGTTGCAGGCTT
 TAATCTCTCAAGCTCTCTCTCATCTTCTCTGCTCTATCTTTTTCATTTTTGCAGCGATCTT
 CAGGATCCGTTCTGCTGAAGGCAGGCACAAAGCCTTTTCTACGTGTGCTTCCCACTGACA
 ATAGTCACTTTGTTTTATGGAACCCTCTTCTGCATGTACGTAAGGCCTCCATCAGAGAAGT
 CTGTAGAGGAGTCCAAAATAACTGCAGTCTTTTATACTTTTTTGTAGCCCAATGCTGAACCC
 35 ATTGATCTATAGCCTACGGAACACAGATGTAATCCTTGCCATGCAACAAATGATTAGGGGA
 AAATCCTTTCATAAAATTGCAGTTTAG (SEQ ID NO: 280)

AOLFR152 sequences:

40 MDQINHNTNVEFFLELTRSRELEFFLVVFFAVYVATVLGNALIVVTITCESRLHTPMYFLLRN
 KSVLDIVFSSITVPKFLVDLLSDRKTISYND CMAQIFFHFAGGADIFFLSVMA YDRYLAIKPL
 HYVTMMRKEVWVALVVASWVSGGLHSIIQVILMLPFPFCGPNTLDAFYCYVLQVVKLACTDT
 FALELFMISNNGLVTLWFLLLGSYTVILVMLRSHSGEGRNKALSTCTSHMLVVTLHFVPCV
 YIYCRPFMTLPMDTTISINNTVITPMLNPIIYSLRNQEMKSAMQRLQRRLLGPSES RKGW (SEQ ID
 NO: 281)

45 ATGGACCAGATCAACCACACTAATGTGAAGGAGTTTTTCTTCTGGAACCTTACACGTTCCC
 GAGAGCTGGAGTTTTTCTTGTGTTTGGTCTTCTTTGCTGTGTATGTAGCAACAGTCCTGGG
 AAATGCACTCATTGTGGTCACTATTACCTGTGAGTCCCGCCTACACACTCCTATGTACTTTC
 TCCTGCGGAACAAATCAGTCCTGGACATCGTTTTTTTCATCTATCACCCTGCCCAAGTTCTGT
 50 GTGGATCTTTTATCAGACAGGAAAACCATCTCCTACAATGACTGCATGGCACAGATCTTTT
 TCTTCCACTTTGCTGGTGGGGCAGATATTTTTTCTCTCTGTGATGGCCTATGACAGATAC
 CTTGCAATCGCCAAGCCCTGCACTATGTGACCATGATGAGGAAAGAGGTGTGGGTGGC
 TTGGTGGTGGCTTCTTGGGTGAGTGGTGGTTTGCATTCAATCATCCAGGTAATTCTGATGC
 TTCCATTCCCCTTCTGTGGCCCCAACACACTGGATGCCTTCTACTGTTATGTGCTCCAGGTG
 55 GTAAAACCTGGCCTGCACTGACACCTTTGCTTTGGAGCTTTTCATGATCTCTAACAACGGAC
 TGGTGACCCTGCTCTGGTTCTCTGCTCCTGGGCTCCTACACTGTCATTCTGGTGATGCTG

AGATCCCACTCTGGGGAGGGGCGGAACAAGGCCCTCTCCACGTGCACGTCCCACATGCTG
GTGGTGACTCTTCACTTCGTGCCTTGTGTTTACATCTACTGCCGGCCCTTCATGACGCTGCC
CATGGACACAACCATATCCATTAATAACACGGTCATTACCCCATGCTGAACCCCATCATC
TATTCCTGAGAAATCAAGAGATGAAGTCAGCCATGCAGAGGCTGCAGAGGAGACTTGGG
5 CCTTCCGAGAGCAGAAAATGGGGTGA (SEQ ID NO: 282)

AOLFR153 sequences:

MSKTSLVTAFILTGLPHAPGLDAPLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNLS
FIDMWFSTVTVPKMLMTLVSPSGRAISFHCVAQLYFFHFLGSTECFLYTVMSYDRYLAI SYPL
10 RYTSMMSGSRCALLATSTWLSGSLHSAVQTLTFHLPYCGPNQIQHYLCDAPPILKLACADTSA
NEMVIFVDIGLVASGCFLLIVLSYVSIVCSILRIHTSEGRHRAFQTCASHCIVVLCFFVXCVFYLR
PGSRDVVDGVVAIFYTVLTPLLNPVVYTLRNKEVKKAVLKLRDKVAHSQGE (SEQ ID NO:
283)

15 ATGTCCAAGACCAGCCTCGTGACAGCGTTTCATCCTCACGGGCCCTTCCCCATGCCCCAGGGC
TGGACGCCCCACTCTTTGGAATCTTCCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCATGTACTACTTCTCTCA
CCAACCTGTCCTTCATTGACATGTGGTTCTCCACTGTCACGGTGCCCCAAATGCTGATGAC
CTTGGTGTCCCCAAGCGGCAGGGCTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTTT
20 TCCACTTCCTGGGGAGCACCGAGTGTTCCTCTACACAGTCATGTCTATGATCGCTACTTG
GCCATCAGTTACCCGCTCAGGTACACCAGCATGATGAGTGGGAGCAGATGTGCCCTCCTGG
CCACCAGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCCAT
TTGCCCTACTGTGGACCCAACCAGATCCAGCACTATTTGTGTGATGCACCGCCCCATCCTGA
AACTGGCCTGTGCAGACACCTCAGCCAACGAGATGGTCATCTTTGTGGACATTGGGCTAGT
25 GGCCTCGGGCTGCTTTCTCCTGATAGTGTCTTATGTGTCCATCGTCTGTTCCATCCTGC
GGATCCACACCTCAGAGGGGAGGCACAGAGCCTTTCAGACCTGTGCCTCCCACTGCATCGT
GGTCTTTTGCTTTTTTGTNNCTGTGTTTTCATTTACCTGAGACCAGGCTCCAGGGACGTCG
TGGATGGAGTTGTGGCCATTTTCTACACTGTGCTGACACCCCTTCTCAACCTGTTGTGTAC
ACCCTGAGAAACAAGGAGGTGAAGAAAGCTGTGTTGAAACTGAGAGACAAAGTAGCACAT
30 TCTCAGGGAGAATAA (SEQ ID NO: 284)

AOLFR156 sequences:

MCWAMPSPFTGSSTRNMESRNQSTVTEFIFTGFPQLQDGSLLYFFPLLFITYTFIIDNLLIFSAVRL
DTHLGNPMYNFISFLEIWTATATPKMLSNLISEKKAISMTCILQMYFFHSLENSEGILLTT
35 MAIDRYVAICNPLRYQMIMTPRLCAHLSAGSCLFGFLILLPEIVMISTLPFCGPNQIHQIFCDLVP
VLSLACTDTSMLIEDVIHAVTIIITFLIALSYVRIVTVILRIPSSEGRQKAXSTCAGHLMVFLIFFG
SVSLMYLRFSTNTYPPVLDTAIALMFTVLAPFFNPPIIYSLRNKDMNNAIKKLFCLQKVLNKP GG
(SEQ ID NO: 285)

40 ATGTGCTGGGCTATGCCCTCTCCATTTACAGGTAGCTCTACTAGAAATATGGAGAGCAGAA
ACCAATCAACAGTGACTGAATTTATCTTCACTGGATTCCCTCAGCTTCAGGATGGTAGTCT
CCTGTACTTCTTTCTTTACTTTTCATCTATACTTTTATTATCATTGATAACTTATTAATCTT
CTCTGCTGTAAGGCTGGACACCCATCTGGGCAACCCCATGTATAATTTATCAGTATATTTT
CCTTTCTGGAGATCTGGTACACCACAGCCACCATTCCCAAGATGCTCTCCAACCTCATCAG
45 TGAAAAGAAGGCCATCTCAATGACTGGCTGCATCTTGACAGATGTATTTCTTCCACTCACTT
GAAAACCTCAGAGGGGATCTTGCTGACCACCATGGCCATTGACAGATACGTTGCCATCTGCA
ACCCTCTTCGCTATCAAATGATCATGACCCCCCGGCTCTGTGCTCACCTCTCTGCAGGTTCC
TGCCTCTTCGGTTTCCTTATCCTGCTTCCCAGATTGTGATGATTCCACACTGCCTTTCTG
TGGGCCCAACCAAATCCATCAGATCTTCTGTGACTTGGTCCCTGTGCTAAGCCTGGCCTGT
50 ACAGACACGTCCATGATTCTGATTGAGGATGTGATTGATGCTGTGACCATCATCATTACCT
TCCTAATCATTGCCCTGTCTATGTAAGAATTGTCACTGTGATATTGAGGATTCCCTCTTCT
GAAGGGAGGCAAAAAGGCTNTTCTACCTGTGCAGGCCACCTCATGGTCTTCTGATATTCT
TTGGCAGTGTACTCACTCATGTACTTGCCTTCAGCAACACTTATCCACCAGTTTGTGACAC
AGCCATTGCACTGATGTTTACTGTACTTGTCTCAATCTTCAATCCCATCATTTATAGCCTGA
55 GAAACAAGGACATGAACAATGCAATTAATAAACTGTTCTGTCTTCAAAAAGTGTGAACA
AGCCTGGAGGTAA (SEQ ID NO: 286)

AOLFR157 sequences:

MAMDNVTA VFQFLLIGISNYPQWRDTFFTLVLIYLSLLGNGFMIFLIHFDPNLHTPIYFFLSNL
SFLDLCYGTASMPQALVHCFSTHPYLSYPRCLAQTSVSLALATAECLLLAAMAYDRVVAISNP
5 LRYSVVMNGPVCVCLVATSWGTSVLVTAMLJLSRLHFCGANVINHFACELSLIKLTCSDTSL
NEFMILITSIFTL LLPFGFVLLSYIRIAMAIRIRSLOGRKKAFTTCGSHLTVVTIFYGSAJSMYMKT
QSKSSPDQDKFISVFY GALT PMLNPLIYSLRKKDVKRAIRKVMLKRT (SEQ ID NO: 287)

ATGGCCATGGACAATGTCACAGCAGTGTTCAGTTTCTCCTTATTGGCATTCTAACTATCC
10 TCAATGGAGAGACACGTTTTTCACATTAGTGCTGATAATTTACCTCAGCACATTGTTGGGG
AATGGATTATGATCTTTCTTATTCACTTTGACCCCAACCTCCACACTCCAATCTACTTCTT
CCTTAGTAACCTGTCTTTCTTAGACCTTTGTTATGGAACAGCTTCCATGCCCCAGGCTTTGG
TGCATTGTTTCTCTACCCATCCCTACCTCTCTTATCCCCGATGTTTGGCTCAAACGAGTGTCT
TCCTTGGCTTTGGCCACAGCAGAGTGCCTCCTACTGGCTGCCATGGCCTATGACCGTGTGG
15 TTGCTATCAGCAATCCCCTGCGTTATTCACTGGTATTGAATGGCCAGTGTGTGTCTGCTT
GGTTGCTACCTCATGGGGGACATCACTTGTGCTCACTGCCATGCTCATCCTATCCCTGAGG
CTTCACTTCTGTGGGGCTAATGTCATCAACCATTTTGCCTGTGAGATTCTCTCCCTCATTAA
GCTGACCTGTTCTGATACCAGCCTCAATGAATTTATGATCCTCATCACCAGTATCTTCAACC
TGCTGCTACCAATTTGGGTTTGTCTCTCTCTACATACGAATTGCTATGGCTATCATCAAGG
20 ATTCGCTCACTCCAGGGCAGGCTCAAGGCCTTTACCACATGTGGCTCTCACCTGACCGTGG
TGACAATCTTCTATGGGTCAGCCATCTCCATGTATATGAAAACTCAGTCCAAGTCTCCCC
TGACCAGGACAAGTTTATCTCAGTGTTTTATGGAGCTTTGACACCCATGTTGAACCCCTG
ATATATAGCCTGAGAAAAAAGATGTTAAACGGGCAATAAGGAAAGTTATGTTGAAAAGG
ACATGA (SEQ ID NO: 288)

25

AOLFR158 sequences:

MKAGNFSDTPEFFLLGLSGDPELQPIFLFSLMYLATMLGNLLILAVNSDSHLHTPMYFLLSI
LSLVDICFTSTTMPKMLVNIQAQASINYTGCLTQICFVLVFGLENGILVMMA YDRFVAICHP
LRYNVIMNPKLCGLLLLSFIVSVLDALLHTLMVLQLTFCIDLEIPHFCELAHILKLACSDVLIN
30 NILVYLVTSL LGVVP LSGIIFS YTRIVSSVMKIPSAGGKYKAFSICGSHLIVVSLFYGTGFGVYLS
GATHSSRKGAIASVMYTVVTPMLNPLIYSLRNKMDMLKALRKLISRIPSFH (SEQ ID NO: 289)

ATGAAAGCAGGAACTTCTCAGACACTCCAGAATTCTTTCTCTTGGGATTGTCAGGGGATC
CGGAGCTGCAGCCCATCCTCTTCATGCTGTTCTGTCCATGTACCTGGCCACAATGCTGGG
35 GAACCTGCTCATCATCCTGGCCGTCAACTCTGACTCCACCTCCACACCCCCATGTACTCC
TCCTCTCTATCCTGTCTTGGTCGACATCTGTTTACCTCCACCACGATGCCCAAGATGCTG
GTGAACATCCAGGCACAGGCTCAATCCATCAATTACACAGGCTGCCTCACCCAAATCTGCT
TTGTCCTGGTTTTTGTGGATTGGAATTTCTGGTCATGATGGCCTATGATCGATT
TGTGGCCATCTGTCACCCACTGAGGTACAATGTCATCATGAACCCCAACTCTGTGGGCTG
40 CTGCTTCTGCTGTCTTCATCGTTAGTGTCTGGATGCTCTGCTGCACACGTTGATGGTGCT
ACAGCTGACCTTCTGCATAGACCTGGAAATCCCCACTTTTTCTGTGAACTAGCTCATATT
TCAAGCTCGCCTGTTCTGATGTCTCATCAATAACATCCTGGTGTATTTGGTGACCAGCCT
GTTAGGTGTTGTTCTCTCTCTGGGATCATTTTCTTTACACACGAATTGTCTCTCTGTCA
TGAAAATTCCATCAGCTGGTGAAAGTATAAAGCTTTTCCATCTGCGGGTCACATTTAAT
45 CGTTGTTTCTCTGTTTATGGAACAGGGTTTGGGGTGTACCTTAGTTCTGGGGCTACCCACT
CCTCCAGGAAGGGTGCAATAGCATCAGTGATGTATACCGTGGTCACCCCATGCTGAACCC
ACTCATTTACAGCCTGAGAAACAAGGACATGTTGAAGGCTTTGAGGAAACTAATATCTAG
GATACCATCTTTCCATTGA (SEQ ID NO: 290)

AOLFR159 sequences:

MGPRNQTA VSEFLLMKVTEDPELKLIPFSLFSLMYLVITLGNLLILAVISDSHLHTPMYFLLFN
LSFTDICLTTTTVPKILVNIQAQNSITYTGCLTQICLVLFVAGLESCFLAVMAYDRYVAICHP
RYTVLMNVHFWGLLLSMFMSTMDALVQSLMVLQLSFCKNVEIPLFFCEVVQVIKLACSDTL
INNILIYFASSVFGAIP LSGIIFSYSQIVTSVLRMP SARGKYKAFSTCGHLSVFSLFYGTAFGVYIS
55 SAVAESSRITAVASVMYTVVPQMMNPFYISLRNKEMKKALRKLIGRLFPF (SEQ ID NO: 291)

ATGGGACCCAGAAACCAACAGCTGTTTCAGAATTTCTTCTCATGAAAGTGACAGAGGAC
 CCAGAACTGAAGTTAATCCCTTTTCAGCCTGTTCTGTCCATGTACCTGGTCACCATCCTGG
 GGAACCTGCTCATTTCTCCTGGCTGTCATCTCTGACTCCCACCTCCACACCCCCATGTACTTC
 CTTCTCTTTAATCTCTCCTTTACTGACATCTGTTTAAACCACAACCACAGTCCCAAAGATCCT
 5 AGTGAACATCCAAGCTCAGAATCAGAGTATCATTACACAGGCTGCCTACCCAGATCTGT
 CTTGTCTTGGTTTTTGTGGCTTGGAAAAGTTGCTTTCTTGCAGTCATGGCCTACGACCGCTA
 TGTGGCCATTTGCCACCCACTGAGGTACACAGTCCTCATGAATGTCCATTTCTGGGGCTTG
 CTGATTCTTCTCTCCATGTTTCATGAGCACTATGGATGCCCTGGTTTCAGAGTCTGATGGTATT
 GCAGCTGTCCCTTCTGCAAAAACGTTGAAATCCCTTTGTTCTTCTGTGAAGTCGTTACAGTTC
 10 ATCAAGCTCGCCTGTTCTGACACCCTCATCAACAACATCCTCATATATTTTGAAGTAGTGT
 ATTTGGTGCAATTCCTCTCTCTGGAATAATTTTCTCTTATTCTCAAATAGTCACCTCTGTTTC
 TGAGAAATGCCATCAGCAAGAGGAAAGTATAAAGCGTTTTCCACCTGTGGCTGTACCTCTC
 TGTTTTTTCTTGTCTATGGGACAGCTTTTGGGGTGTACATTAGTTCTGCTGTTGCTGAGT
 CTTCCCGAATTAAGTGTGGCTTCAGTGATGTACACTGTGGTCCCTCAAATGATGAACCC
 15 CTTTCATCTACAGCCTGAGAAATAAGGAGATGAAGAAAGCTTTGAGGAAACTTATTGGTAG
 GCTGTTTCTTTTAG (SEQ ID NO: 292)

AOLFR160 sequences:

MPMQLLLTDFIHSIRFIINSMEARNQTAISKFLLGLIEDPELQPVLFSLFLSMYLVTLGNLLILL
 20 AVISDSHLHTPMYFFLSNLSFLDICLSTTTIPKMLVNIQAQNRSTYSGCLTQICFVLFAGLENC
 LLAAMAYDRYVAICHPLRYTVIMNPRCLGLLILLSLTSVNNALLSLMVLRLSFCTDLEIPLEF
 CELAQVIQLTCSDTLINNLIYFAACIFGGVPLSGIILSYTQITSCVLRMPASGKHKAVSTCGSHL
 SIVLLFYGAGLGVISSVVTDSRKTAVASVMYSVFPQMVNPFYSLRNKDMKGTLRKFIGRIP
 SLLWCAICFGFRLE (SEQ ID NO: 293)

25 ATGCCGATGCAGCTGCTGCTTACAGATTTTATTATCTTTTCCATCAGATTCATCATCAACAG
 CATGGAAGCGAGAAACCAACAGCTATTTCAAATTCCTTCTCCTGGGACTGATAGAGGAT
 CCGGAAGTGCAGCCCGTCTTTTTCAGCCTGTTCTGTCCATGTACTTGGTCACCATCCTGGG
 GAACCTGCTCATCCTCTTGGCTGTCATCTCTGACTCTCACCTCCACACCCCCATGTACTTCT
 30 TCCCTCTCCAATCTCTCCTTTTGGACATTTGTTTAAGCACAACCACGATCCCAAAGATGCTG
 GTGAACATCCAAGCTCAGAATCGGAGCATCACGTACTCAGGCTGCCTCACCAGATCTGCT
 TTGTCTTGTTTTTTGTGGCTTGGAAAATTGTCTCCTTGCAGCAATGGCCTATGACCGCTAT
 GTGGCCATTTGTACCCCCCTTAGATACACAGTCATCATGAACCCCGCCTCTGTGGCCTGC
 TGATTCTTCTCTCTGTTGACTAGTGTGTGAATGCCCTTCTTCTCAGCCTGATGGTGTG
 35 AGGCTGTCTTCTGCACAGACCTGGAAATCCCGCTCTTCTTCTGTGAAGTGGCTCAGGTCA
 TCCAAGTACCTGTTTGCAGACACCTCATCAATAACATCCTGATATATTTTGCAGCTTGCATA
 TTTGGTGGTGTCTCTGTCTGGAATCATTTTGTCTTACACTCAGATCACCTCCTGTGTTTT
 GAGAATGCCATCAGCAAGTGGAAGCACAAAGCAGTTTCCACCTGTGGGTCTCACCTCTCC
 ATTGTTCTTGTCTATGGGGCAGGTTTGGGGGTGTACATTAGTTCTGTGGTTACTGACTC
 40 ACCTAGGAAGACTGCAGTGGCTTCAGTGATGTATTCTGTGTTCCCTCAAATGGTGAACCCC
 TTTATCTATAGTCTGAGGAATAAGGACATGAAAGGAACCTTGAGGAAGTTCATAGGGAGG
 ATACCTTCTTCTGTGGTGTGCCATTTGCTTTGGATTACAGTTTCTAGAGTAA (SEQ ID
 NO: 294)

AOLFR161 sequences:

45 MEPRNQTSAQFILLGLSEKPEQETLLFSLFFCMYLVMMVGNLLIILAISSIDSHLHTPMYFFLANL
 SLVDFCLATNTIPKMLVSLQTGSKAISYPCCLIQMYFFHFFGIVDSVILAMMAYDRFVAICHPLH
 YAKIMSLRLCRLLVGALWAFSCFISLTHILLMARLVFCGSHEVPHYFCDLTPILRLSCTDTSVNR
 IFILIVAGMVIATPFVCILASYARILVAIMKVPSAGGRKKAFTSCSSHLSVVALFYGTTIGVYLCF
 50 SSVLTTVKEKASAVMYTAVTPMLNPFYSLRNRLKALRKLVRNKITSSS (SEQ ID NO: 295)

ATGGAACCAAGAAACCAACAGTGCATCTCAATTCATCCTCCTGGGACTCTCAGAAAAGC
 CAGAGCAGGAGACGCTTCTTTTCCCTGTTCTTCTGCATGTACCTGGTCATGGTCGTGGG
 GAACCTGCTCATCCTGGCCATCAGCATAGACTCCCACCTCCACACCCCCATGTACTTCT
 55 TCCTGGCCAACCTGTCCCTGGTTGATTTCTGTCTGGCCACCAACACCATCCCTAAGATGCT
 GGTGAGCCTTCAAACCGGGAGCAAGGCCATCTCTTATCCCTGCTGCCTGATCCAGATGTAC

TTCTTCCATTTCTTTGGCATCGTGGACAGCGTCATAATCGCCATGATGGCTTATGACCGGTT
 CGTGGCCATCTGCCACCCATTGCACTACGCCAAGATCATGAGCCTACGCCTCTGTGCCTGT
 CTGGTCGGCGCCCTCTGGGCGTTTTCTTGCTTCATCTCACTCACTCACATCCTCCTGATGGC
 CCGTCTCGTTTTCTGCGGCAGCCATGAGGTGCCTCACTACTTCTGCGACCTCACTCCCATCC
 5 TCCGACTTTTCGTGCACGGACACCTCTGTGAATAGGATCTTCATCCTCATTGTGGCAGGGAT
 GGTGATAGCCACGCCCTTTGTCTGCATCCTGGCCTCCTATGCTCGCATCCTTGTGGCCATCA
 TGAAGGTCCCCTCTGCAGGCGGCAGGAAGAAAGCCTTCTCCACCTGCAGCTCCCACTGTCT
 TGTGGTTGCTCTCTTCTATGGGACCACCATTTGGCGTCTATCTGTGTCCCTCCTCGGTCTCA
 CCACTGTGAAGGAGAAAGCTTCTGCGGTGATGTACACAGCAGTCACCCCATGCTGAATCC
 10 CTTTCATCTACAGCTTGAGGAACAGAGACCTGAAAGGGGCTCTCAGGAAGCTGGTCAACAG
 AAAGATCACCTCATCTTCTCTGA (SEQ ID NO: 296)

AOLFR162 sequences:

MMRLMKEVRGRNQTEVTEFLLGLSDNPDLQGVLFALFLLIYMANMVGNLGMIVLIKIDLCLH
 15 TPMYFFLSSLSFVDASYSSSVTPKMLVNLMAENKAISFHGCAAQFYFFGSFLGTECFLLAMMA
 YDRYAAIWNPLLVPVLVSGRICFLLIATSLAGCGNAIHTGMTFRLSFCGSNRINHIFYCDTPPL
 LKLSGSDTHFNQIVIMAFSSFIVISCVMIVLISYLIFIAVLKMPSEGRHKAFSTCASYLMAVTIF
 FGILFMYLRPTSSYSMEQDKVVSFVTVIIPVLNPLIYSLKNKDVKKALKKILWKHIL (SEQ ID
 NO: 297)

ATGATGAGACTTATGAAAGAGGTTTCGAGGCAGAAATCAAACAGAAGTAACAGAATTTCTC
 CTCTTAGGACTTTCCGACAATCCAGATCTACAAGGAGTCTCTTTGCATTGTTTCTGTTGAT
 CTATATGGCAAACATGGTGGGCAATTTGGGGATGATTGTATTGATTAAAGATTGATCTCTGT
 CTCCACACCCCATGTATTTCTTTCTCAGTAGCCTCTCTTTTGTAGATGCCTCTTACTCTTCT
 25 TCCGTCACCTCCCAAGATGCTGGTGAACCTCATGGCTGAGAATAAGGCCATTTCTTTTCATG
 GATGTGCTGCCAGTTCTACTTCTTTGGCTCCTTCTGGGGACTGAGTGCTTCTGTTGGCC
 ATGATGGCATATGACCGCTATGCAGCCATTTGGAACCCCTGCTCTACCCAGTTCTCGTGT
 CTGGGAGAATTTGCTTTTTGCTAATAGCTACCTCCTTCTTAGCAGGTTGTGGAAATGCAGC
 CATAACATACAGGGATGACTTTTAGGTTGTCTTTTGTGGTTCTAATAGGATCAACCATTTCT
 30 ACTGTGACACCCCGCCACTGCTCAAACCTCTCTTGCTCTGATACCCACTTCAATGGCATTGTG
 ATCATGGCATTCTCAAGTTTTATTGTATCAGCTGTGTTATGATTGTCCTCATTTCCTACCT
 GTGTATCTTTCATTGCCGTCTTGAAGATGCCTTCGTTAGAGGGCAGGCACAAAGCCTTCTCC
 ACCTGTGCCTCTTACCTCATGGCTGTCAACATATTCTTTGGAACAATCCTCTTCATGTAATT
 GCGCCCTACATCTAGCTACTCAATGGAGCAAGACAAGGTTGTCTCTGTCTTTTATACAGTA
 35 ATAATCCCTGTGCTAAATCCCTCATCTATAGTTTAAAAAATAAGGATGTAAAAAAGGCC
 TAAAGAAGATCTTATGAAACACATCTTGTAG (SEQ ID NO: 298)

AOLFR163 sequences:

MQRSNHTVTEFILLGFTTDPGMQLGLFVVLGVYSLTVVGNSTLIVLICNDSCLHTPMYFFTG
 40 LSFLDLWYSSVYTPKILVTCISEDKSISFAGCLCQFFFSAGLAYSECYLLAAVAYDRYVAISKPL
 LYAQAMSIKLCALLVAVSYCGGFINSIITKKTFSFNFCRENIIDDFCDLLPLVELACGEKGGYK
 IMMYFLLASNVICPAVLILASYLFIITSVLRISSEKGYLKAFSTCSSHLTSVTLYYGSILYIALPRS
 SYSFDMDKIVSTFYTVVFPMLNLMISLRNKDVKEALKKLLP (SEQ ID NO: 299)

ATGCAGAGGAGCAATCATACAGTGAAGTGTATGCTGGGCTTACCACAGACCCCA
 GGAATGCAGCTGGGCTCTTCGTGGTGTCTCTGGGCGTGTACTCTCTCACTGTGGTAGGAA
 ATAGCACCCCTCATCGTGTGATCTGTAATGACTCCTGCCTCCACACACCCATGTATTTTTTC
 ACTGGAAATCTGTCTGTTTCTGGATCTCTGGTATTCTCTGTCTACACCCCAAAGATCCTAGT
 GACCTGCATCTCTGAAGACAAAAGCATCTCCTTTGCTGGCTGCCTGTGTCACTTCTTCTCT
 50 CTGCAGGGCTGGCCTATAGTGAGTGCTACCTGCTGGCTGCCGTGGCTTATGACCGCTACGT
 GGCCATCTCCAAGCCCCTGCTTTATGCCAGGCCATGTCCATAAAGCTGTGTGCATTGCTG
 GTAGCAGTCTCATATTGTGGTGGCTTTATTAACCTCTCAATCATCACCAAGAAAACGTTTTTC
 CTTAACCTTCTGCGGTGAAAACATCATGACTTTTTCTGTGATTGCTTCCCTTGGTGG
 AGCTGGCCTGTGGCGAGAAGGGCGGTATATAAATTATGATGTACTTCTGCTGGCCTCCAA
 55 TGTCATCTGCCCCGAGTGCTCATCTGGCCTCCTACCTCTTTATCATCACCAGTGTCTTGA
 GGATCTCCTCCTCCAAGGGCTACCTCAAAGCCTTCTCCACATGCTCCTCCACCTGACCTCT

GTCACCTTTATACTATGGCTCCATTCTCTACATCTACGCTCTCCCCAGATCTAGCTATTCTTT
TGATATGGACAAAATAGTTTCTACATTTTACACTGTGGTATTCCCCATGTTGAATCTCATG
ATCTACAGCCTAAGGAATAAGGATGTGAAAGAGGCTCTGAAAAAATTCTCCCATAA (SEQ
ID NO: 300)

5

AOLFR164 sequences:

MFLTERNTTSEATFTLLGFS DYLELQIPLFFVFLAVYGFSVVG NLMIVIIKINPKLHTPMYFFLN
HLSFVDFCYSSIIAPMMLVNLVVEDRTISFSGCLVQFFFFCTFVVTELILFAVMAYDHFVAICNP
LLYTVAISQKLCAMLVVVLYAWGVACSLTLACSALKLSFHGFNTINHHFCELSSLISLSYPDSYL
10 SQLLLFTVATFNEISTLLILTSYAFIIVTTLKMPSASGHRKVFS TCASHLTAITIFHGTLILFLYCV
NSKNSRHTVKVASVFTVVIPLLNPLIYSLRNKDVKDAIRKIINTKYFHIKHRHWYPFNFVIEQ
(SEQ ID NO: 301)

15 ATGTTTCTGACAGAGAGAAATACGACATCTGAGGCCACATTCACTCTCTTGGGCTTCTCAG
ATTACCTGGAAGTGC AAAATCCCCCTCTTCTTTGTATTTCTGGCAGTCTACGGCTTCAGTGTG
GTAGGGAATCTTGGGATGATAGTGATCATCAAAATTAACCCAAAATTGCATACCCCCATGT
ATTTTTTCTCAACCACCTCTCCTTTGTGGATTTCTGCTATTCTCCATCATTGCTCCCATGA
TGCTGGTGAACCTGGTTGTAGAAGATAGAACCATTTCATTCTCAGGATGTTTGGTGCAATT
CTTTTTCTTTTGACCTTTGTAGTGACTGAATTAATTCTATTTGCGGTGATGGCCTATGACC
20 ACTTTGTGGCCATTTGCAATCCTCTGCTCTACACAGTTGCCATCTCCCAGAAACTCTGTGCC
ATGCTGGTGGTTGTATTGTATGCATGGGGAGTCGCATGTTCCCTGACACTCGCGTGCTCTG
CTTTAAAGTTATCTTTTCATGGTTTCAACACAATCAATCATTCTTCTGTGAGTTATCCTCC
CTGATATCACTCTCTTACCCTGACTCTTATCTCAGCCAGTTGCTTCTTTTCACTGTTGCCAC
TTTAAATGAGATAAGCACACTACTCATCTATTCTGACATCTTATGCATTATCATTTGTACCCA
25 CCTTGAAGATGCCTTCAGCCAGTGGGCACCGCAAAGTCTTCTCCACCTGTGCCTCCACCT
GACTGCCATCACCATCTTCCATGGCACCATCCTCTTCTCTACTGTGTACCCAACTCCAAAA
ACTCCAGGCACACAGTCAAAGTGGCCTCTGTGTTTTACACCGTGGTGATCCCCTTGTGAA
TCCCCTGATCTACAGTCTGAGAAATAAAGATGTTAAGGATGCAATCCGAAAAATAATCAAT
ACAAAATATTTTCATATTAACATAGGCATTGGTATCCATTTAATTTTGTATTGAACAATA
30 A (SEQ ID NO: 302)

AOLFR165 sequences:

MAVGRNNTIVTKFILLGLSDHPQMKIFLFLGLYLLTLAWNLSLIALIKMDSHLHMPMYFFL
SNLSFLDICYVSSSTAPKMLSDITEQKTISFVGCATQYFVFCGMGLTECFLLAAMAYDRYAAICN
35 PLLYTVLISHTLCLKMVVGAYVGGFLSSFIETYSVYQHDFCGPYMINHFFCDLPPVLALSCSDTF
TSEVVTFIVSVVGVSVLVVLISYGYIVA AVVKISSATGRTKAFSTCASHLTAVTLFYGSGFFM
YMRPSSSYSLNRDKVVSIFYALVIPVNP IYSFRNKEIKNAMRKAMERDPGISHGPPFIFMTLG
(SEQ ID NO: 303)

40 ATGGCTGTAGGAAGGAACAACACAATTGTGACAAAATTCATTCTCCTGGGACTTTCAGACC
ATCCTCAAATGAAGATTTTCTTTTCATGTTATTTCTGGGGCTCTACCTCCTGACGTTGGCC
TGGAACCTTAAGCCTCATTGCCCTCATTAAAGATGGACTCTCACCTGCATGCCCCATGTACT
TCTTCCTCAGTAACTGTCTTCTCTGGACATCTGCTATGTGTCTCCACCGCCCTAAGATG
CTGTCTGACATCATCACAGAGCAGAAAAACCATTTCTTTGTTGGCTGTGCCACTCAGTACT
45 TTGTCTTCTGTGGGATGGGGCTGACTGAATGCTTTCTCCTGGCAGCTATGGCCTATGACCG
GTATGCTGCAATCTGCAACCCCTTGCTTTACACAGTCCTCATATCCCATACACTTTGTTTAA
AGATGGTGGTTGGCGCCTATGTGGGTGGATTCTTAGTTCTTTTATTGAAACATACTCTGT
CTATCAGCATGATTTCTGTGGGCCCTATATGATCAACCACTTTTCTGTGACCTCCCTCCAG
TCCTGGCTCTGTCTGCTCTGATACCTTACCCAGCGAGGTGGTGACCTTCATAGTCAGTGTT
50 GTCGTTGGAATAGTGTCTGTGCTAGTGGTCTCATCTCTTATGGTTACATTGTTGCTGCTGT
TGTGAAGATCAGCTCAGCTACAGGTAGGACAAAGGCCTTCAGCACTTGTGCCTCTCACCTG
ACTGCTGTGACCCTCTTCTATGGTTCTGATTCTTCATGTACATGCGACCCAGTCCAGCTA
CTCCCTAAACAGGGACAAAGGTGGTGTCCATATTCTATGCCTTGGTGATCCCCGTGGCAAT
CCCATCATCTACAGTTTTAGGAATAAGGAGATTAAAAATGCCATGAGGAAAGCCATGGAA
55 AGGGACCCCGGGATTTCTCAGGTGGACCATTCATTTTATGACCTTGGGCTAA (SEQ ID
NO: 304)

AOLFR166 sequences:

MEMENCTR VKEFIFLGLTQNREVS LVLFLFLLLVYVTTLLGNLLIMVTVTCESRLHTPMYFLLH
 NLSIADICFSSITVPKVLVDLLSERKTISFNHCFTQMFLFHLIGGVDVFSLSVMALDRYVAISKPL
 5 HYATIMSRDHICIGLTVAAWLGGFVHSIVQISLLLPFCGPNVLDTFYCDVHRVLKLAHTDIFIL
 ELLMISNNGLLTTLWFFLLLVSYIVILSLPKSQAGEGRRKAISTCTSHITVVTLHFVPCIYVYARP
 FTALPMDKAISVTFTVISPLLNPLIYTLRNHEMKSAMRRLKRRLVPSDRK (SEQ ID NO: 305)

ATGGAGATGGAAAAGCTGCACCAGGGTAAAAGAATTTATTTTCCTTGGCCTGACCCAGAATC
 10 GGGAAGTGAGCTTAGTCTTATTTCTTTCTACTCTTGGTGTATGTGACAACTTTGCTGGGA
 AACCTCCTCATCATGGTCACTGTTACCTGTGAATCTCGCCTTCACACGCCCATGTATTTTT
 GCTCCATAATTTATCTATTGCCGATATCTGCTTCTCTTCCATCACAGTGCCCAAGGTTCTGG
 TGGACCTTCTGTCTGAAAGAAAGACCATCTCCTTCAATCATTGCTTCACTCAGATGTTTCTA
 TTCCACCTTATTGGAGGGGTGGATGTATTTTCTCTTTCGGTGATGGCATTGGATCGATATG
 15 TGGCCATCTCCAAGCCCCTGCACTATGCGACTATCATGAGTAGAGACCATTGCATTGGGCT
 CACAGTGGCTGCCTGGTTGGGGGGCTTTGTCCACTCCATCGTGAGATTTCCTGTGTGCTC
 CCACTCCCTTTCTGCGGACCCAATGTTCTTGACACTTTCTACTGTGATGTCCACCGGGTCT
 CAAACTGGCCCATACAGACATTTTCATACTTGAACACTAATGATTTCCAACAATGGACTG
 CTCACCACTGTGGTTTTTCTGTCTCTGGTGTCTACATAGTCATATTATCATTACCCAA
 20 GTCTCAGGCAGGAGAGGGCAGGAGGAAAGCCATCTCCACCTGCACCTCCACACACTGT
 GGTGACCGCTGATTTCTGTCCCTGATCTATGTCTATGCCCGGCCCTTCACTGCCCTCCCCA
 TGGATAAGGCCATCTCTGTACCTTCACTGTCTATCTCCCTCTGCTCAACCCCTTGATCTAC
 ACTCTGAGGAACCATGAGATGAAGTCAGCCATGAGGAGACTGAAGAGAAGACTTGTGCT
 TCTGATAGAAAATAG *SEQ ID NO: 306)

25

AOLFR167 sequences:

MSITKAWNSSSVTMFILLGFTDHPQLALLFVTFGLGIYLTTLAWNLAIFLIRGDTHLHTPMYFF
 LSNLSFIDICYSSAVAPNMLTDFWEQKTSIFVGCQAQFFFFVGMGLSECLLLTAMAYDRYAAI
 SSPLLYPTIMTQGLCTRMVVGAYVGGFLSSLIQASSIFRLHFPGPNINHHFFCDLPPVLALSCSDT
 30 FLSQVNVNLFVVTVGGTSFLQLLISYGYTVSAVLKIPSAEGRWKACNTCASHLMVVTLLFGTAL
 FVYLRPSSSYLLGRDKVVSFVSLVIPMLNPLIYSLRNKEIKDALWKVLERKKVFS (SEQ ID
 NO: 307)

ATGTCCATAACCAAAGCCTGGAACAGCTCATCAGTGACCATGTTTCATCCTCCTGGGATTCA
 35 CAGACCATCCAGAACTCCAGGCCCTCCTCTTTGTGACCTTCTGGGCATCTATCTTACCACC
 CTGGCCTGGAACCTGGCCCTCATTTTTCTGATCAGAGGTGACACCCATCTGCACACACCCA
 TGTACTTCTTCTAAGCAACTTATCTTTCAATTGACATCTGCTACTCTTCTGCTGTGGCTCCC
 AATATGCTCACTGACTTCTTCTGGGAGCAGAAGACCATATCATTTGTGGGCTGTGCTGCTC
 AGTTTTTTTTTCTTTGTGCGCATGGGTCTGTCTGAGTGCCCTCCTGACTGCTATGGCATA
 40 GACCGATATGCAGCCATCTCCAGCCCCCTTCTCTACCCCACTATCATGACCCAGGGCCTCT
 GTACACGCATGGTGGTTGGGGCATATGTTGGTGGCTTCTGAGCTCCCTGATCCAGGCCAG
 CTCCATATTTAGGCTTCACTTTTGCAGGACCAACATCATCAACCACTTCTTCTGCGACCTCC
 CACCAGTCTGGCTCTGTCTTGTCTGACACCTTCTCAGTCAAGTGGTGAATTTCTCGTG
 GTGGTCACTGTGCGAGGAACATCGTTTCTCCAACTCCTTATCTCCTATGGTTACATAGTGT
 45 CTGCGGTCTGAAGATCCCTTCAGCAGAGGGCCGATGGAAAGCCTGCAACACGTGTGCT
 CGCATCTGATGGTGGTGACTCTGCTGTTTGGGACAGCCCTTTTCTGTGACTTGCGACCCAG
 CTCCAGCTACTTGCTAGGCAGGGACAAGGTGGTGTCTGTTTTCTATTCAATTGGTGATCCCC
 ATGCTGAACCTCTCATTTACAGTTTGAGGAACAAAGAGATCAAGGATGCCCTGTGGAAG
 GTGTTGGAAAGGAAGAAAGTGTTCCTTAG (SEQ ID NO: 308)

50

AOLFR168 sequences:

MEKINNVTETIFWGLSQSPEIEKVCFVVSFFYIILLGNLLIMLTVCLSNLFKSPMYFFLSFV
 DICYSSTVAPKMIVDLLAKDKTISYVGCMLQLLGVHFFGCTEIFILTVMAYDRYVAICKPLHYM
 TIMNRETCKMMLLGTWVGGFLHSIIQVALVVQLPFCGPNEIDHYFCDVHPVLKLACTETYIVG
 55 VVVTANSGTIALGSFVILLISYSIILVSLRKQSAEGRRKALSTCGSHIAMVVIFFGPCTFMYMRPD

TTFSEDKMVAVFYTTITPMLNPLIYTLRNAEVKNAMKKLWGRNVFLEAKGK (SEQ ID NO: 309)

5 ATGGAAAAAATAAACACGTAACCTGAATTCATTTTCTGGGGTCTTTCTCAGAGCCCAGAGA
TTGAGAAAGTTTGTGTTTGTGGTGTGTTTCTTTCTTCTACATAATCATTCTTCTGGGAAATCTC
CTCATCATGCTGACAGTTTGCCTGAGCAACCTGTTTAAAGTCACCCATGTATTTCTTTCTCAG
CTTCTTGTCTTTTGTGGACATTTGTTACTCTTCAGTCACAGCTCCCAAGATGATTGTTGACC
TGTTAGCAAAGGACAAAACCATCTCCTIATGTGGGGTGCATGTTGCAACTGCTTGGAGTAC
ATTTCTTTGGTTGCACTGAGATCTTCATCCTTACTGTAATGGCCTATGATCGTTATGTGGCT
10 ATCTGTAAACCCCTACATTATATGACCATCATGAACCGGGAGACATGCAATAAAATGTTAT
TAGGGACGTGGGTAGGTGGGTCTTACACTCCATTATCCAAGTGGCTCTGGTAGTCCAACCT
ACCTTTTGTGGACCCAAATGAGATAGATCACTACTTTTGTGATGTTACCCCTGTGTTGAAA
CTTGCTGCACAGAAACATACATTGTTGGTGTGTTGTGACAGCCAAACAGTGGTACCATTG
CTCTGGGGAGTTTTGTTATCTTGCTAATCTCCTACAGCATCATCCTAGTTTCCCTGAGAAAG
15 CAGTCAGCAGAAGGCAGGCGCAAAGCCCTCTCCACCTGTGGCTCCACATTGCCATGGTGC
TTATCTTTTTCGGCCCTGTACTTTTATGTACATGCGCCCTGATACGACCTTTTCAGAGGAT
AAGATGGTGGCTGTATTTTACACCATTATCACTCCCATGTTAAATCCTCTGATTTATACACT
GAGAAATGCAGAAGTAAAGAATGCAATGAAGAAACTGTGGGGCAGAAATGTTTTCTTGA
GGCTAAAGGGAAATAG (SEQ ID NO: 310)

20

AOLFR169 sequences:

MMDNHSSATEFHLLGFPQSQGLHHILFAIFFFFYLVTLMGNTVIIIVCVDKRLQSPMYFFLSHL
STLEILVTIIVPMMWLWLLFLGCRQYLSLHVSINFSCGTMEFALLGVMAVDRYVAVCNPLRY
NIMNSSTCIWVIVSWVFGFLSEIWPIYATFQFTFRKSNSLDHFYCDRGQLKLSCDNTLLTEFI
25 LFLMAVFILIGSLIPTIVSYTYIISTILKIPSASGRKAFSTFASHFTCVVIGYGSCLFLYVKPKQTQ
GVEYNKIVSLLVSVLTPFLNPFIFTLRNDKVKEALRDGMKRCCQLLKD (SEQ ID NO: 311)

ATGATGGACAACCACTCTAGTGCCACTGAATTCACCTTCTAGGCTTCCCTGGGTCCCAAG
GACTACACCACATTTCTTTTGTCTATATTTCTTTTCTTCTATTTAGTGACATTAATGGGAAAC
30 ACGGTCATCATTGTGATTGTCTGTGTGGATAAACGTCTGCAGTCCCCCATGTATTTCTTCTC
CAGCCACCTCTCTACCCTGGAGATCCTGGTCACAACCATAATTGTCCCATGATGCTTTGG
GGATTGCTCTTCTGGGATGCAGACAGTATCTTTCTCTACATGTATCGCTCAACTTTTCTCTG
TGGGACCATGGAGTTTGCACTTCTGGAGTGATGGCTGTGGACCGTTATGTGGCTGTGTGT
AACCCTTTGAGGTACAACATCATTATGAACAGCAGTACCTGTATTTGGGTGGTAATAGTGT
35 CATGGGTGTTTGGATTTCTTTCTGAAATCTGGCCCATCTATGCCACATTTCACTTTACCTTC
CGCAAATCAAATTCATTAGACCAATTTTACTGTGACCGAGGGCAATTGCTCAAACCTGTCTC
GCGATAACACTCTTCTCACAGAGTTTATCCTTTTCTTAATGGCTGTTTTTATTCTCATTGGT
TCTTTGATCCCTACGATTGTCTCCTACACCTACATTATCTCCACCATCCTCAAGATCCCGTC
AGCCTCTGGCCGGAGGAAAGCCTTCTCCACTTTTGCTCCCACTTCACCTGTGTTGTGATTG
40 GCTATGGCAGCTGCTTGTCTCTACGTGAAACCAAGCAAACACAGGGAGTTGAGTACAA
TAAGATAGTTTCCCTGTTGGTTTCTGTGTTAACCCCTTCTGAATCCTTTTCATCTTTACTCT
TCGGAATGACAAAGTCAAAGAGGCCCTCCGAGATGGGATGAAACGCTGCTGTCAACTCCT
GAAAGATTAG (SEQ ID NO: 312)

45 **AOLFR170 sequences:**

MSFTSLIPSLCFSLTLPLFCYLSLLPFLSAFLFITRWLLAFLSLFSVSVVPVSSVSSSMVLCYLSVS
ASPSVFCFSCMQGPILWIMANLSQPSEFVLLGFSSFGELQALLYGPFLMLYLLAFMGNTIIIVMVI
ADTHLHTPMYFFLGNFSLLEILVTMTAVPRMLSDLLVPHKVITFTGCMVQFYFHFSLGSTFLLIL
TDMALDRFVAICHPLRYGTLMRAMCVQLAGAAWAAPFLAMVPTVLSRAHLDYCHGDVINH
50 FFCDNEPLLQLSCSDTRLLEFWDFLMALTFVLSFLVTLSYGYIVTTVLRIPSASSCQKAFSTCG
SHLTLVFIGYSSITFLYVRPGKAHSVQVRKVVALVTSVLTPLNPFILTFCNQTVKTVLQGMQ
RLKGLCKAQ (SEQ ID NO: 313)

ATGTCTTTCACTTCTCTCATACCCCTCACTCTGTTTCTCCTTGACTCTCCCATTCCTGTTTTGT
55 TATCTTTCTTTATTGCCGTTTCTTTCTGCTTTTCTGTTTATCACTCGCTGGCTACTTGCCCTT
CTCTCTCTATTCTCTGTCTCTGTCCCTGTTTCTTCTGTTTCAAGTTCAATGGTCTCTGTCTC

TATCTCTCTGTTTCTGCCTCTCCGTCTGTCTTTTGTCTCTTGCATGCAGGGCCCCATACTG
 TGGATCATGGCAAATCTGAGCCAGCCCTCCGAATTTGTCTCTTGGGCTTCTCCTCCTTTGG
 TGAGCTGCAGGCCCTTCTGTATGGCCCCCTTCTCATGCTTTATCTTCTCGCCTTCATGGGAA
 ACACCATCATCATAGTTATGGTCATAGCTGACACCCACCTACATACACCCATGTACTTCTTC
 5 CTGGGCAATTTTTCCCTGCTGGAGATCTTGGTAACCATGACTGCAGTGCCCAGGATGCTCT
 CAGACCTGTTGGTCCCCACAAAGTCATTACCTTCACTGGCTGCATGGTCCAGTTCTACTTC
 CACTTTTCCCTGGGGTCCACCTCCTTCTCATCTGACAGACATGGCCCTTGATCGCTTTGT
 GGCCATCTGCCACCCACTGCGCTATGGCACTCTGATGAGCCGGGCTATGTGTGTCCAGCTG
 GCTGGGGCTGCCTGGGCAGCTCCTTTCTAGCCATGGTACCCACTGTCCTTCTCCCGAGCTC
 10 ATCTTGATTACTGCCATGGCGACGTCATCAACCACTTCTTCTGTGACAATGAACCTCTCCTG
 CAGTTGTCATGCTCTGACACTCGCCTGTTGGAATTCTGGGACTTTCTGATGGCCTTGACCTT
 TGTCTCAGCTCCTTCTGCTGGTGACCTCATCTCCTATGGCTACATAGTGACCACTGTGCTGC
 GGATCCCCCTCTGCCAGCAGCTGCCAGAAGGCTTTTCTCCACTTGCGGGTCTCACCTCACACT
 GGTCTTCATCGGCTACAGTAGTACCATCTTTCTGTATGTCAGGCCTGGCAAAGCTCACTCT
 15 GTGCAAGTCAGGAAGGTCGTGGCCTTGGTGACTTCAGTTCTCACCCCTTTCTCAATCCCT
 TTATCCTTACCTTCTGCAATCAGACAGTTAAACAGTGCTACAGGGGCAGATGCAGAGGCT
 GAAAGGCCCTTTGCAAGGCACAATGA (SEQ ID NO: 314)

AOLFR171 sequences:

20 MVGNLLIWVTTIGSPSLGSLMYFFLAYLSLMDAISTAMSPKLMIDLLCDKIAISLSACMGQLFI
 EHLGGAEVFLVVMAYDRYVAISKPLHYLNIMNRLVCILLVAMIGGFVHSVQIVFLYSLP
 ICGPNVIDHSVCDMYPLLELLCLDTYFIGLTVVANGGIICMVIFTLISCGVILNFKTYSQEER
 HKALPTCISHIIVVALVFPCIFMYVRPVSNEPFDKLMTVFYSHITLMLNPLIYSLRQSEMKNAM
 KNLWCEKLSIVRKRVSPTLNIFIPSSKATNRR (SEQ ID NO: 315)

25 ATGGTGGGAAACCTCCTCATTTGGGTGACTACTATTGGCAGCCCCCTCCTTGGGCTCCCTAA
 TGTACTTCTTCTTGCCTACTTGTCACTTATGGATGCCATATATCCACTGCCATGTCACCC
 AAATTGATGATAGACTTACTCTGTGATAAAATCGCTATTTCTTGTGAGCTTGCATGGGTC
 AGCTCTTCATAGAACACTTACTTGGTGGTGCAGAGGTCTTCTTTTGGTGGTGATGGCCTA
 30 TGATCGCTATGTGGCTATCTCTAAGCCGCTGCACTATTTGAACATCATGAATCGACTGGTT
 TGCATCCTTCTGTGGTGGTGGCCATGATTGGAGGTTTGTGCACTCTGTGGTTCAAATTGT
 CTTTCTGTACAGTCTACCAATCTGTGGCCCCAATGTTATTGACCACTCTGTCTGTGACATGT
 ACCCATTTGGAACTGTTGTGCCTTGACACCTACTTTATAGGACTCACTGTGGTTGCCAA
 TGGTGAATAATTTGTATGGTCATCTTACCTTTCTGCTAATCTCCTGTGGAGTCATCCTAA
 35 ACTTCCTTAAACTTACAGTCAGGAAGAGAGGCATAAAGCCCTGCCTACCTGCATCTCCCA
 CATCATTGTGGTTGCCCTCGTTTTTGTTCCTGTATTTTATGTATGTTAGACCCGTTTCCA
 ACTTTCCCTTTGATAAATAATGACTGTGTTTTATTCAATTATCACACTCATGTTGAATCCT
 TTAATATACTCGTTGAGACAATCAGAGATGAAAAATGCTATGAAAAATCTCTGGTGTGAA
 AAGTTAAGTATAGTTAGAAAAAGAGTATCTCCCACTGAACATATTTATTCCTAGTTCTA
 40 AGGCAACAAATAGGCGGTAA (SEQ ID NO: 316)

AOLFR172 sequences:

MAETLQLNSTFLHPNFFILTGFPGLGSAQTWLTLVFGPIYLLALLGNGALPAVVWIDSTLHQPM
 FLLAILAATDLGLATSIAPGLLAVLWLGPRSVPYAVCLVQMFFVHALTAMESGVLLAMACDR
 45 AAAIGRPLHYPVLVTKACVGYAALALALKAVAIVVPFLLVAKFEHFQAKTIGHTYCAHMAV
 VELVVGNTQATNLYGLALSIAISGMDILGITGSYGLIAHAVLQLPTREAHAKAFGTCSSHICVIL
 AFYIPGLFSYLAHRFGHHTVPKPVHILLSNIYLLPPLNPLIYGARTKQIRDRLLETFTFRKSPL
 (SEQ ID NO: 317)

50 ATGGCAGAACTCTACAACTCAATTCCACCTTCTACACCCAACTTCTTCATACTGACTG
 GCTTTCCAGGGCTAGGAAGTGCCAGACTTGGCTGCACTGGTCTTTGGGCCCATTTATCT
 GCTGGCCCTGCTGGGCAATGGAGCACTGCCGGCAGTGGTGTGGATAGACTCCACACTCA
 CCAGCCCCACTGTTTCTACTGTTGGCCATCTGCGCAGCCACAGACCTGGGCTTAGCCACATCT
 ATAGCCCCAGGGTTGCTGGCTGTGCTGTGGCTTGGGCCCCGATCTGTGCCATATGCTGTGT
 55 GCCTGGTCCAGATGTTCTTTGTACATGCACTGACTGCCATGGAATCAGGTGTGCTTTTGGC
 CATGGCCTGTGATCGTGTGCGGCAATAGGGCGTCCACTGCACTACCCTGTCTGGTCACC

AAAGCCTGTGTGGGTTATGCAGCCTTGGCCCTGGCACTGAAAGCTGTGGCTATTGTTGTAC
CTTTCCCACTGCTGGTGGCAAAGTTTGAGCACTTCCAAGCCAAGACCATAGGCCATACCTA
TTGTGCACACATGGCAGTGGTAGAACTGGTGGTGGGTAACACACAGGCCACCAACTTATA
TGGTCTGGCACTTCACTGGCCATCTCAGGTATGGATATTCTGGGTATCACTGGCTCCTAT
5 GGACTCATTGCCCATGCTGTGCTGCAGCTACCTACCCGGGAGGCCCATGCCAAGGCCTTTG
GTACATGTAGTTCTCACATCTGTGTCATTCTGGCCTTCTACATACCTGGTCTCTTCTCCTAC
CTCGCACACCGCTTTGGTCACTACACTGTCCCAAAGCCTGTGCACATCCTTCTCTCCAACAT
CTACTTGCTGCTGCCACCTGCCCTCAACCCCTCATCTATGGGGCCCCGACCAAGCAGATC
AGAGACCGACTCCTGGAAACCTTCACATTCAAAAAAGCCCGTTGTAA (SEQ ID NO: 318)
10

AOLFR173 sequences:

MSHTNVTIFHPAVFVLPGLPGLEAYHIWLSIPLCLIYTTAVLGNSILVIVMERNLHVPMYFFLS
MLAVMDILLSTTTVPKALAFWLQAHNIAFDACVTQGGFFVHMMFVGESAILLAMAFDRFVAIC
APLRYTTVLTWPVVGRIALAVITRSFCHFPVIFLLKRLPFCLTNIVPHSYCEHIGVARLACADITV
15 NIWYGFSVPVIMVILDVILLAVSYSLILRAVFLPSQDARHKALSTCGSHLCVILMFYVPSFFTL
THHFGRNIPQHVHILLANLYVAVPPMLNPVYGVKTKQIREGVAHRFFDIKTWCCTSPGLS
(SEQ ID NO: 319)

ATGAGTCACACCAATGTTACCATCTTCCATCCTGCAGTTTTTGTCTTCCTGGCATCCCTGG
20 GTTGGAGGCTTATCACATTTGGCTGTCAATACCTCTTTCCTCATTTACATCACTGCAGTCC
TGGGAAACAGCATCCTGATAGTGGTTATTGTCATGGAAACGTAACCTTCATGTGCCCATGTA
TTTCTTCTCTCAATGCTGGCCGTGTCATGGACATCCTGCTGTCTACCACTGTCGCCCAAGG
CCCTAGCCATCTTTTGGCTTCAAGCACATAACATTGCTTTTGATGCCTGTGTCAACCAAGG
TTCTTTGTCCATATGATGTTTGTGGGGGAGTCAGCTATCCTGTTAGCCATGGCCTTTGATCG
25 CTTTGTGGCCATTTGTGCCCCACTGAGATATACAACAGTGCTAACATGGCCTGTTGTGGGG
AGGATTGCTCTGGCCGTGTCACCCGAAGCTTCTGCATCATCTTCCCAGTCATATTCTTGCT
GAAGCGGCTGCCCTTCTGCCTAACCAACATTGTTCTCTCACTCCTACTGTGAGCATATTGGA
GTGGCTCGTTTAGCCTGTGCTGACATCACTGTAAACATTTGGTATGGCTTCTCAGTGCCCAT
TGTCATGGTCATCTTGATGTTATCCTCATCGCTGTGTCTTACTCACTGATCCTCCGAGCAG
30 TGTTTCGTTTGCCCTCCCAGGATGCTCGGCACAAGGCCCTCAGCACTTGTTGGCTCCACCT
CTGTGTCATCCTTATGTTTATGTTCCATCCTTCTTTACCTTATTGACCCATCATTTTGGGCG
TAATATTCCTCAACATGTCCATATCTTGCTGGCCAACTTTTATGTGGCAGTGCCACCAATGC
TGAACCCCATTTGCTATGGTGTGAAGACTAAGCAGATACGTGAGGGTGTAGCCACCCGGTT
CTTTGACATCAAGACTTGGTGTGTACCTCCCCTCTGGGCTCATGA (SEQ ID NO: 320)
35

AOLFR175 sequences:

MHFLSQNDLNLNIPHLCLHRHSVIAGAFTHRHMKIFNSPNSSTFTGFILLGFPCPREGQILLFV
LFTVVYLLTLMGNGSIICAVHWDQRLHAPMYILLANFSFLEICYVTSTVPSMLANFLSDTKHSF
SGCFLQFYFFSLGSTECFLAVMAFDRLAJACRPLRYPTIMTRRLCTNLVNCWVLGFIWFLPI
40 VNISQMSFCGSRIDHFLCDPAPLLTLTCKKGPVIELVFSVLSPLPVFMLFLFVGSYALVVRVL
RVPSAAGRRAKAFSTCGSHLAVVSLFYGSVLVVMYGSPPSKNEAGKQKTVTLFYSVVTPLNPVI
YSLRNKDMRKALKKFWGT (SEQ ID NO: 321)

ATGCATTTTCTTTCCCAAATGATTAAATATAAATCTGATTCCCCATCTATGTTTGCACCG
45 TCATTAGTAATTGCTGGTGCTTTTACAATTCACAGGCACATGAAAATCTTCAACAGCCCC
AGCAACTCCAGCACCTTCACTGGCTTCATCCTCCTGGGCTTCCCTTGCCCCAGGGAGGGGC
AGATCCTCCTCTTTGTGCTCTTCACTGTTGTTTACCTCCTGACCCCTCATGGGCAATGGTTCC
ATCATCTGTGCTGTGCACTGGGATCAGAGACTCCACGCCCCCATGTACATCCTGCTCGCCA
ACTTCTCCTTCTTGGAGATATGTTATGTCACCTCCACAGTCCCCAGCATGCTGGCCAACTTC
50 CTCTCTGACACCAAGATCATCTCGTTCTCTGGCTGCTTCCCTCCAGTTCTACTTTTCTTCTCC
TTGGGCTCTACAGAATGCTTTTCTTGGCAGTTATGGCATTGATCGATACCTTGCCATCTG
TCGGCCTCTACGCTATCCAACCATTATGACCAGACGCTCTCTGTACCAATCTTGTGGTCAATT
GCTGGGTACTTGGTTTCACTGCTGTTCTTCTGATTCTTATCGTCAACATCTCCCAAATGTCCTTC
TGTGGATCTAGGATTATTGACCACTTCTATGTGACCCAGCTCCTCTTCTAACTCTCACTTG
55 CAAAAAAGGCCCTGTGATAGAGCTTGTCTTTCTGTCTTAAAGTCTCTGCTGTCTTTATGC
TCTTTCTCTTCAATTGTGGGGTCTATGCTCTGGTCTGAGAGCTGTGTTGAGGGTCCCTTCA

GCAGCTGGGAGAAGAAAGGCTTTCTCCACCTGTGGGTCTCACCTGGCTGTGGTTTCACTGT
TCTACGGCTCAGTACTGGTCATGTATGGGAGCCACCATCTAAGAATGAAGCTGGAAAGC
AGAAGACTGTGACTCTGTTTTATTCTGTTGTACCCCACTGCTTAACCCTGTGATATATAGT
CTTAGGAACAAAGATATGAGAAAAGCTCTGAAGAAATTTTGGGGAACATAA (SEQ ID NO:
5 322)

AOLFR176 sequences:

MFFIIHSLVTSVFLTALGPQNRTMHFVTEFVLLGFHGGQREMQSCFFSFLVLYLLTLLGNGAIVC
AVKLDRLRLHTPMYILLGNFAFLEIWIYSSITVPNMLVNILSEIKTISFSGCFLQFYFFFSGLTTECF
10 LSVMA YDRYLAICRPLHYPSIMTGKFCILVCVCWVGGFLCYPVPIVLISQLPFCGPNIDHLVCD
PGLFALACISAPSTELICYTFNSMIIFGPFLSILGSYTLVIRAVLCIPSGAGRTKAFSTCGSHLMV
VSLFYGTLMVMYVSPSTSGNPAGMQKIITLVYTAMTFFLNPLIYSLRNKDMKDALKRVLGLTVS
QN (SEQ ID NO: 323)

ATGTTCTTTATTATTTCATTCTTTGGTTACTTCTGTTTTTCTAACAGCTTTGGGACCCAGAA
CAGAACAAATGCATTTTGTGACTGAGTTTGTCTCCTGGGTTTCCATGGTCAAAGGGAGATG
CAGAGCTGCTTCTTCTCATTTCATCCTGGTTCTCTATCTCCTGACACTGCTAGGGAATGGAGC
TATTGTCTGTGCACTGAAATTGGACAGGCGGCTCCACACACCCATGTACATCCTTCTGGGA
AATTTGCTTTTCTAGAGATCTGGTACATTTCTCCTCACTGTCCCAAACATGCTAGTCAATAT
20 CCTCTCTGAGATTAAAACCATCTCCTTCTCTGGTTGCTTCTGCAATTCTATTTCTTTTTTCT
ACTGGGTACAACAGAGTGTTTCTTTTATCAGTTATGGCTTATGATCGGTACCTGGCCATC
TGTCGTCCTTACACTACCCCTCCATCATGACTGGGAAGTTCTGTATAATTCTGGTCTGTGT
ATGCTGGGTAGGCGGATTTCTCTGCTATCCAGTCCCTATTGTTCTTATCTCCCAACTTCCCT
TCTGTGGGCCCAACATCATTGACCACTTGGTGTGTGACCCAGGCCCATGTTTGCACCTGGC
25 CTGCATCTCTGCTCCTTCCACTGAGCTTATCTGTTACACCTTCAACTCGATGATTATCTTTG
GGCCCTTCTCTCCATCTTGGGATCTTACACTCTGGTCATCAGAGCTGTGCTTTGTATTCCC
TCTGGTGCTGGTCAACTAAAGCTTTCTCCACATGTGGGTCCACCTAATGGTGGTGTCTC
TATTCTATGGAACCCCTTATGGTGATGTATGTGAGCCCAACATCAGGGAACCCAGCAGGAAT
GCAGAAGATCATCACTCTGGTATACACAGCAATGACTCCATTCTTAAATCCCCCTATCTAT
30 AGTCTTCGAAACAAAGACATGAAAGATGCTCTAAAGAGAGTCTGGGGTTAACAGTTAGC
CAAACTGA (SEQ ID NO: 324)

AOLFR177 sequences:

MSFFFVDLRPMNRSATHIVTEFILLGFPGCWKIQIFLSFLVIYVLTLLGNGAIIYAVRCNPLLH
35 TPMYFLLGNFAFLEIWIYVSSTIPNMLVNILSKTKAISFSGCFLQFYFFFSGLTTECLFLAVMAYD
RYLAICHPLQYPAIMTVRFCKLVSFCWLIGFLGYPIPIFYISQLPFCGPNIDHFLCDMDPLMAL
SCAPAPITECIFYTQSSLVLFFTSMYILRSYILLTAVFQVPSAAGRRKAFSTCGSHLVVVSFLFYG
TVMVMYVSPTYGIPTLLQKILTLVYSVTPLFNPLIYTLRNKDMKMLALRNVLFGMRIRQNS
(SEQ ID NO: 325)

ATGTCTTTCTTCTTTGTAGACTTAAGACCCATGAACAGGTCAGCAACACACATCGTGACAG
AGTTTATTCTCCTGGGATTCCCTGGTTGCTGGAAGATTGAGATTTTCTCTTCTCATTGTTT
TTGGTGATTTATGTCTTGACCTTGCTGGGAAATGGAGCCATCATCTATGCAGTGAGATGCA
ACCCACTACTACACACCCCATGTACTTTCTGCTGGGAAATTTGCCTTCTTGAGATCTGG
45 TATGTGCTCCTCACTATTCTAACATGCTAGTCAACATTCTCTCCAAGACCAAGGCCATCTC
ATTTTCTGGGTGCTTCTCCTCAGTTCTATTTCTTCTTTTCACTGGGAACAACTGAATGTCTCT
TTCTGGCAGTAATGGCTTATGATCGATACCTGGCCATCTGCCACCCACTGCAGTACCCTGC
CATCATGACTGTAAGGTTCTGTGGTAAGCTGGTGTCTTTCTGTTGGCTTATTGGATTCTTG
GATACCCAATTCCCATTTTCTACATCTCCCAACTCCCCCTTCTGTGGTCCCTAATATCATTGAT
50 CACTTCTGTGTGACATGGACCCATTGATGGCTCTATCCTGTGCCCCAGCTCCCACTAATG
AATGTATTTTCTATACTCAGAGCTCCCTTGTCTCTTTTCTACTAGTATGTACATTCTTCGA
TCCTATATCCTGTTACTAACAGCTGTTTTTCAAGTCCCTTCTGCAGCTGGTCCGAGAGAAAAG
CCTTCTCTACCTGTGGTTCTCATTGGTTGTTGATCTCTTTTCTATGGGACATGTCATGGTA
ATGTATGTAAGTCTACATATGGGATCCCACTTTATTGCAGAAGATCCTCACACTGGTAT
55 ATTCAGTAACGACTCCTCTTTTAACTCTGATCTATACTCTTCGTAATAAGGACATGAAA

CTCGCTCTGAGAAATGTCCTGTTTGGGAATGAGAATTCGTCAAAATTCGTGA (SEQ ID NO: 326)

AOLFR178 sequences:

- 5 MVGANHSVSEFVFLGLTNSWEIRLLLLVFSSMFYMASMMGNSLILLTVTSDPHLHSPMYFLL
ANLSFIDLGVSSVTSPKMIYDLFRKHEVISFGGCIQIFFIHVIGGVEMVLLIAMAFDRYVAICKP
LQYLTIMSPRMCMMFFLVAWVTGLIHSVVQLVFVNLPCGPNVSDSFYCDLPRFIKLACTDSY
RLEFMVTANSGFISLGSFFILISYVVIIITVLKHSSAGLSKALSTLSAHVSVVVLFFGPLIFVYTW
PSPSTHLDKFLAIFDAVLTPVLNPIIYTFRN (SEQ ID NO: 327)
- 10 ATGGTTGGGGCAAATCACTCCGTGGTGTCAGAGTTTGTGTTCTCTGGGACTACCAATTCCT
GGGAGATCCGACTTCTCCTCCTTGTGTTCTCCTCCATGTTTTACATGGCCAGTATGATGGGA
AACTCTCTCATTTTGTCTACTGTGACTTCTGACCCTCACTTGCACTCCCCCATGTATTTCT
GTTAGCCAACCTCTCCTTCATTGACCTGGGTGTTTCTCTGTCACTTCTCCAAAATGATTT
15 ATGACCTGTTGAGAAAGCACGAAGTCATCTCCTTTGGAGGCTGCATCGCTCAAATCTTCTT
CATCCACGTCATTGGCGGTGTGGAGATGGTGCTGCTCATAGCCATGGCCTTTGACAGATAT
GTGGCCATATGTAAGCCCTCCAGTACCTGACCATTATGAGCCCAAGAATGTGCATGTTCT
TCTTAGTGGCTGCCTGGGTGACCGGCCTTATCCACTCTGTAGTTCAATTGGTTTTTGTAGTA
AACTTGCCCTTCTGTGGTCCTAATGTATCGGACAGCTTTTACTGTGACCTTCTCGGTTTCAT
20 CAAACTTGCTGCACAGACAGCTACCGACTGGAGTTCATGGTTACAGCCAACAGTGGATTCT
ATCTCTCTGGGCTCCTTCTTCATACTGATCATTTCTATGTGGTCATCATTCTCACTGTTCT
GAAACACTCTCAGCTGGTTTATCCAAGGCTCTGTCCACCCTTTCAGCTCAGCTCAGTGTG
GTAGTTTTGTTCTTTGGTCTTTGATTTTTGTCTATACGTGGCCATCTCCCTCCACACACCT
GGATAAGTTTCTGGCCATCTTTGATGCAGTTCTCACTCCTGTTTTAAATCCTATCATCTACA
25 CATTAGGAATTGA (SEQ ID NO: 328)

AOLFR179 sequences:

- MNGMNHSVSEFVFMGLTNSREIQLLLFVFSLLFYFASMMGNLVIVFTVTMDAHLHSPMYFLL
ANLSIIDMAFCSITAPKMICDIFKKHKAIISFRGCTQIFFSHALGGTEMVLLIAMAFDRYMAICKP
30 LHYLTIMSPRMCLYFLATSSIIGLIHLVQLVFVVDLPFCGPNIFDSFYCDLPRLLRLACTNTQEL
EFMVTVNSGLISVGSFVLLVISYIFLFTVWKHSSGGLAKALSTLSAHVTVVILFFGPLMFFYTW
PSPTSHLDKYLAIFDAFITPFLNPVIYTFRNKDMKVAMRRLCSRLAHFTKIL (SEQ ID NO: 329)
- 35 ATGAATGGAATGAATCACTCTGTGGTATCAGAATTTGTATTTCATGGGACTACCAACTCAC
GGGAGATTCAGCTTCTACTTTTTGTTTTCTCTTTGTTGTTCTACTTTGCGAGCATGATGGGA
AACCTTGTCATTGTATTCACTGTAACCATGGATGCTCATCTGCACTCCCCCATGTATTTCT
CCTGGCTAACCTCTCAATCATTGATATGGCATTGCTCAATTACAGCCCTAAGATGATTT
GTGATATTTTCAAGAAGCACAAAGGCCATCTCCTTTCGGGGATGTATTACTCAGATCTTCTT
TAGCCATGCTCTTGGGGGCACTGAGATGGTGCTGCTCATAGCCATGGCCTTTGACAGATAC
40 ATGGCCATATGTAAACCTCTCCACTACCTGACCATCATGAGCCCAAGAATGTGTCTATACT
TTTTAGCCACTTCTCTATCATTGGCCTTATCCACTCATTGGTCCAATTAGTTTTTGTGGTA
GATTTACCTTTTTGTGGTCCTAATATCTTGACAGTTTTTACTGTGATCTCCCTCGGCTCCT
CAGACTTGCCCTGTACCAACACCCAAGAAGTTCATGGTCACTGTCAATAGTGGACTC
ATTTCTGTGGGCTCCTTTGTCTTGCTGGTAATTTCTTACATCTTCATTCTGTTCACTGTTTG
45 GAAACATTCTTCTGGTGGTCTAGCCAAGGCCCTCTCTACCCTGTCAGCTCATGTCACTGTG
GTCATCTTGTCTTTGGGCCACTGATGTTTTTCTACACATGGCCTTCTCCACATCACACCT
GGATAAATATCTTGCTATTTTTGATGCATTTATTACTCCTTTTCTGAATCCAGTTATCTACA
CATTAGGAACAAAGACATGAAAGTGGAATGAGGAGACTGTGCAGTCGTCTTGCGCATT
TTACAAAGATTTTGTA (SEQ ID NO: 330)

50

AOLFR180 sequences:

- MTNKMYYAIYIKNLNYFSFLVQCLQPTMAIFNNTTSSSNFLLTAFPGLECAHVWISIPVCCLYTI
ALLGNSMIFLVIITKRRLHKPMYYFLSMLAAVDLCLTITLPTVLGVLFHAREISFKACFIQMF
FVHAFSLLESSVLVAMAFDRFVAICNPLNYATILTDRMVLVIGLVICIRPAVFLPLLVAINTVSF
55 HGGHELHSHFPCYHPEVIKYTYSKPVWISSFWGLFLQLYLNGLTDVLFILFSYVLLRTVLGIVARKK

QQKALSTCVCHICAVTIFYVPLJLSLSLAHRLFHSTPRVLCSTLANIYLLPPVLNPIIYSLKTKTIR
QAMFQLLQSKGSWGFNVRGLRGRWD (SEQ ID NO: 331)

5 ATGACTAATAAAATGTATGCTATATATATAAAGAATCTTAATTATTTTCTTTCCTCATAGT
TCAGTGTCTTCAACCAACCATGGCAATATTCAATAACACCACTTCGTCTTCTCAAACCTTCC
TCCTCACTGCATTCCCTGGGCTGGAATGTGCTCATGTCTGGATCTCCATTCCAGTCTGCTGT
CTCTACACCATTTGCCCTCTTGGGAAACAGTATGATCTTTCTTGTCATCATTACTAAGCGGA
GACTCCACAAACCCATGTATTATTTCTCTCCATGCTGGCAGCTGTTGATCTATGTCTGACC
ATTACGACCCCTTCCCACTGTGCTTGGTGTCTCTGGTTTCATGCCCAGGAGATCAGCTTTAA
10 AGCTTGCTTCATTCAAATGTTCTTTGTGCATGCTTCTCTCTGCTGGAGTCCCTCGGTGCTGG
TAGCCATGGCCTTTGACCGCTTCGTGGCTATCTGTAACCCCACTGAACTATGCTACTATCCTC
ACAGACAGGATGGTCCCTGGTGATAGGGCTGGTCATCTGCATTAGACCAGCAGTTTCTTAC
TTCCCTTCTTGTAGCCATAAACACTGTGTCTTTTCATGGGGGTCACGAGCTTTCCCATCCA
TTTTGCTACCACCCAGAAGTGATCAAATACACATATTCCAAACCTTGGATCAGCAGTTTTT
15 GGGGACTGTTTCTTCAGCTCTACCTGAATGGCACTGACGTATTGTTTATTCTTTCTCTAT
TCTCTGATCCTCCGTACTGTTCTGGGCATTGTGGCCCGAAAGAAGCAACAAAAAGCTCTCA
GCACTTGTGTCTGTACATCTGTGCAGTCACTATTTTCTATGTGCCACTGATCAGCCTCTCT
TTGGCACACCGCCTCTTCCACTCCACCCCAAGGGTGTCTGTAGCACTTTGGCCAATATTTA
TCTGCTCTTACCACCTGTGCTGAACCCTATCATTTACAGCTTGAAGACCAAGACAATCCGC
20 CAGGCTATGTTCCAGCTGCTCCAATCCAAGGGTTCATGGGGTTTTAATGTGAGGGGTCTTA
GGGGAAGATGGGATTGA (SEQ ID NO: 332)

AOLFR181 sequences:

25 MSVLNNSEVKLFLGIPGLEHAHIWFSIPICLMYLLAIMGNCTILFIKTEPSLHEPMYYFLAML
AVSDMGLSLSSLPTMLRVFLFNAMGISPNACFAQEFFIHGFTVMESSVLLIMSLDRFLAIHNPLR
YSSILTSNRVAKMGLILAIRSILLVPPFFTLLRLKYCQKNLLSHSYCLHQDTMKLACSDNKTIV
IYGFIALCTMLDLALIVLSYVLILKILSLIASLAERLKALNTCVSHICAVLTFYVPIITLAAMHFF
AKHKSPLVILLIADMFLVPLMNPVYCVKTRQIWEKILGKLLNVCGR (SEQ ID NO: 333)

30 ATGTCTGTTCTCAATAACTCCGAAGTCAAGCTTTTCTTCTGATTGGGATCCCAGGACTGG
AACATGCCCACATTTGGTCTCCATCCCCATTTGCCTCATGTACCTGCTTGCCATCATGGGG
AACTGCACCATTTCTTTATTATAAAGACAGAGCCCTCGCTTCATGAGCCCATGTATTATT
CCTTGCCATGTTGGCTGTCTCTGACATGGGCCTGTCCCTCTCCTCCCTTCCCTACCATGTTGA
GGGTCTTCTTGTTCAATGCCATGGGAATTTACCTAATGCCTGCTTTGCTCAAGAATTCTTC
35 ATTCATGGATTCACTGTCAATGGAATCCTCAGTACTTCTAATTATGTCTTTGGACCGCTTCT
TGCCATTACAATCCCTTAAGATACAGTTCTATCCTCACTAGCAACAGGGTTGCTAAAATG
GGACTATTTTAGCCATTAGGAGCATTCTCTTAGTGATTCCATTTCCCTTACCTTAAGGAG
ATTAAAATATTGTCAAAAAGAATCTTCTTCTCACTCATACTGTCTTCATCAGGATACCATGA
AGCTGGCCTGCTCTGACAACAAGACCAATGTCACTATGGCTTCTTCATTGCTCTCTGTACT
40 ATGCTGGACTTGGCACTGATTGTTTTGTCTTATGTGCTGATCTTGAAGACTATACTCAGCAT
TGCATCTTTGGCAGAGAGGCTTAAGGCCCTAAATACCTGTGTCTCCACATCTGTGCTGTG
CTCACCTTCTATGTGCCATCATCACCTGGCTGCCATGCATCACTTTGCCAAGCACAAAA
GCCCTCTTGTTGTGATCCTTATTGCAGATATGTTCTTGTGTTGGTGCCGCCCTTATGAACCC
ATTGTGTAAGTGTGTAAGACTCGACAAATCTGGGAGAAGATCTTGGGGAAGTTGCTTAAT
45 GTATGTGGGAGATAA (SEQ ID NO: 334)

AOLFR182 sequences:

50 MTLGSLGNSSSVSATFLLSGIPGLERMHIWISIPLCFMYLVSIPGNCTILFIKTERSLHEPMYFL
SMLALIDLGLSLCTLPVLGIFWVGAREISHDACAQLFFIHCFSLFLESSVLLSMAFDRFVAICHP
LHYVSILTNTVIGRIGLVSIGRSVALIFPLPFMLKRFYCGSPVLSHSHYCLHQEVMKLACADMK
ANSIYGMFVIVSTVGIDSLILFSYALILRTVLSIASRAERFKALNTCVSHICAVLLFYTPMIGLSV
IHRFGKQAPHLVQVVMGFMYLLFPPVMNPVYSVKTKQIRDRVTHAFY (SEQ ID NO: 335)

55 ATGACCCTGGGATCCCTGGGAAACAGCAGCAGCAGCGTTTCTGCTACCTTCTGCTGAGTG
GCATCCCTGGGCTGGAGCGCATGCACATCTGGATCTCCATCCCACTGTGCTTCATGTATCT
GGTTTCCATCCCGGGCAACTGCACAATTCTTTTATCATTAACAGAGCGCTCACTTCAT

GAACCTATGTATCTCTTCTGTCATGCTGGCTCTGATTGACCTGGGTCTCTCCCTTTGCAC
 TCTCCCTACAGTCTCTGGGCATCTTTTGGGTGGAGCACGAGAAATTAGCCATGATGCCTGC
 TTTGCTCAGCTCTTTTTCATTCAGTCTCTCTTCTCGAGTCTCTGTGCTACTGTCTATG
 GCCTTTGACCGCTTTGTGGCTATCTGCCACCCCTTGCACTATGTTTCCATTCTCACCAACAC
 5 AGTCATTGGCAGGATTGGCCTGGTCTCTCTGGGTGCTAGTGTAGCACTCATTTTTCCATTA
 CCTTTTATGCTCAAAAAGATTCCCCTATTGTGGCTCCCCAGTTCTCTCACATTCTTATTGTCT
 CCACCAAGAAGTGATGAAATTGGCCTGTGCCGACATGAAGGCCAACAGCATCTACGGCAT
 GTTTGTCTATCGTCTCTACAGTGGGTATAGACTCACTGCTCATCCTCTTCTCTTATGCTCTGA
 TCCTGCGCACCGTGCTGTCCATCGCCTCCAGGGCTGAGAGATTCAAGGCCCTTAACACCTG
 10 TGTTTCCACATCTGTGCTGTGCTGCTCTTCTACACTCCCATGATTGGCCTCTCTGTCTATCC
 ATCGCTTTGGAAAGCAGGCACCCACCTGGTCCAGGTGGTCAATGGGTTTTCATGTATCTTCT
 CTTTCTCTGTGATGAATCCCATTTGTCTACAGTGTGAAGACCAAAACAGATCCGGGATCGA
 GTGACGCATGCCTTTTGTACTAA (SEQ ID NO: 336)

15 **AOLFR183 sequences:**

MTNLNASQANHRNFILTGIPGTPDKNPWLAFPLGFLYTLTLLGNGTILAVIKVEPSLHEPTYFL
 SILALTDVSLMSLTLPMSLSIYWFNAPQIVFDACIMQMFFIHVFGIVESGVLVSMADFDRFVAINR
 PLHYVLSILTHDVIRKTVISVLTRA VCVVFPVFLIKCLPFCHSNVLSHSYCLHQNMRLACASTR
 INSLYGLIVVIFTLGLDVLTLTLLSYVLTLLKTVLGVSRGERLKTLLSTCLSHMSTVLLFYVPPMGA
 20 ASMIHRFWHELSPVVHVMVADIYLLLPVLNPIVYSVKTKQI (SEQ ID NO: 337)

ATGACGAACTTGAATGCATCACAGGCCAACCCACCGTAACCTTCATTCTGACAGGTATCCCGA
 GAACGCCAGACAAGAACCCATGGTTGGCCTTTCCCTGGGATTTCTCTACACACTCACACT
 CCTGGGAAATGGTACCATCCTAGCTGTCATCAAGGTGGAGCCAAGTCTCCATGAGCCACAG
 25 TATTACTTCTTTTCTATCTTGGCTCTCACTGACGTTAGTCTCTCCATGTCCACCTTGCCTCC
 ATGCTCAGCATCTACTGGTTTAATGCCCTCAGATTGTTTTTATGTCATGCATCATGCAGAT
 GTTCTTCATCCATGTATTTGGAATAGTAGAATCAGGAGTCTAGTGTCCATGGCCTTTGAC
 AGATTGTGGCCATCCGAAACCCATTACACTATGTTTCCATCCTCACTCACGATGTTATTCCG
 AAAGACTGGAATATCTGTCCTCACCCGGGCAGTCTGTGTGGTATTCCCTGTGCCCTTCTT
 30 ATAAAGTGCCTACCCTTCTGCCATTCCAATGTCTTGTCTCATTCTACTGTCTTACCAAAA
 CATGATGCGGCTAGCTTGTGCCAGCACCCGCATCAACAGCCTCTACGGCCTCATCGTCGTC
 ATCTTCACACTGGGGCTCGATGTTCTCTCACTCTACTGTCTTATGTACTCACCTCAAGAC
 TGTGCTGGGCTAGTCTCCAGAGGTGAAAGGCTGAAAACCCCTCAGCACATGCCCTCTCTCAC
 ATGTCTACCGTGCTCCTCTTCTATGTTTCTTTTATGGGTGCTGCCTCCATGATCCACAGATT
 35 TTGGGAGCATTTATCACCAGTAGTGACATGGTCATGGCTGATATATACCTACTGCTCCCG
 CCTGTGCTAAACCCCATTTGTCTACAGTGTGAAGACCAAGCAAATTTGA (SEQ ID NO: 338)

AOLFR184 sequences:

MSTLPTQIAPNSSTSMAPTFLLVGMPGLSGAPSWWTLPLIAVYLLSALGNGTILWHIALQPALHR
 40 PMHFFLFLSVSDIGLVLTALMPTLLGIALAGAHTVPASACLLQMVFHVFVSMESSVLLAMSID
 RALAI CRPLHYPALLTNGVISKISLAISFRCLGLHLPLPFLLAYMPYCLPQVLTHSYCLHPDVARL
 ACPEAWGAAYSFLFVLSAMGLDPLLIFFSYGLIGKVLQGVESREDRWKAGQTCAAHLSAVLLF
 YIPMILLALINHPITQHTHTLLSYVHFLPLINPILYSVKMKRILNRLQPRKVGGAQ
 (SEQ ID NO: 339)

ATGTCAACATTACCAACTCAGATAGCCCCAATAGCAGCACTTCAATGGCCCCCACCTTCT
 TGCTGGTGGGCATGCCAGGCCTATCAGGTGCACCCTCCTGGTGGACATTGCCCTCATGTC
 TGTCTACCTTCTCTCTGCACTGGGAAATGGCACCATCCTCTGGATCATTGCCCTGCAGCCC
 GCCCTGCACCGCCCAATGCACTTCTTCTCTTCTTGTCTAGTGTGTCTGATATTGGATTGGT
 50 CACTGCCCTGATGCCACACTGCTGGGCATCGCCCTTGTGGTGTCTCACTGTCCCTGCC
 TCAGCCTGCCCTTCTACAGATGGTTTTTATCCATGTCTTTTCTGTCTGAGTCTCTGTCTT
 GCTCGCATGTCCATTGATCGGGCACTGGCCATCTGCCGACCTCTCCACTACCCAGCGCTC
 CTCACCAATGGTGTAATTAGCAAAATCAGCCCTGGCCATTTCTTTTCGATGCCTGGGTCTCC
 ATCTGCCCTGCCATTCTGCTGGCCTACATGCCCTACTGCCTCCACAGGTCTTAACCCAT
 55 TCTTATTGCTTGCATCCAGATGTGGCTCGTTTGGCCTGCCAGAAAGCTTGGGGTGCAGCCT
 ACAGCCTATTTGTGGTCTTTTACGCCATGGGTTTGGACCCCTGCTATTTTCTCTCTAT

GGCCTGATTGGCAAGGTGTTGCAAGGTGTGGAGTCCAGAGAGGATCGCTGGAAGGCTGGT
CAAACCTGTGCTGCCCACCTCTCTGCAGTGCTCCTCTTCTATATCCCTATGATCCTCCTGGC
ACTGATTAACCATCCTGAGCTGCCAATCACTCAGCATAACCATACTCTTCTATCCTATGTCC
ATTTCTTCTTCTCCTCCATTGATAAACCTATTCTCTATAGTGTCAGATGAAGGAGATTAGA
5 AAGAGAATACTCAACAGGTTGCAGCCCAGGAAGGTGGGTGGTGCTCAGTGA (SEQ ID NO:
340)

AOLFR185 sequences:

MFYPILNDISTKNNSNIMSCCNILFIKTVEIILVYNQTSQSPWYPIVPSKSLVYNNNTCFDCYHLQR
10 VDCVPSRDHINQSMVLASGNSSHPVSFILLGIPGLEFQLWIAFPFCATYAVAVVGNITLLHVIR
IDHTLHEPMYLFLAMLAITDLVLSSTQPKMLAIFWFHAHEIQYHACLIQVFFIHAFSSVESGVL
MAMALDCYVATCFPLRHSSILTPSVVIKLGITVMLRGLLWVSPFCFMVSRMPFCQHQAIPQSYC
EHMAVLKLVCADTSISRGYGLFVAFSVAGFDMIVIGMSYVMILRAVLQLPSGEARLKAFSTRA
SHICVILALYIPALFSFLTYRFGHDVPRVVHILFANLYLLIPMLNPIIYGVRTKQIGDRVIQGCCG
15 NIP (SEQ ID NO: 341)

ATGTTCTACCCCATTTTGAATGACATAAGTACGAAAAACAACAGTAACATCATGTGTCATGTT
GTAACATATTATTTATTAACAGTTGAAATTATTCTAGTTTATAATCAAACCCAATCACC
20 CTGGTATCCAATAGTCCCATCCAAAAGCCTTGATATAATAAACAACCTGTTTTGATTGTT
ATCATCTGCAGAGAGTAGATTGCGTTCCCAGCAGAGACCATATTAACAGTCCATGGTGCT
GGCTTCAGGGAACAGCTCTTCTCATCCTGTGTCTTTCATCCTGCTTGGAAATCCCAGGCCTG
GAGAGTTTCCAGTTGTGGATTGCCTTTCCGTTCTGTGCCACGTATGCTGTGGCTGTTGTGG
AAATATCACTCTCCTCCATGTAATCAGAATTGACCACACCCTGCATGAGCCCATGTACCTC
25 TTTCTGGCCATGCTGGCCATCACTGACCTGGTCCTCTCCTCCTCCACTCAACCTAAGATGTT
GGCCATATTCTGGTTTTCATGCTCATGAGATTGAGTACCATGCCTGCCTCATCCAGGTGTTCT
TCATCCATGCCTTTTCTTCTGTGGAGTCTGGGGTGCTCATGGCTATGGCCCTGGACTGCTAC
GTGGCTACCTGCTTCCCACTCCGACACTCTAGCATCCTGACCCCATCGGTGCTGATCAAAC
TGGGGACCATCGTGATGCTGAGAGGGCTGCTGTGGGTGAGCCCCTTCTGCTTCATGGTGCT
30 TAGGATGCCCTTCTGCCAACACCAAGCCATTCCCCAGTCATACTGTGAGCACATGGCTGTG
CTGAAGTTGGTGTGTGCTGATACAAGCATAAGTCGTGGGTATGGGCTCTTTGTGGCCTTCT
CTGTGGCTGGCTTTGATATGATTGTCATTGGTATGTCATACGTGATGATTTTGAGAGCTGT
GCTTCAGTTGCCCTCAGGTGAAGCCCGCCTCAAAGCTTTTAGCACACGTGCCTCCCATATC
TGTGTCATCTTGGCTCTTTATATCCCAGCCCTTTTTTCTTCTCCTACCTACCGCTTTGGCCAT
35 GATGTGCCCCGAGTTGTACACATCCTGTTTGCTAATCTCTATCTACTGATACCTCCCATGCT
CAACCCCATCATTTATGGAGTTAGAACCAAACAGATCGGGGACAGGGTTATCCAAGGATG
TTGTGGAAACATCCCCTGA (SEQ ID NO: 342)

AOLFR186 sequences:

MSNASLVTAFLTGLPHAPGLDALLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNL
40 FIDMWFSTVTVPKMLMTLVSPSGRAISFHSCVAQLYFFHFLGSTECFLYTVMSYDRYLAISYPL
RYTSMMSGSRCALLATGTWLSGSLHSAVQTLTFHLPYCGPNQIQHYFCDAPPILKLACADTSA
NVMVIFVDIGIVASGCFVLIVLSYVSIVCSILRRTSDGRRRAFQTCASHCIVVLCFFVPCVVIYLR
PGSMDAMDGVVAIFYTVLTPLLNPVVYTLRNKEVKKAVLKLKRDKVAHPQRK (SEQ ID NO:
343)

ATGTCCAACGCCAGCCTCGTGACAGCATTTCATCCTCACAGGCCTTCCCCATGCCCCAGGGC
TGGACGCCCTCCTCTTTGGAATCTTCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCATGTACTACTTCTCTCA
50 CCAACCTGTCTTCATTGACATGTGGTTCTCCACTGTCACGGTGCCCAAATGCTGATGAC
CTTGGTGTCCCCAAGCGGCAGGGCTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTTT
TCCACITCCTGGGGAGCACCGAGTGTTCCTCTACACAGTCATGTCCTATGATCGCTACTTG
GCCATCAGTTACCCGCTCAGGTACACCAGCATGATGAGTGGGAGCAGGTGTGCCCTCCTGG
CCACCGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCCAT
TTGCCCTACTGTGGACCCAACCAGATCCAGCACTACTTCTGTGACGCACCGCCCATCCTGA
55 AACTGGCCTGTGCAGACACCTCAGCCAACGTGATGGTCATCTTTGTGGACATTGGGATAGT
GGCCTCAGGCTGCTTTGTCTGATAGTGCTGTCTATGTGTCCATCGTCTGTTCCATCCTGC

GGATCCGCACCTCAGATGGGAGGCGCAGAGCCTTTCAGACCTGTGCCTCCCACTGTATTGT
GGTCTTTTGCTTCTTTGTTCCTGTGTTGTCAATTTATCTGAGGCCAGGCTCCATGGATGCCA
TGGATGGAGTTGTGGCCATTTTCTACACTGTGCTGACGCCCCTTCTCAACCCTGTTGTGTAC
ACCCTGAGAAACAAGGAGGTGAAGAAAGCTGTGTTGAAACTTAGAGACAAAGTAGCACAT
5 CCTCAGAGGAAATAA (SEQ ID NO: 344)

AOLFR187 sequences:

MAQVRALHKIMALFSANSIGAMNNSDTRIAGCFLTGIPGLEQLHIWLSIPFCIMYIAALEGNGLI
CVILSQAILHEPMYIFLSMLASADVLLSTTTMPKALANLWLGYSHISFDGCLTQKFFIHFLFIHSA
10 VLLAMAFDRYVAICSPRLRYVTILTSKVIGKIVTATLSRSFIIMFPSIFLLEHLHYCQINIAHTFCEH
MGIAHLSCSDISINVWYGLAAALLSTGLDIMLITVSYIHILQAVFRLLSQDARSKALSTCGSHICV
ILLFYVPALFSVFAYRFGGRSIPCYVHILLASLYVVIPMLNPVIYGVRTKPILEGAKQMFSNLAK
GSK (SEQ ID NO: 345)

15 ATGGCACAGGTGAGGGCGCTGCATAAAATCATGGCCCTTTTTTCTGCTAACAGCATAGGTG
CTATGAACAACTCTGACACTCGCATAGCAGGCTGCTTCTCACTGGCATCCCTGGGCTGGA
GCAACTACATATCTGGCTGTCCATCCCCTTCTGCATCATGTACATCGCTGCCCTGGAAGGC
AATGGCATCCTAATTTGTGTCATCCTCTCCCAGGCAATCCTGCATGAGCCCATGTACATAT
TCTTATCTATGCTGGCCAGTGCTGATGTCTTGCTCTCTACCACCACCATGCCTAAGGCCCTG
20 GCCAATTTGTGGCTAGGTTATAGCCACATTTCTTTGATGGCTGCCTCACTCAAAAGTTCTT
CATTCACTTCTCTTCACTCTGCTGTCTGCTGGCCATGGCCTTTGACCGCTATGTGG
CCATCTGCTCCCCCTGCGATATGTCACAATCCTCACAAGCAAGGTCATTGGGAAGATCGT
CACTGCCACCTGAGCCGCAGCTTCATCATTATGTTTCCATCCATCTTTCTCCTTGAGCACC
TGCACTATTGCCAGATCAACATCATTGCACACACATTTTGTGAGCACATGGGCATTGCCCA
25 TCTGTCTGTTCTGATATCTCCATCAATGTCTGGTATGGGTTGGCAGCTGCTCTTCTCTCCA
CAGGCCCTGGACATCATGCTTATTACTGTTTCTACATCCACATCCTCCAAGCAGTCTTCCGC
CTCCTTTCTCAAGATGCCCGCTCCAAGGCCCTGAGTACCTGTGGATCCCATATCTGTGTCAT
CCTACTCTTCTATGTCCCTGCCCTTTTTTCTGTCTTTGCCTACAGGTTTGGTGGGAGAAGCA
TCCCATGCTATGTCCATATCTCCTGGCCAGCCTCTACGTTGTCATTCTCCTATGCTCAAT
30 CCCGTTATTTATGGAGTGAGGACTAAGCCAATACTGGAAGGGGCTAAGCAGATGTTTTCA
AATCTTGCCAAAGGATCTAAATAA (SEQ ID NO: 346)

AOLFR188 sequences:

MFPSLPCPVLLVQLPLMNENMQCFVFCSDSLRMMVSRFIHVFPVKMKRIIVGGYSKHFFSN
35 ELLCVRPWGKTWSIRHHIFDMELLTNNLKFITDPFVCRLRHLSPPTSEEHMKNKNNVTEFILL
GLTQNPGEQKVLFFVTFLLIYMTIMGNLLIIVTIMASQSLGSPMYFFLASLSFIDTVYSTAFAPK
MIVDLLSEKKTISFQGCMAQLFMDHLFAGAEVILLVVMAYDRYMAICKPLHELITMNNRVCVL
MLLAAWIGGFLHSLVQFLFIYQLPFCGPNVIDNFLCDLYPLLKLACTNTYVTGLSMIANGGAIC
AVTFFITILLSYGVILHSLKTQSLEGRKRAFYTASHVTVVILFFVPCIFLYARPNSFTPIDKSMTV
40 VLTFITPMLNPLIYTLKNAEMKSAMRKLWSKKVSLAGKWLYHS (SEQ ID NO: 347)

ATGTTCCCTCCCTGTGTCCATGTGTTCTCCTTGTTCAACTCCCACTTATGAATGAGAACAT
GCAGTGTTTTGTTTTCTGTTCTTGTGATAGTTTGCTGAGAATGATGGTTTCCCGCTTCATCC
ATGTCCCATTTGTAAAAATGAAAAGGATAATTGTGGGAGGATATTCTAAACACTTCTTTTC
45 TAATGAGCTGCTCTGTGTGAGGCCCTGGTCAGGGAACCGTGGTCGATAAGGCATCACAT
TTTTGACATGGAGCTTCTGACAAATAATCTCAAATTTATCACTGACCCTTTTGTGTTAGGC
TCCGACACCTGAGTCCAACACCTTCAGAAGAACACATGAAAAATAAGAACAATGTGACTG
AATTTATCCTCTTAGGGCTCACACAGAACCCTGAGGGGCAAAAGGTTTTATTTGTACAT
CTTACTAATCTACATGGTGACGATAATGGGCAACCTGCTTATCATAGTGACCATCATGGCC
50 AGCCAGTCCCTGGGTTCCCCCATGTACTTTTTTCTGGCTTCTTTATCATTATAGATACCGT
CTATTCTACTGCATTTGCTCCCAAAATGATTGTTGACTTGCTCTCTGAGAAAAAGACCATT
CCTTTCAGGGTTGTATGGCTCAACTTTTTATGGATCATTTATTTGCTGGTGTGAAGTCATT
CTTCTGGTGGTAATGGCCTATGATCGATACATATGGCCATCTGTAAGCCTCTTCATGAATTGA
TCACCATGAATCGTTCGAGTCTGTGTTCTTATGCTGTTGGCGGCCTGGATTGGAGGCTTTCT
55 TCACTCATTGGTTCATTTCTCTTTATTTATCAGCTCCCTTTCTGTGGACCCAATGTCATTG
ACAACCTCCTGTGTGATTTGTATCCCTTATTGAAACTTGCTTGACCAATACCTATGTCATT

GGGCTTTCTATGATAGCTAATGGAGGAGCGATTTGTGCTGTACCTTCTTCACTATCCTGC
TTTCCTATGGGGTCATATTACACTCTCTTAAGACTCAGAGTTTGGAAGGGAAACGAAAAGC
TTTCTACACCTGTGCATCCACGTCACGTGGTCAATTTTATTCTTTGTCCCCTGTATCTTCTT
GTATGCAAGGCCCAATTCTACTTTTCCCATTGATAAATCCATGACTGTAGTTCTAACTTTTA
5 TAACTCCCATGCTGAACCCACTAATCTATACCCTGAAGAATGCAGAAATGAAAAGTGCCAT
GAGGAAACTTTGGAGTAAAAAAGTAAGCTTAGCTGGGAAATGGCTGTATCACTCATGA
(SEQ ID NO: 348)

AOLFR189 sequences:

10 MQQNSVPEFILLGLTQDPLRQKIVFVIFLIFYMGTVVGNMLIIVTIKSSRTLGSMPYFFLFYLSF
ADSCFSTSTAPRLIVDALSEKKIITYNECMTQVFALHLFGCMEIFVLILMAVDRYVAICKPLRYP
TIMSQQVCMLIVLAWIGSLIHSTAQILALRLPFCGPYLIDHYCCDLQPLLKLACMDTYMINLLL
VSNSGAICSSSFMLIISYIVILHSLRNHSAKGGKKALSACTSHIIVVILFFGPCIFYTRPPTTFPMD
KMVAVFYTIGTGPLNPLIYTSEECRSEKCHEK (SEQ ID NO: 349)

15 ATGCAGCAAAATAACAGTGTGCCTGAATTCATACTGTTAGGATTAACACAGGATCCCCTGA
GGCAGAAAATAGTGTTTGTAACTCTTCTTAATTTTCTATATGGGAACTGTGGTGGGGAATAT
GCTCATTATTGTGACCATCAAGTCCAGCCGGACACTAGGAAGCCCCATGTACTTCTTTCTA
TTTTATTGTCCCTTTCAGATTCTTGCTTTTCAACTTCCACAGCCCCTAGATTAAATTGTGGA
20 TGCTCTCTCTGAAAAGAAAATTATAACCTACAATGAGTGCATGACACAAGTCTTGCACATA
CATTTATTTGGCTGCATGGAGATCTTTGTCCTCATTCTCATGGCTGTTGATCGCTATGTGGC
CATCTGTAAGCCCTTGCGTTACCCAACCATCATGAGCCAGCAGGTCTGCATCATCCTGATT
GTTCTTGCCTGGATAGGGTCTTTAATACTCTACAGCTCAGATTATCCTGGCCTTAAGATT
GCCTTTCTGTGGACCTATTTGATTGATCATTATTGCTGTGATTTGCAGCCCTTGTGAAAC
25 TTGCCTGCATGGACACTTACATGATCAACCTGCTGTTGGTGTCTAACAGTGGGGCAATTTG
CTCAAGTAGTTTCATGATTTTGTAAATTTTATATATTGTCATCTTGCATTCACTGAGAAACC
ACAGTGCCAAAGGGAAGAAAAGGCTCTCTCCGCTTGACAGTCTCACATAATTGTAGTCAT
CTTATTCTTTGGCCCATGTATATTCATATATACACGCCCCCGACCACTTTCCCCATGGACA
AGATGGTGGCAGTATTTTATACTATTGGAACACCCTTTCTCAATCCACTCATCTACACATCT
30 GAGGAATGCAGAAAGTGAAAATGCCATGAGAAAG (SEQ ID NO: 350)

AOLFR190 sequences:

MQRSNHTVTEFILLGFTTDPGMQLGLFVFLGVYCLTVVGSSTLIVLICNDSRLHTPMYFVIGN
LSFLDLWYSSVHTPKILVTCISEDKSISFAGCLCQFFSARLAYSECYLLAAMAYDHYVAISKPLL
35 YAQTMPPRLCICLVLYSYTGGFVNAILTSNTFTLDFCGDNVIDDFCDVPPLVKLACSVRESYQ
AVLHFLLASNVISPTVLILASYLSIITILRIHSTQGRKVFSTCSSHLISVTLYYGSILYNYSRPS
YSLKRDKMVSTFYTMLFPMNLNPMIYSLRSKDMKDALKKFFKSA (SEQ ID NO: 351)

ATGCAGAGGAGCAATCACACAGTGAAGTTCATCCTGCTGGGCTTCACCACAGATCCAG
40 GGATGCAACTGGGCCTCTTTGTGGTGTCTCTGGGTGTACTGTCTGACTGTGGTAGGAAG
TAGCACCCCTCATCGTGTGATCTGTAATGACTCCCGCCTACACACACCCATGTATTTTGTCA
TTGGAAATCTGTCAATTTCTGGATCTCTGGTATTCTTCTGTCCACACCCCAAGATCCTAGTG
ACCTGCATCTCTGAAGACAAAAGCATCTCCTTTGCTGGCTGCCTGTGTGAGTTCTTCTCTGC
CAGGCTGGCCTATAGTGAGTGTACCTACTGGCTGCCATGGCTTATGACCACTACGTGGCC
45 ATCTCCAAGCCCCTGCTTTATGCTCAGACCATGCCAAGGAGATTGTGCATCTGTTTGGTTTT
ATATTCTATACTGGGGGTTTTGTCAATGCAATAATATTAACCAGCAACACATTACATTG
GATTTTTGTGGTGACAATGTCAATTGATGACTTTTTCTGTGATGTTCACCCCTCGTGAAGCT
GGCATGCAGTGTGAGAGAGAGCTACCAGGCTGTGCTGCACTTCCTTCTGGCCTCCAATGTC
ATCTCCCCTACTGTGCTCATCCTTGCCCTCTTACCTCTCCATCATCACCACCATCCTGAGGAT
50 CCACTCTACCCAGGGCCGCATCAAAGTCTTCTCCACATGCTCCTCCACCTGATCTCCGTTA
CCTTATACTACTGGCTCCATTCTCTACAACACTCCCGGCCAAGTTCAGCTACTCCCTCAAG
AGGGACAAAATGGTTTCTACCTTTTATACTATGCTGTTCCCCATGTTGAATCCCATGATCTA
CAGTCTGAGGAGTAAAGACATGAAAGACGCTCTGAAAAAATCTTCAAGTCAGCATAA
(SEQ ID NO: 352)

55

AOLFR191 sequences:

MTGGGNITEITYFILLGFSDFPRIKVLFTIFLVIYITSLAWNLSLIVLIRMDSHLHTPMYFFLSNLS
 FIDVCYISSTVPKMLSNLLQEQQTITFVGCIQYFIFSTMGLSESLMTAMAYDRYAAICNPLLYS
 SIMSPTLCVWMVLGAYMTGLTASLFQIGALLQLHFCGSNVIRHFFCDMPQLLILSCTDITFFVQV
 5 MTAILTMFFGIASALVIMISYGYIGISIMKITSAGSPKAFNTCASHLTAVSLFYTSIGIFVYLRSSS
 GGSSSFDREASVFYTVVIPMLNPLIYSLRNKEIKDALKRLQKRKCC (SEQ ID NO: 353)

ATGACTGGGGGAGGAAATATTACAGAAATCACCTATTTTCATCCTGCTGGGATTCTCAGATT
 TTCCCAGGATCATAAAAGTGCTCTTCACTATATTCCTGGTGATCTACATTACATCTCTGGCC
 10 TGGAACCTCTCCCTCATTGTTTTAATAAGGATGGATTCCCACCTCCATACACCCATGTATTT
 CTTCTCAGTAACCTGTCTTCATAGATGTCTGCTATATCAGCTCCACAGTCCCCAAGATGC
 TCTCCAACCTCTTACAGGAACAGCAAATATCACTTTTGTGGTTGTATTATTAGTACTTT
 ATCTTTTCAACGATGGGACTGAGTGAGTCTTGTCTCATGACAGCCATGGCTTATGATCGTT
 ATGCTGCCATTTGTAAACCCCTGCTCTATTCATCCATCATGTACCCACCCTCTGTGTTTGG
 15 ATGGTACTGGGAGCCTACATGACTGGCCTCACTGCTTCTTTATTCCAAATTGGTGCTTTGCT
 TCAACTCCACTTCTGTGGGTCTAATGTCATCAGACATTTCTTCTGTGACATGCCCCAACTGT
 TAATCTTGTCTGTACTGACACTTTCTTTGTACAGGTCATGACTGCTATATTAACCATGTTC
 TTTGGGATAGCAAGTGCCCTAGTTATCATGATATCCTATGGCTATATTGGCATCTCCATCA
 TGAAGATCATCTCAGCTAAAGGCATCCAAAGGCATTCAACACCTGTGCTTCTCATCTAAC
 20 AGCTGTTTCCCTCTTCTATACATCAGGAATCTTTGTCTATTTGAGGTCCAGCTCTGGAGGTT
 CTTCAAGCTTTGACAGATTTGCATCTGTTTTCTACACTGTGGTCATTCCCATGTTAAATCCC
 TTGATTTACAGTTTGAGGAACAAAGAAATTAAGATGCCTTAAAGAGGTTGCAAAAGAGA
 AAGTGCTGCTGA (SEQ ID NO: 354)

AOLFR192 sequences:

MENNTEVTEFILVGLTDDPELQIPLFVFLFIYLTITLVGNLGMIELILLDSCLHTPMYFFLSNLSLV
 DFGYSSAVTPKVMVGFLTGDKFILYNACATQFFFFVAFITAESFLLASMA YDRYAALCKPLHY
 TTTMTTNVCACLAIGSYICGFLNASIHTGNTFRLSFCRSNVVEHFFCDAPLLTLSCSDNYISEM
 VIFFVVGFNDFSILVILISYLFIFITIMKMRSPGRQKAFSTCASHLTAVSIFYGTGIFMYLRPNSS
 30 HFMGTDKMASVFYAIVIPMLNPLVYSLRNKEVKSAFKKTVGKAKASIGFIF (SEQ ID NO: 355)

ATGGAGAACAACACAGAGGTGACTGAATTCATCCTTGTGGGGTTAACTGATGACCCAGAA
 CTGCAGATCCCACTCTTCATAGTCTTCTTTTCATCTACCTCATCACTCTGGTTGGGAACCT
 GGGGATGATTGAATTGATTCTACTGGACTCCTGTCTCCACACCCCCATGTACTTCTTCTCTCA
 35 GTAACCTCTCCCTGGTGGACTTTGGTTATTCCTCAGCTGTCACTCCCAAGGTGATGGTGGG
 GTTTCTCAGAGGAGACAAATTCATATTATATAATGCTTGTGCCACACAATTCCTTCTTTG
 TAGCCTTTATCACTGCAGAAAGTTTCTCTGGCATCAATGGCCTATGACCGCTATGCAGC
 ATTGTGTAAACCCCTGCATTACACCACCACCATGACAACAAATGTATGTGCTTGCCTGGCC
 ATAGGCTCCTACATCTGTGGTTTCTCTGAATGCATCCATTCACTGCGGAACACTTTCAGGC
 40 TCTCCTTCTGTAGATCCAATGTAGTTGAACACTTTTTCTGTGATGCTCCTCCTCTCTTGA
 CTCTCATGTTGAGACAACCTACATCAGTGAGATGGTTATTTTTTTTGTGGTGGGATTCAATG
 ACCTCTTTTCTATCCTGGTAATCTTGATCTCCTACTTATTTATATTTATCACCATCATGAAG
 ATGCGCTCACCTGAAGGACGCCAGAAAGGCCTTTTCTACTTGTGCTTCCACCTTACTGCAG
 TTTCCATCTTTTATGGGACAGGAATCTTTATGTACTTACGACCTAACTCCAGCCATTTTCATG
 45 GGCACAGACAAAATGGCATCTGTGTTCTATGCCATAGTCATTCCCATGTTGAATCCACTGG
 TCTACAGCCTGAGGAACAAAGAGGTTAAGAGTGCCTTTAAAAAGACTGTAGGGAAGGCAA
 AGGCCTCTATAGGATTCATATTTTAA (SEQ ID NO: 356)

AOLFR193 sequences:

MENKTEVTQFILLGLTNDSELQVPLFITFPFIYITLVGNLGIIVLIFWDSCLHNPMYFFLSNLSLV
 DFCYSSAVTPIVMAGFLIEDKVISYNACAAQMYIFVAFATVENYLLASMA YDRYAAVCKPLHY
 TTTMTTTVCARLAIGSYLCGFLNASIHTGDTFSLSFCKSNVHFFCDIPAVMVLSCSDRHISEL
 VLIYVVSFNIFIALLVILISYTFIFITLKMHSASVYQKPLSTCASHFLAVGIFYGTIIFMYLQPSSS
 50 SMDTDMKMAPVFYTMVIPMLNPLVYSLRNKEVKSAFKKVVEKAKLSVGWSV (SEQ ID NO:
 357)

ATGGAAAATAAGACAGAAGTAACACAATTTCATTCTTCTAGGACTAACCAATGACTCAGAA
CTGCAGGTTCCCTCTTTATAACGTTCCCTTCATCTATATTATCACTCTGGTTGGAAACCT
GGGAATTATTGTATTGATATTCTGGGATTCTGTCTCCACAATCCCATGTACTTTTTTCTCA
GTAACCTGTCTCTAGTGGACTTTTGTACTCTTCAGCTGTCACTCCCATCGTCATGGCTGGA
5 TTCCTTATAGAAGACAAGGTCATCTCTTACAATGCATGTGCTGCTCAAATGTATATCTTTGT
AGCTTTTGCCACTGTGGAAAATTACCTCTTGGCCTCAATGGCCTATGACCGCTATGCAGCA
GTGTGCAAACCCCTACATTACACCACAACCATGACAACAACCTGTGTGTGCTCGTCTGGCCA
TAGGCTCCTACCTCTGTGGTTTCCTGAATGCCTCCATCCACACTGGGGACACATTTAGTCTC
TCTTTCTGTAAGTCCAATGAAGTCCATCACTTTTTCTGTGATATTCCAGCAGTCATGGTTCT
10 CTCTTGCTCTGATAGACATATTAGCGAGCTTGTCTTATTTATGTTGTGAGCTTCAATATCT
TTATAGCTCTCCTGGTTATCTTGATATCCTACACATTCATTTTATCACCATCCTAAAGATG
CACTCAGCTTCAGTATACCAGAAGCCTTTGTCCACCTGTGCCTCTCATTTTCATTGCAGTCGG
CATCTTCTATGGGACTATTATCTTCATGTACTTACAACCCAGCTCCAGTCACTCCATGGACA
CAGACAAAATGGCACCTGTGTTCTATACAATGGTCATCCCCATGCTGAACCCCTCTGGTCTA
15 TAGTCTGAGGAACAAGGAAGTGAAGAGTGCATTCAAGAAAGTTGTTGAGAAGGCAAAATT
GTCTGTAGGATGGTCAGTTTAA (SEQ ID NO: 358)

AOLFR194 sequences:

MERQNOQSCVVEFILLGFSNYPELQGGQFLVAFVLVYLVTLIGNAIIIVIVSLDQSLHVPMYLFLNL
20 SVVDLSFSAVIMPEMLVVLSTEKTTISFGGCFQMYFILLFGGAECFLLGAMAYDRFAAICHPL
NYQMIMNKGVMKLIIFSWALGFMLGTVQTSWVSSFPFCGLNEINHISCETPAVLELACADTFL
FEIYAFTGTFLIILVPFLILLSYIRVLFALIKMPSTTGRQKAFSTCAAHLTSVTLFYGTASMTYLO
PKSGYSPETKKVMSLSYSLLTPLNLLIYSLRNSEMKRALMKLWRRRVVLHTI (SEQ ID NO:
359)

25

ATGGAAAGACAAAATCAAAGCTGTGTGGTTGAATTCATCCTCTTGGGCTTTTCTAACTATC
CTGAGCTCCAGGGGCAGCTCTTTGTGGCTTTCTGGTTATTTATCTGGTGACCCTGATAGG
AAATGCCATTATTATAGTCATCGTCTCCCTAGACCAGAGCCTCCACGTTCCCATGTACCTGT
TTCTCCTGAACCTTATCTGTGGTGGACCTGAGTTTCAGTGCAGTTATTATGCCTGAAATGCT
30 GGTGGTCCTCTCTACTGAAAAAACTACAATTTCTTTTGGGGGCTGTTTGCACAGATGTAT
TTCATCCTTCTTTTGGTGGGGCTGAATGTTTTCTTCTGGGAGCAATGGCTTATGACCGATT
TGCTGCAATTTGCCATCCTCTCAACTACCAATGATTATGAATAAAGGAGTTTTTATGAAA
TTAATTATATTTTCATGGGCCTTAGGTTTTATGTTAGGTACTGTTCAAACATCATGGGTATC
TAGTTTTCCCTTTTGTGGCCTTAATGAAATTAACCATATATCTTGTGAAACCCAGCAGTGT
35 TAGAACTTGCATGTGCAGACACGTTTTTGTGTTGAAATCTATGCATTACAGGCACCTTTTTG
ATTATTTTGGTTCCTTTCTTGTGATACTCTTGTCTTACATTGAGTTCTGTTTGCCATCCTG
AAGATGCCATCAACCACTGGGAGACAAAAGGCCTTTTCCACCTGTGCCGCTCACCTCATAT
CTGTGACCCTATTCTATGGCACAGCCAGTATGACTTATTTACAACCCAAATCTGGCTACTC
ACCGGAAACCAAGAAAGTGATGTCATTGTCTTACTCACTTCTGACACCACTGCTGAATCTG
40 CTTATCTACAGTTTGCGAAATAGTGAGATGAAGAGGGCTTTGATGAAATTATGGCGAAGG
CGAGTGGTTTTACACACAATCTGA (SEQ ID NO: 360)

AOLFR195 sequences:

MIVQLICTVCFLAVNTFHVRSSEFLKADDMGEINQTLVSEFLLLGLSGYPKIEIVYFALILVMY
45 LVILIGNGVLIASIFDSHFHTPMYFFLGNLSFLDICYTSSSVPSLTVSLISKRNISFSGCAVQMFF
GFAMGSTECLLLGMMAFDYVAICNPLRYPIILSKVAYVLMASVSWLSGGINSVQTLAMRL
PFCGNNIINHFACEILAVLKLACADISLNIITMVISNMAFLVPLMVIFFSYMFILYTLQMNSATG
RRKAFSTCSAHLTVVIFYGTIFFMYAKPKSQDLIGEEKLQALDKLISLFYGVVTPMLNPILYSR
NKDVKAADVLYLNKKPIH (SEQ ID NO: 361)

50

ATGATTGTTTCAGTTAATTTGTACTGTTTGTCTTGGCAGTAAATACATTTTCATGTTAGATC
TTCTTTTGATTTCCTGAAAGCAGATGACATGGGTGAGATTAAACCAGACACTTGTGTCAGAA
TTCTTCTTCTGGGTCTTTCTGGATACCCAAAGATTGAGATTGTTTACTTTGCTCTCATTCT
AGTTATGTACCTAGTGATTCTAATTGGCAATGGTGTCTAATCATAGCCAGCATCTTTGATT
55 CTCATTTTCACACACCAATGTACTTCTTCTGGGCAACCTCTCTTCTGGATATCTGCTAT
ACATCCTCCTCTGTTCCCTCAACATTGGTGAGCTTAATCTCAAAGAAAAGAAACATTTCT

TCTCTGGATGTGCAGTGCAGATGTTCTTTGGGTTTGCAATGGGGTCAACAGAATGTCTGCT
 TCTTGGCATGATGGCATTGATCGTTATGTGGCCATCTGCAACCCACTGAGATACCCCATC
 ATCCTGAGCAAGGTGGCGTATGTATTGATGGCTTCTGTGCTGGCTGTCCGGTGAATAA
 ATTACAGCTGTGCAAACATTACTTGCCATGAGACTGCCTTTCTGTGGGAATAATATTATCAA
 5 TCATTTTCGCATGTGAAATATTAGCTGTCCTCAAGCTGGCCTGTGCTGATATATCCCTCAATA
 TTATCACCATGGTGATATCAAATATGGCCTTCCTGGTTCTTCCACTGATGGTCATTTTTTTC
 TCCTATATGTTTCATCTCTACACCATCTTGCAAATGAATTCAGCCACAGGAAGACGCAAGG
 CATTTTCCACGTGCTCAGCTCACCTGACTGTGGTGATCATATTTTACGGTACCATCTTCTTT
 ATGTATGCGAAACCGAAGTCTCAAGACCTGATTGGGGAAGAAAAATTGCAAGCATTAGAC
 10 AAGCTCATTTCTCTGTTTTATGGGGTAGTGACACCCATGCTGAATCCTATACTCTATAGCTT
 GAGAAATAAGGATGTAAAAGCTGCTGTAAATATTGCTGAACAAAAAACCAATTCACTA
 A (SEQ ID NO: 362)

AOLFR196 sequences:

15 MLESNYTMPTEFLFVGFTDYLPLRVTLFLVFLVYTLTMVGNILLIILVNINSSLQIPMYFLSNL
 SFLDISCSTAITPKMLANFLASRKSISPYGCALQMFFFAFADAECLILAAAMAYDRYAAICNPLL
 YTTLMSSRRVCVCFIVLAYFSGSTTSLVHVCLTFRLSFCGSNIVNHFFCDIPLLALSCTDQTQINQL
 LLFALCSFIQTSTFVIFISYFCILITVLSIKSSGGRSKTFSTCASHLIAVTLFYGALLFMYLQPTTS
 YSLDTDKVVAVFYTVVFPFMFNPIIYSFRNKDVKNALKKLLERIGYSNEWYLNRLRIVNI (SEQ
 20 ID NO: 363)

ATGTTGGAGAGTAATTACACCATGCCAACTGAGTTCCTATTTGTTGGATTACAGATTATC
 TACCTCTCAGAGTCACACTGTTCTTGGTATTCCTTCTGGTATATACATTAATATGGTCGGA
 AATATACTCTTAATAATTCTAGTTAATATTAATTCAAGCCTTCAAATCCCATGTATTATTT
 25 TCTTAGCAACTTATCTTTCTTAGACATCAGCTGTTCTACAGCAATCACTCCTAAAATGCTGG
 CAAACTTCTTGGCATCCAGGAAAAGCATCTCTCCTTATGGGTGTGCACTACAAATGTTTTT
 CTTGCTTCTTTTGTGCTGATGCTGAGTGCCTTATCCTGGCAGCAATGGCTTATGACCGCTATG
 CAGCCATCTGCAACCCACTGCTCTATACTACACTGATGTCTAGGAGAGTCTGTGTCTGCTT
 CATTGTGTTGGCATATTTCAAGTGAAGTACAACATCACTGGTCCATGTGTGCCTCACATTC
 30 AGGCTGTCAATTTGTGGCTCCAATATCGTCAATCATTTTTTCTGTGATATCCCACCTCTTCT
 GGCTTTATCATGTACAGACACTCAGATCAACAGCTTCTGCTCTTGTGCTTGTGCAGCTTCA
 TCCAGACCAGCACTTTTGTGGTAATATTTTCTTACTTCTGCATCCTCATCACTGTGTTG
 AGCATCAAGTCCTCAGGTGGCAGAAAGCAAAACATTCTCCACTTGTGCTTCCCACCTCATAG
 CAGTCACCTTATTCTATGGAGCGCTCCTGTTTATGTACTTACAGCCCACCACTAGCTATTCC
 35 CTAGACACTGATAAGGTGGTGGCAGTGTTTTATACTGTTGTATTTCCCATGTTTAATCCAA
 TAATTTATAGTTTTCAGAAACAAGGATGTGAAAAATGCTCTCAAAAAGCTATTAGAAAGAA
 TTGGATATTCAAATGAATGGTATTTAAATCGTTTAAGAATAGTCAATATCTAA (SEQ ID NO:
 364)

AOLFR197 sequences:

40 MCYLSQLCLSLGEHTLHMGMVRHTNESNLAGFILLGFSDYPQLQKVLFLILILYLLTILGNTTI
 ILVSRLEPKLHMPMYFFLSHLSFLYRCFTSSVIPQLLVNLWEPMKTIAYGGCLVHLYNSHALGS
 TECVLLALMSCDRYVAVCRPLHYTVLMHIHLCMALASMAWLSGIATTLVQSTLTQLPFCGH
 RQVDHFICEVPVLIKLACVGTTTFNEAELFVASILFLIVPVSFILVSSGYIAHAVLRIKSATRRQKAF
 45 GTCFSLHTVVTIFYGTIIFMYLQPAKRSRSDQKGFVSLFYTVVTRMLNPLIYTLRIKEVKGALKK
 VLAKALGVNII (SEQ ID NO: 365)

ATGTGTTATCTTTCTCAGCTATGCCTCAGCCTTGGGGAACACACTTTACATATGGGGATGG
 TGAGACATACCAATGAGAGCAACCTAGCAGGTTTCATCCTTTTAGGGTTTTCTGATTATCC
 50 TCAGTTACAGAAGGTTCTATTTGTGCTCATATTGATTCTGTATTTACTAACTATTTTGGGGA
 ATACCACCATCATTCTGGTTTCTCGTCTGGAACCCAAAGCTTCATATGCCGATGTATTTCTTC
 CTTTCTCATCTCTCCTTCTGTAACCGCTGCTTACCAGCAGTGTTATTCCCCAGCTCCTGGT
 AAACCTGTGGGAACCCATGAAAACATATCGCCTATGGTGGCTGTTTGGTTACCTTTACAAC
 TCCCATGCCCTGGGATCCACTGAGTGCCTCCTTGGCTCTGATGTCCTGTGACCGCTATGT
 55 GGCTGTCTGCCGCTCCTCTCCATTACACTGTCTTAATGCATATCCATCTCTGCATGGCCTTGG
 CATCTATGGCATGGCTCAGTGGAATAGCCACCACCTGGTACAGTCCACCTCACCTGCA

GCTGCCCTTCTGTGGGCATCGCCAAGTGGATCATTTTCATCTGCGAGGTCCCTGTGCTCATC
 AAGCTGGCTTGTGTGGGCACACGTTTAAACGAGGCTGAGCTTTTTGTGGCTAGTATCCTTT
 TCCTTATAGTGCCTGTCTCATTTCATCCTGGTCTCCTCTGGCTACATTGCCACGCAGTGTG
 AGGATTAAGTCAGCTACCAGGAGACAGAAAGCATTGCGGACCTGCTTCTCCACCTGACA
 5 GTGGTCACCATCTTTTATGGAACCATCATCTTCATGTATCTGCAGCCAGCCAAGAGTAGAT
 CCAGGGACCAGGGCAAGTTTGTCTCTCTTCTACACTGTGGTAACCCGCATGCTTAACCC
 TCTTATTTATACCTTGAGGATCAAGGAGGTGAAAGGGGCATTAAAGAAAGTTCTAGCAAA
 GGCTCTGGGAGTAAATATTTTATGA (SEQ ID NO: 366)

10 **AOLFR198 sequences:**

MENCTEVTKFILLGLTSVPELQIPLFILFTFIYLLTLCGNLGMMLLILMDSCLHTPMYFFLSNLSL
 VDFGYSSAVTPKVMAGFLRGDKVISYNACAVQMFVVALATVENYLLASMA YDRYA AVCKP
 LH YTTTMTASVGAC LALGSYVCGFLNASFHIGGIFSLSFCKSNLVHHFFCDVPAVMALSCSDKH
 TSEVILVFMSSFNIFVLLVIFISYLFIFITILKMHS AKGHQKALSTCASHFTAVSVFYGT VIFIFYLQ
 15 PSSSHSMDTDKMASVFYAMIIPMLNPVVYSLRNREVQNAFKKVLRRQKFL (SEQ ID NO: 367)

ATGGAGAATTGTACGGAAGTGACAAAGTTCATTCTTCTAGGACTAACCAGTGTCCCAGAAC
 TACAGATCCCCCTCTTTATCTTGTTCACCTTCATCTACCTCCTCACTCTGTGTGGGAACCTG
 GGGATGATGTTGCTGATCCTGATGGACTCTTGTCTCCACACCCCCATGTACTTTTTCTCAG
 20 TAACCTGTCTCTGGTGGACTTTGGATACTCCTCAGCTGTCACTCCCAAGGTCATGGCTGGG
 TTCCTTAGAGGAGACAAGGTCATCTCCTACAATGCATGTGCTGTTCAAGATGTTCTTCTTGT
 AGCCTTGGCCACGGTGGAAAATTACTTGTGGCCTCAATGGCCTATGACCGCTATGCAGCA
 GTGTGCAAAACCCCTACACTACACCACCACCATGACGGCCAGTGTAGGTGCTGTCTGGCCC
 TAGGCTCATATGTCTGTGGCTTCTTAAATGCCTCATTCCACATTGGGGGCATATTCAGTCTC
 25 TCTTTCTGTAAATCCAATCTGGTACATCACTTTTTCTGTGATGTTCCAGCAGTCATGGCTCT
 GTCTTGCTCTGATAAACACACTAGTGAGGTGATTCTGGTTTTTATGTCAAGCTTTAATATCT
 TTTTTGTTCTTCTAGTTATCTTTATCTCCTACTTGTTCATATTCATCACCATCTTGAAGATGC
 ATTCACTAAGGGACACCAAAAAGCATTGTCCACCTGTGCCTCTCACTTCACTGCAGTCTC
 CGTCTTCTATGGGACAGTAATCTTCATCTACTTGACGCCAGCTCCAGCCACTCCATGGAC
 30 ACAGACAAAATGGCATCTGTGTTCTATGCTATGATCATCCCCATGCTGAACCCTGTGGTCT
 ACAGCCTGAGGAACAGAGAAGTCCAGAATGCATTCAAGAAAGTGTGAGAAGGCAAAAAT
 TTCTATAA (SEQ ID NO: 368)

AOLFR199 sequences:

MDTGNTLPQDFLLGFPQSQTLLSLFMLFLVMYILTVSGNVAILMLVSTSHQLHTPMYFFLS
 NLSFLEIWTAAV PKALAILLGRSQTISFTSCLLQMYFVFSLGCTEYFLAAMAYDRCLAICY P
 LHYGAIMSSLLSAQLALGSWVCGFVAIAVPTALISGLSFCGPRAINHHFFCDIAPWIALACTNTQA
 VELVAFVIAVVILSSCLITFVSYYIISTILRIPSASGRSKAFSTCSSHLTVVLIWYGSTVFLHVR
 TSIKDALDLIAVHVLNTVVPVLPNPFYTLRNKEVRETLKKWK GK (SEQ ID NO: 369)

ATGGACACAGGCAACAAAACCTCTGCCCCAGGACTTTCTCTTACTGGGCTTTCCTGGTTCTC
 AAACCTCTTCAGCTCTCTCTTTATGCTTTTTCTGGTGATGTACATCCTCACAGTTAGTGGT
 AATGTGGCTATCTTGATGTTGGTGAGCACCTCCCATCAGTTGCATACCCCATGTACTTCTT
 TCTGAGCAACCTCTCCTTCTGGAGATTGGTATACCACAGCAGTGCCTCAAGCACTG
 45 GCCATCCTACTGGGGAGAAGTCAGACCATATCATTTACAAGCTGTCTTTTGAGATGTACT
 TTGTTTTCTCATTAGGCTGCACAGAGTACTTCTCCTGGCAGCCATGGCTTATGACCGCTGT
 CTTGCCATCTGCTATCCTTTACACTACGGAGCCATCATGAGTAGCCTGCTCTCAGCGCAGC
 TGGCCCTGGGCTCCTGGGTGTGTGGTTTTCTGGCCATTGCAGTGCCACAGCCCTCATCAG
 TGGCCTGTCTTCTGTGGCCCCCGTGCCATCAACCACTTCTTCTGTGACATTGCACCCTGGA
 50 TTGCCCTGGCCTGCACCAACACACAGGCAGTAGAGCTTGTGGCCTTTGTGATTGCTGTTGT
 GGTTATCCTGAGTTCATGCCTCATCACTTTGTCTCCTATGTGTACATCATCAGCACCATCC
 TCAGGATCCCCTCTGCCAGTGGCCGGAGCAAAGCCTTCTCCACGTGCTCCTCGCATCTCAC
 CGTGGTGCTCATTTGGTATGGGTCCACAGTTTTCTTCACGTCCGCACCTCTATCAAAGAT
 GCCTTGGATCTGATCAAAGCTGTCCACGTCTGAACACTGTGGTGA CTCCAGTTTTAAACC
 55 CCTTCATCTATACGCTTCGTAATAAGGAAGTAAGAGAGACTCTGCTGAAGAAATGGAAGG
 GAAAATAA (SEQ ID NO: 370)

AOLFR200 sequences:

MTRKNYTSLTEFVLLGLADTLELQIILFFLVITYTLTVLGNLGMILLIRIDSQ LHTPMYFFLANL
 SFVDVCNSTTTTPKMLADLLSEKKTISFAGCFLQMYFFISLATTECILFGLMAYDRYAAICRPLL
 5 YSLIMSRTVYLKMAAGAFAGLLNFMVNTSHVSSLSFCDNSVIHHFFCDSPPLFKLSGSDTILKE
 SISSILAGVNIVGTLVLSSYSYVLSIFSMHSGEGRHAFSTCASHLTAILFYATCIYTYLRPSS
 SYSLNQDKVASVFYTVVIPMLNPLIYSLRSKEVKKALANVISRKRTSSFL (SEQ ID NO: 371)

ATGACCAGAAAAAATTATACCTCACTGACTGAGTTCGTCCTATTGGGATTAGCAGACACGC
 10 TGGAGCTACAGATTATCCTCTTTTTGTTTTTCTTGTGATTTATACACTTACAGTACTGGGA
 AATCTCGGGATGATCCTCTTAATCAGGATCGATTCCCAGCTTCACACACCCATGTATTTCTT
 CCTGGCTAACCTGTCCTTTGTGGACGTTTGTAACTCAACTACCATCACCCCAAAGATGCTG
 GCAGATTTATTATCAGAGAAGAAAAACCATCTCTTTTGTGGCTGCTTCCTACAGATGTACT
 TCTTTATCTCCCTGGCGACAACCGAATGCATCCTCTTTGGGTAAATGGCCTATGACAGGTA
 15 TGCGGCCATATGTCGCCCGCTGCTTTACTCCTTGATCATGTCCAGGACCGTCTACCTAAAA
 ATGGCAGCCGGGGCTTTTGTGTCAGGGTTGCTGAACTTCATGGTCAACACAAGCCATGTCA
 GCAGCTTGTCATTCTGTGACTCCAATGTCATCCATCACTTCTTCTGTGACAGTCCCCCACTT
 TTCAAGCTCTCTTGTCTGACACAATCCTGAAAGAAAGCATAAGTTCTATTTTGGCTGGTG
 TGAATATTGTGGGGACTCTGCTTGTCATCCTCTCCTCCTACTCCTACGTTCTCTTCTCCATT
 20 TTTTCTATGCATTGCGGGGAGGGGAGGCACAGAGCTTTCTCCACGTGTGCCTCTCACCTGA
 CAGCCATAATTCTGTCTATGCCACCTGCAGACTTATACCTGAGACCTAGTGTCCAGTAC
 TCCCTGAATCAGGACAAAGTGGCTTCTGTGTTCTACACAGTGGTGATTCCCATGTTGAATC
 CTCTGATCTACAGCCTCAGGAGTAAGGAAGTAAAGAAGGCTTTAGCGAATGTAATTAGCA
 GGAAAAGGACCTCTTCCTTTCTGTGA (SEQ ID NO: 372)

AOLFR201 sequences:

MEWENHTILVEFFLKGLSGHPRLLELFFVLIFIMYVVILLGNGTLILISILDPHLHTPMYFFLGNL
 SFLDICYTTTSIPSTLVSFSLERKTISLSGCAVQMFLGLAMGTTECVLLGMMAFDRYVAICNPLR
 YPIIMSKDAYVPMAGSWIIGAVNSAVQSVFVQLPFCRNNIINHFTCEILAVMKLACADISDN
 30 EFIMLVATTFLIPTLLIIVSYTLIIVSIFKISSSEGRSKASSTCSAHLTVVIFYGTILFMYMKPKS
 KETLNSDDLDAATDKIISMFGVMTMPMMNPLIYSLRNKDVKEAVKHLLNRRFFSK (SEQ ID NO:
 373)

ATGGAATGGGAAAACACACCATTTCTGGTGGAATTTTTTCTGAAGGGACTTTCTGGTCACC
 35 CAAGACTTGAGTTACTCTTTTTTGTGCTCATCTTCATAATGTATGTGGTCATCCTTCTGGGG
 AATGGTACTCTCATTTTAATCAGCATCTTGGACCCTCACCTTCACACCCCTATGTACTTCTT
 TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCACTCTATTCCCTCCACGCTAG
 TGAGCTTCCCTTTCAGAAAGAAAGACCATTTCCCTTTCTGGCTGTGCAGTGCAGATGTTCTT
 CGGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCATGATGGCCTTTGACCGCTAT
 40 GTGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGAGTAAGGATGCCTATGTACCCA
 TGGCAGCTGGGTCTGGATCATAGGAGCTGTCAATTCTGCAGTACAATCAGTGTTTGTGGT
 ACAATTGCCTTTCTGCAGGAATAACATCATCAATCATTTACCTGTGAAATTCTGGCTGTC
 ATGAAACTGGCCTGTGCTGACATCTCAGACAATGAGTTCATCATGCTTGTGGCCACAACAT
 TGTTCATATTGACACCTTTGTTATTAATCATTGTCTCTTACACGTTAATCATTGTGAGCATC
 45 TTCAAAATTAGCTCTTCCGAGGGGAGAAGCAAAGCTTCCTCTACCTGTTCAGCCCATCTGA
 CTGTGGTCATAATATTCTATGGGACCATCCTCTTCATGTACATGAAGCCCAAGTCTAAAGA
 GACACTTAATTTCGGATGACTTGGATGCTACCGACAAAATTATATCCATGTTCTATGGGGTG
 ATGACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAAGAGGCA
 GTAAAACACCTACTGAACAGAAGGTTCTTTAGCAAGTGA (SEQ ID NO: 374)

AOLFR202 sequences:

MEWENHTILVEFFLKGLSGHPRLLELFFVLIFIMYVVILLGNGTLILISILDPHLHTPMYFFLGNL
 SFLDICYTTTSIPSTLVSFSLERKTISLSGCAVQMFLSLAMGTTECVLLGVMAFDRYVAICNPLR
 YPIIMSKDAYVPMAGSWIIGAVNSAVQTVFVQLPFCRNNIINHFTCEILAVMKLACADISGN
 55 EFILLVTTTLFLLTPLLLIIVSYTLIILSIFKISSSEGRSKPSSTCSARLTVVITFCGTIFLMMYMKPKSQ

ETLNSDDLDATDKLIFIFYRVMTMPMMNPLIYSLRNKDVKEAVKHLLRRKNFNK (SEQ ID NO: 375)

5 ATGGAATGGGAAAACACACCATTTCTGGTGGAAATTTTTTCTGAAGGGACTTTCTGGTCACC
CAAGACTTGAGTTACTCTTTTTTGTGCTCATCTTCATAATGTATGTGGTCATCCTTCTGGGG
AATGGTACTCTCATTTTAATCAGCATCTTGACCCCTCACCTTCACACCCCTATGTACTTCTT
TCTGGGGAAACCTCTCCTTCTTGGACATCTGCTACACCACCACTCTATTCCCTCCACGCTAG
TGAGCTTCCTTTTCAGAAAGAAAGACCATTTCCCTTTCTGGCTGTGCAGTGCAGATGTTCCCT
CAGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCGTGATGGCCTTTGACCGCTAT
10 GTGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGAGTAAGGATGCCTATGTACCCA
TGGCAGCTGGGTCTGGATCATAGGAGCTGTCAATTCTGCAGTACAAACAGTGTTTGTGGT
ACAATTGCCTTTCTGCAGGAATAACATCATCAATCATTTTCACCTGTGAAATTCTAGCTGTC
ATGAAACTGGCCTGTGCTGACATCTCAGGCAATGAGTTCATCCTGCTTGTGACCACAACAT
TGTTCCATTGACACCTTTGTTATTAATTATTGTCTCTTACACGTTAATCATTTTGAGCATC
15 TTCAAATTAGCTCTTCGGAGGGGAGAACCTTCCTCTACCTGCTCAGCTCGTCTGA
CTGTGGTGATAACATTCTGTGGGACCATCTTCCTCATGTACATGAAGCCCAAGTCTCAAGA
GACACTTAATTCAGATGACTTGGATGCCACTGACAACTTATATTCATATTCTACAGGGTG
ATGACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAGGAGGCA
GTAAACACCTACTGAGAAGAAAAAATTTTAACAAGTAA (SEQ ID NO: 376)

20

AOLFR203 sequences:

5 MKRQNSQSVVEFILLGFSNFBELQVQLFGVFLVIYVVTLMGNAITVIISLNQSLHVPMYLFLLN
LSVVEVSFAVITPEMLVVLSTEKTMSIFVGCFAQMYFILLFGGTECFLLGAMAYDRFAAICHPL
NYPVIMNRGVFMKLVIFSWISGIMVATVQTTWVFSFPFCGPNEINHLFCETPPVLELVCADTFLE
25 EIYFTGTILIVMVPFLILLSYIRVLFALKMPSTTGRQKAFSTCASHLTSVTLFYGTANMTYLO
PKSGYSPETKKLISLAYTLLTPLLNPLIYSLRNSEMKRTLKLRWKVILHTF (SEQ ID NO: 377)

30 ATGAAAAGACAAAATCAAAGCTGTGTGGTGAATTCATCCTCCTGGGCTTTTCTAACTTTC
CTGAGCTCCAGGTGCAGCTCTTTGGGGTTTTCTAGTTATTTATGTGGTGACCCTGATGGG
AAATGCCATCATTACAGTCATCATCTCCTTAAACCAGAGCCTCCACGTTCCCATGTACCTGT
TCCTCCTGAACCTATCTGTGGTGGAGGTGAGTTTCAGTGCAGTCATTACGCCTGAAATGCT
GGTGGTGCTCTCTACTGAGAAAATATGATTTCTTTTGTGGGCTGTTTTCACAGATGTAT
TTCATCCTTCTTTTGGTGGGACTGAATGTTTTCTCCTGGGAGCGATGGCTTATGACCGATT
TGCTGCAATTTGCCATCCTCTGAACTACCCAGTGATTATGAACAGAGGGGTTTTATGAAA
35 TTAGTAATATTCTCATGGATCTCAGGGATCATGGTGGCTACTGTGCAGACCACTTGGGTAT
TTAGTTTTCCTATTTTGGGCCCCAATGAAATTAATCATCTCTTCTGTGAGACTCCCCCGTA
CTAGAGCTTGTGTGTGCAGACACCTTCTTATTTGAAATCTATGCCTTCACAGGCACCATTTT
GATTGTTATGGTTCCTTTCTTGTGATCCTCTTGTCTTACATTTCGAGTTCTGTTGCCATCCT
GAAGATGCCATCAACTACTGGGAGACAAAAGGCCTTTTCCACCTGTGCCTCTCACCTCACA
40 TCTGTGACCCTGTTCTATGGCACAGCCAATATGACTTATTTACAACCCAAATCTGGCTACTC
ACCCGAAACCAAGAAACTGATCTCATTGGCTTACACGTTGCTTACCCCTCTGCTCAATCCG
CTCATCTATAGCTTACGAAACAGTGAGATGAAGAGGACTTTGATAAAACTATGGCGAAGA
AAAGTGATTTTACACACATTCTGA (SEQ ID NO: 378)

AOLFR204 sequences:

45 MEKKKNVTEFILGLTQNPIMEKVTFVFLVLYMTLSGNLLIVVTTTTQALSSPMYFFLTHLSL
IDTVYSSSSAPKLIVDSFQEKIISFNGCMAQAYAEHIFGATEIILLTVMACDCYVAICKPLNYTT
IMSHSLCILLVAVAVVGGFLHATIQILFTVWLPFCGPNVIGHFMCDLYPLLKLVCIDHTLGLFV
AVNSGFICLLNFLILVVSIVILRSKNSLEGRCKALSTCISHIVVVLFFVPCIFVYLRSVTTLPI
50 DKAVAVFYTMVVPMLNPVVYTLRNBVKSAIRKLWRKKVTSND (SEQ ID NO: 379)

55 ATGGAGAAGAAAAAGAATGTGACTGAATTCATTTTAATAGGTCTTACACAGAACCCCATTA
ATGGAGAAAGTCACGTTTGTAGTATTTTGGTTCTTTACATGATAACACTTTCAGGCAACC
TGCTCATTGTGGTTACCATACCACCAGCCAGGCTCTGAGCTCCCCCATGTACTTCTTCCTG
ACCCACCTTTCTTTGATAGACACAGTTTATTCTTCTTCTTCAGCTCCTAAGTTGATTGTGGA
TTCCTTTCAAGAGAAGAAAAATCATCTCCTTTAATGGGTGTATGGCTCAAGCCTATGCAGAA

CACATTTTTGGTGCTACTGAGATCATCCTGCTGACAGTGATGGCCTGTGACTGCTATGTGG
 CCATCTGCAAACCTCTGAACTACACAACCATTATGAGCCACAGCCTGTGCATTCTCCTGGT
 GGCAGTGGCCTGGGTGGGAGGATTTCTTCATGCAACTATTCAGATTCTCTTTACAGTATGG
 CTGCCCTTCTGTGGCCCCAATGTCATAGGCCACTTCATGTGTGACTTGTACCCATTGTTAA
 5 ACTTGTTCATAGACACTCATACCCTTGGTCTCTTTGTTGCTGTGAACAGTGGGTTTATCT
 GCTTATTAACACTTCCTTATCTTGGTGGTATCCTATGTGATCATCTTGAGATCTTTAAAGAAC
 AATAGCTTGGAGGGGAGGTGTAAAGCCCTCTCCACCTGTATTTCTCACATCATAGTAGTTG
 TCTTATTCTTTGTGCCCTGTATATTTGTGTATCTGCGCTCAGTGACCACTCTGCCCATGAT
 AAAGCTGTTGCTGTATTTTATACTATGGTGGTCCCAATGTTAAATCCCGTGGTCTACACAC
 10 TCAGAAATGCTGAGGTAAAAAGTGCAATAAGGAAGCTTTGGAGAAAAAAGTGACTTCAG
 ATAATGATTAA (SEQ ID NO: 380)

AOLFR205 sequences:

MESENRTVIREFILLGLTQSQDIQLLVFVLVLIFYFILPGNFLIIFTIKSDPGLTAPLYFFLGNLAF
 15 DASYSFTVAPRMLVDFLSAKKIISYRGCTQLFFLHFLGGEGELLVVMFAFDRIAICRPLHYPT
 VMNPRTCYAMMLALWLGGFVHSIIQVVLRLPFCGPNQLDNFFCDVPQVIKLACTDTFVVEL
 LMFVNSGLMTLLCFLGLLASVAVILCRIRGSSSEAKNKAMSTCITHIIVIFFMFGPGIFITRPFRA
 FPAKVVVSLFHTVIFPLNPVIYTLRNQEVKASMKKVFNKHIA (SEQ ID NO: 381)
 20 ATGGAAAGCGAGAACAGAACAGTGATAAGAGAATTCATCCTCCTTGGTCTGACCCAGTCT
 CAAGATATTCAGTCTCCTGGTCTTTGTGCTAGTTTAAATATTCTACTTCATCATCCTCCCTGG
 AAATTTTCTCATTATTTTACCATAAAGTCAGACCCCTGGGCTCACAGCCCCCTCTATTCT
 TTCTGGGCAACTTGGCCTTCTGGATGCATCCTACTCCTTCACTGTGGCTCCCCGGATGTTG
 GTGGACTTCTCTCTGCGAAGAAGATAATCTCCTACAGAGGCTGCATCACTCAGCTCTTTT
 25 TCTTGCACTTCTTGGAGGAGGGGAGGGATTACTCCTTGTGTGATGGCCTTTGACCGCTA
 CATCGCCATCTGCCGGCCTCTGCACTATCCTACTGTGATGAACCTAGAACCTGCTATGCA
 ATGATGTTGGCTCTGTGGCTTGGGGGTTTTGTCCACTCCATTATCCAGGTGGTCTCATCCT
 CCGCTTGCCTTTTTGTGGCCCAAACCAGCTGGACAACCTTCTTCTGTGATGTCCACAGGTC
 ATCAAGCTGGCCTGCACCGACACATTTGTGGTGGAGCTTCTGATGGTCTTCAACAGTGGCC
 30 TGATGACACTCCTGTGCTTTCTGGGGCTTCTGGCCTCCTATGCAGTCATTCTTTGTGCATA
 CGAGGGTCTTCTCTGAGGCAAAAAACAAGGCCATGTCCACGTGCATCACCCATATCATTTG
 TTATATTCTTCATGTTTGGACCTGGCATCTTCACTATACACGCGCCCTTCAGGGCTTTCCCA
 GCTGCAAGGTGGTTTCTCTCTTCCACACAGTGATTTTCTTTGTTGAATCCTGTCTATTA
 TACCCTTCGAACAGGAAGTGAAAGCTTCCATGAAAAAGGTGTTTAATAAGCACATAGC
 35 CTGA (SEQ ID NO: 382)

AOLFR206 sequences:

MANRNNVTEFILLGLTENPKMQKIIFVFSVIYINAMIGNVLIVVTTASPSLRSPMYFFLAYLSFI
 40 DACYSSVNPTELITDSLYENKTLFNGCMTQVFGHEFFRGVEVILLTVMAYDHYVAICKPLHYT
 TIMKQHVCSLLVGVSWVGGFLHATIQLFICQLPFCGPNVIDHFMCDLYTLINLACTNHTLGLF
 IAANSFICLLNCLLLLVSVCVILYSLKTHSLEARHEALSTCVSHITVVILSFIPCIFVYMRPPATL
 PIDKAVAVFYTMITSMLNPLIYTLRNAQMKNAIRKLCRKAISSVK (SEQ ID NO: 383)
 45 ATGGCGAATAGAAACAATGTGACAGAGTTTATTCTATTGGGGCTTACAGAGAATCCAAAA
 ATGCAGAAAATCATATTTGTTGTGTTTTCTGTCTATCATCAACGCCATGATAGGAAATG
 TGCTCATTGTGGTCACCATCACTGCCAGCCCATCACTGAGATCCCCCATGTACTTTTCTCTG
 GCCTATCTCTCCTTTATTGATGCCTGCTATTCCTCTGTCAATACCCCTAAGCTGATCACAGA
 TTCACTCTATGAAAACAAGACTATCTTATTCAATGGATGTATGACTCAAGTCTTTGGAGAA
 CATTITTTTTCAGAGGTGTTGAGGTCACTCTACTTACTGTAATGGCCTATGACCACTATGTGG
 50 CCATCTGCAAGCCCTTGCACTATACCACCATCATGAAGCAGCATGTTTGTAGCCTGCTAGT
 GGGAGTGTGATGGGTAGGAGGCTTTCTTCATGCAACCATAACAGATCCTCTTCTATCTGTCAA
 TTACCTTTCTGTGGTCCTAATGTCATAGTACTTTATGTGTGATCTCTACACTTTGATCAA
 TCTTGCCCTGCACTAATAACCCACACTTAGGACTCTTCAATTGCTGCCAACAGTGGGTTTCATAT
 GCCTGTAAACTGTCTCTTGCTCCTGGTCTCCTGCGTGGTGCATACTGTACTCCTTAAAGACC
 55 CACAGCTTAGAGGCAAGGCATGAAGCCCTCTCTACCTGTGTCTCCACATCACAGTTGTCA
 TCTTATCCTTTATACCCTGCATATTTGTGTACATGAGACCTCCAGCTACTTTACCCATTGAT

AAAGCAGTTGCTGTATTCTACACTATGATAAATTCTATGTTAAACCCCTTAATCTACACCTT
GAGGAATGCTCAAATGAAAAATGCCATTAGGAAATTGTGTAGTAGGAAAGCTATTTCAAG
TGTCAAATAA (SEQ ID NO: 384)

5 **AOLFR207 sequences:**

MERTNDSTSTEFFLVGLSAHPKLQTVFFVLILWMYLMILLGNGVLISVIIFDShLHTPMYFFLCN
LSFLDVCYTSSSVPLILASFLAVKKKVSFSGCMVQMFISFAMGATECMILGTMALDRYVAICYP
LRYPVIMSKGAYVAMAAGSWVTGLVDSVVQTAFAMQLPFCANNVIKHFVCEILAILKLACADI
SINVISMTGSNLIVLVIPLLVISISYIFIVATILRIPSTEGKHKAFSTCSAHLTVVIIFYGTIFFMYAKP
10 ESKASVDSGNEDIIEALISLFYGVMTPLNPLIYSLRNKDVKA AVKNILCRKNFSDGK (SEQ ID
NO: 385)

ATGGAAAGGACCAACGATTCCACGTCGACAGAATTTTTCCTGGTAGGGCTTTCTGCCCCACC
CAAAGCTCCAGACAGTTTCTTCGTTCTAATTTTGTGGATGTACCTGATGATCCTGCTTGGAC
15 AATGGAGTCTTATCTCAGTTATCATCTTTGATTCTCACCTGCACACCCCCATGTATTTCTT
CCTCTGTAATCTTTCCTTCCTCGACGTTTGCTACACAAGTTCCTCTGTCCCACTAATTCTTG
CCAGCTTTCTGGCAGTAAAGAAAAAGGTTTCTTCTCTGGGTGTATGGTGCAAATGTTTAT
TTCTTTTGCCATGGGGGCCACGGAGTGCATGATCTTAGGCACGATGGCACTGGACCGCTAT
GTGGCCATCTGCTACCCACTGAGATACCCTGTCATCATGAGCAAGGGTGCCTATGTGGCCA
20 TGGCAGCTGGGTCTGGGTCACTGGGCTTGTGGACTCAGTAGTGCAGACAGCTTTTGCAAT
GCAGTTACCATCTGTGCTAATAATGTCATTAAACATTTTGTCTGTGAAATTCTGGCTATCT
TGAAACTGGCCTGTGCTGATATTTCAATCAATGTGATTAGTATGACAGGGTCAATCTGAT
TGTTCTGGTTATTCCATTGTTAGTAATTTCCATCTCTTACATATTTATTGTTGCCACTATTCT
GAGGATTCCTTCCACTGAAGGAAAACATAAGGCCTTCTCCACCTGCTCAGCCACCTGACA
25 GTGGTGATTATATTCTATGGAACCATCTTCTTCATGTACGCAAAGCCTGAGTCTAAAGCCT
CTGTTGATTACAGTAATGAAGACATCATTGAGGCCCTCATCTCCCTTTTCTATGGAGTGAT
GACTCCCATGCTTAATCCTCTCATCTATAGTCTGCGAAACAAGGATGTAAAGGCTGCTGTC
AAAAACATACTGTGTAGGAAAAACTTTTCTGATGGAAAAATGA (SEQ ID NO: 386)

30 **AOLFR208 sequences:**

MFPANWTSVKVFFFLGFFHYPKVQVIFAVCLLMYLITLLGNIFLISITILDSHLHTPMYFLSNL
SFLDIWYSSSALSPMLANFVSGRNTISFSGCATQMYLSLAMGSTECVLLPMMAYDRYVAICNP
LRYPVIMNRRTCVQIAAGSWMTGCLTAMVEMMSVLPLSLCGNSIINHFTCEILAILKLVCVDT
LVQLMLVISVLLPMPMLLICISYAFILASILRISSVEGRSKAFSTCTAHLMVVVLFGTALS MH
35 LKPSAVDSQEIDKFMA LVYAGQTPMLNPIIYSLRNKEVKVALKKLLIRNHFNTAFISILK (SEQ
ID NO: 387)

ATGTTCCCGGCAAATTGGACATCTGTAAAAGTATTTTCTTCTCCTGGGATTTTTTCACTACCC
CAAAGTTCAAGGTCATCATATTTGCGGTGTGCTTGCTGATGTACCTGATCACCTTGCTGGGC
40 AACATTTTTCTGATCTCCATCACCATTCTAGATTCCACCTGCACACCCCTATGTACCTCTT
CCTCAGCAATCTCTCCTTTCTGGACATCTGGTACTCCTCTTCTGCCCTCTCTCCAATGCTGG
CAAACCTTTGTTTCAGGGAGAAACACTATTTCAATTCTCAGGGTGCGCCACTCAGATGTACCT
CTCCCTTGCCATGGGCTCCACTGAGTGTGTGCTCCTGCCCATGATGGCATATGACCGGTAT
GTGGCCATCTGCAACCCCTGAGATACCCTGTCATCATGAATAGGAGAACCTGTGTGCAGA
45 TTGCAGCTGGCTCCTGGATGACAGGCTGTCTCACTGCCATGGTGGAAATGATGTCTGTGCT
GCCACTGTCTCTGTGGTAATAGCATCATCAATCATTTCACTTGTGAAATTCTGGCCATCT
TGAAATTGGTTTGTGTGGACACCTCCCTGGTGCAGTTAATCATGCTGGTGATCAGTGTACT
TCTTCTCCCATGCCAATGCTACTCATTTGTATCTCTTATGCATTTATCCTCGCCAGTATCC
TGAGAATCAGCTCAGTGGAAGGTCGAAGTAAAGCCTTTTCAACGTGCACAGCCACCTGA
50 TGGTGGTAGTTTTGTTCTATGGGACGGCTCTCTCCATGCACCTGAAGCCCTCCGCTGTAGA
TTCACAGGAAATAGACAAATTTATGGCTTTGGTGATGCCGGACAAACCCCATGTTGAAT
CCTATCATCTATAGTCTACGGAACAAAGAGGTGAAAGTGGCCTTGAAAAAATTGCTGATTA
GAAATCATTTTAAATACTGCCTTCATTTCCATCCTCAAATAA (SEQ ID NO: 388)

AOLFR209 sequences:

- MDKINQTFVREFILLGLSGYPKLEIFFALILVMYVVILIGNGVLIASILDSRLHMPMYFFLGNL
 FLDICYTTSSIPSTLVSLISKRNISFSGCAVQMFFGFAMGSTECFLGMMAFDYVAICNPLRY
 5 PIIMNKVVYVLLTSVSWLSGGINSTVQTSLAMRWPF CGNNIINHFLCEILAVLKLACSDISVNIV
 TLAVSNIAFLVPLLVIFFSYMFILYTLIRTSNATGRHKAFSTCSAHLTVVIIFYGTIFFMYAKPKS
 QDLLGKDNLQATEGLVSMFYGVVTPMLNPIIYSLRNKDVKAAIKYLLSRKAINQ (SEQ ID NO:
 389)
- 10 ATGGACAAGATAAACCAGACATTTGTGAGAGAATTCATTCTTCTGGGACTCTCTGGTTACC
 CCAAACCTTGAGATCATTTTCTTTGCTCTGATTCTAGTTATGTACGTAGTGATTCTAATTGGC
 AATGGTGTCTGATCATAGCAAGCATCTTGGATTCTCGTCTTCACATGCCCATGTACTTCTT
 CCTGGGCAACCTCTCTTTCTGGATATCTGCTATACAACCTCCTCCATTCCCTCAACACTGG
 TGAGCTTAATCTCAAAGAAAAGAAACATTTCTTCTCTGGATGTGCAGTGCAGATGTTCTT
 15 TGGGTTTGCAATGGGGTCAACAGAATGTTTCTCTTGGCATGATGGCATTGTATCGTTAT
 GTGGCCATCTGTAACCTCTGAGATACCCCATCATCATGAACAAGGTGGTGTATGTACTGC
 TGACTTCTGTATCATGGCTTTCTGGTGGAATCAATTCAACTGTGCAAACATCACTTGCCAT
 GCGATGGCCTTTCTGTGGGAACAATATTATTAATCATTTCTTATGCGAGATCTTAGCTGTCC
 TAAAAATTAGCTTGTCTGATATATCTGTCAATATTGTTACCCTAGCAGTGTCAAATATTGCT
 20 TTCTAGTTCTTCTCTGCTCGTGATTTTCTCTCTATATGTTTCATCTCTACACCATCTTG
 CGAACGAACTCGGCCACAGGAAGACACAAGGCATTTTCTACATGCTCAGCTCACCTGACTG
 TGGTGATCATATTTTATGGTACCATCTTCTTTATGTATGCAAAACCTAAGTCCCAGGACCTC
 CTTGGGAAAGACAACCTGCAAGCTACAGAGGGGCTTGTTCATGTTTTATGGGGTTGTGA
 CCCCCATGTTAAACCCATAATCTATAGCTTGAGAAATAAAGATGTAAAAGCTGCTATAAA
 25 ATATTTGCTGAGCAGGAAAGCTATTAACCAGTAA (SEQ ID NO: 390)

AOLFR210 sequences:

- MMGRRNDTNVADFILTGLSDSEEVQMALFMLFLLIYLITMLGNVGMILLIRLDLQLHTPMYFFL
 THLSFDLSYSTVVTPKTLANLLTSNYISFTGCF AQMFCFVFLGTAECYLLSSMAYDRYAAICSP
 30 LHVTVMIPKRLCLALITGPYVIGFMDSFVNVVSMRSLHFCD SNIIHHFFCDTSPILALSCTDTDN
 TEMLIIFIAGSTLMVSLITISASYVSILSTILKINSTSGKQKAFSTCVSHLLGVTFIFYGTIMFTYLPK
 RKSYSYSLGRDQVAPVFYTVIPMLNPLIYSLRNREVKNALIRVMQRRQDSR (SEQ ID NO: 391)
- 35 ATGATGGGTAGAAAGGAATGACACAAATGTGGCTGACTTCATCCTTACGGGACTGTCAGAC
 TCTGAAGAGGTCCAGATGGCTCTGTTTATGCTATTTCTCCTCATATACCTAATTACTATGCT
 GGGGAATGTGGGGATGCTATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTAT
 TTTTTCCTTACTCACCTGTCAATTTATTGACCTCAGTTACTCAACTGTCGTCACACCTAAAAC
 CTTAGCGAACTTACTGACTTCCAACATATTTTCTTACGGGGCTGCTTTGCCAGATGTTCT
 GTTTTGTCTTCTTGGGTACTGCTGAATGTTATCTTCTCTCCTCAATGGCCTATGATCGCTAT
 40 GCAGCGATCTGCAGTCTCTACACTACACAGTTATTATGCCAAAAGGCTCTGCCTCGCTC
 TCATCACTGGGCCTTATGTGATTGGCTTTATGGACTCCTTTGTCAATGTGGTTTCCATGAGC
 AGATTGCATTTCTGTGACTCAAACATAATTCATCACTTTTTCTGTGACACTTCCCCAATTTT
 AGCTCTGTCTGCACTGACACAGACAACACTGAAATGCTGATATTCATTATCGCTGGTTCC
 ACCCTGATGGTGTCCCTTATCACAATATCTGCATCCTATGTGTCCATTCTCTTACCATCCT
 45 GAAAATTAATCCACTTCAGGAAAGCAGAAAGCTTTCTCTACTTGCGTCTCTCATCTCTTG
 GGAGTCACCATCTTCTATGGAACATGATTTTTACTTACTTAAAGCCAAGAAAGTCTTATT
 CCTTGGGAAGAGATCAAGTGGCTCCTGTGTTTTATACTATTGTGATTCCCATGCTGAATCC
 ACTCATTTATAGTCTTAGAAACAGAGAAGTGAAAAATGCTCTCATTAGAGTCATGCAGAG
 AAGACAGGACTCCAGGTAG (SEQ ID NO: 392)
- 50

AOLFR211 sequences:

- MMGRRNNTNVADFILMGLTLSEEIQMALFMLFLLIYLITMLGNVGMILLIRLDLQLHTPMYFFL
 THLSFDLSYSTVVTPKTLANLLTSNYISFTGCF AQMFFFAFLGTAECYLLSSMAHDRYAAICSP
 LHVTVIMSKRLCLALITGPYVIGFIDSFVNVVSMRSLHFYDSNVIHHFFCDTSPILALSCTDTYNT
 55 BILFIIVGSTLMVSLFTISASYVFILFTILKINSTSGKQKAFSTCVSHLLGVTFYSTLIFTYLPKPK
 SYSYSLGRDQVASVFYTVIPVLNPLIYSLRNKEVKNVIRVMQRRQDSR (SEQ ID NO: 393)

ATGATGGGTAGAAAGGAATAACACAAATGTGGCTGACTTCATCCTTATGGGACTGACACTTT
 CTGAAGAGATCCAGATGGCTCTGTTTATGCTATTTCTCCTGATATACCTAATTACTATGCTG
 GGGAAATGTGGGGATGATATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTATT
 5 TTTTCTTACTCACCTGTCATTTATTGACCTCAGTTACTCAACTGTCGTACACCTAAAACC
 TTAGCGAACTTACTGACTTCCAATAATTTCTTTACGGGCTGCTTTGCCAGATGTTCTT
 TTTTGCCTTCTTGGGTACTGCTGAATGTTACCTTCTCCTCAATGGCCCATGATCGCTATG
 CAGCGATCTGCAGTCCTCTACACTACACAGTTATTATGTCCAAAAGGCTCTGCCTCGCTCT
 CATCACTGGGCTTATGTGATTGGCTTTATAGACTCCTTTGTCAACGTGGTTTCCATGAGCA
 10 GATTGCATTTCTACGACTCAAACGTAATTCATCACTTTTTCTGTGACACTTCCCCAATTTTA
 GCTCTGTCTGCACTGATACATAACAACCCGAAATCCTGATATTCATTATTGTTGGTTCAC
 CCTGATGGTGTCCCTTTTCAACAATATCTGCATCCTATGTGTTCACTTCTTTTACCATCCTGA
 AAATTAATTCCACTTCAGGAAAGCAGAAAGCTTTCTACTTGGCTCTCTCATCTCTTGGG
 AGTCACCATCTTTTATAGCACTCTGATTTTACTTATTTAAAACCAAGAAAGTCTTATTCTT
 15 TGGGAAGAGATCAAGTGGCTTCTGTTTTTATACTATTGTGATTCCCGTGTGAATCCACT
 CATTTATAGTCTTAGAAACAAAGAGGTGAAAAATGCTGTCATCAGAGTCATGCAGAGAAG
 ACAGGACTCCAGGTAA (SEQ ID NO: 394)

AOLFR212 sequences:

20 MAGNNFTEVTVFILSGFANHPQLVSLFLMFLFYLFVTLGNLGLITLIRMDSQLHTPMYFFLSN
 LAFIDIFYSSVTPKALVNFQSNRRSISFVGVQMYFFVGLVCCECFLLGSMAYNRYIAICNPL
 LYSVVMQKVSNNWLGVMFYVIGFTSSLSVWVISSLAFCDSINHHFCDTTALLALSCVDFTGT
 EMVSFVLGFTLLSLLITVTYIIISAILRIQSAAGRQKAFSTCASHLMAVTIFYGSLIFTYLQPD
 NTSSLTQAQVASVFYTTIVPMLNPLIYSLRNKDVKNALLRVIHRKLP (SEQ ID NO: 395)

25 ATGGCTGGCAACAATTTCACTGAGGTTACCGTCTTCATCCTCTCTGGATTTGCAATCACC
 CTGAATTACAAGTCAGTCTTTTCTTGATGTTTCTCTTCATTTATCTATTCAGTGTTTGGGA
 AACCTGGGACTGATCACGTTAATCAGAATGGATTCTCAGCTTCACACCCCTATGTACTTTT
 30 TCCTGAGCAATTTAGCATTTATTGACATATTTTACTCCTCTACTGTAACACCTAAGGCATTG
 GTGAATTTCCAATCCAATCGGAGATCCATCTCCTTTGTTGGCTGCTTTGTTCAAATGTACTT
 TTTTGTGGATTGGTGTGTTGTGAGTGTTTCCTTCTGGGATCAATGGCCTACAATCGCTACA
 TAGCAATCTGCAATCCCTTACTGTATTAGTAGTCATGTCCAAAAAGTGCCAACCTGGCT
 GGGAGTAATGCCATATGTGATAGGCTTCACAAGCTCGCTGATATCTGTCTGGGTGATAAGC
 AGTTTGGCGTTCGTGATTCCAGCATCAATTTTTTTTTGTGACACCACAGCTCTTTTAGC
 35 ACTCTCCTGTGTAGATACATTTCGGCACAGAAATGGTGAGCTTTGTCTTAGCTGGATTCACT
 CTTCTTAGCTCTCTCCTTATCATCACAGTCACTTATATCATCATCATCTCAGCCATCCTGAG
 GATCCAGTCAGCAGCAGGCAGGCAGAAAGGCCTTCTCCACCTGCGCATCCCACCTCATGGCT
 GTAACATCTTTTATGGGTCTCTGATTTTACCTATTTGCAACCTGATAACACATCATCGCT
 GACCCAGGCGCAGGTGGCATCTGTATTCTATACGATTGTCAATCCCATGCTGAATCCACTC
 40 ATCTACAGTCTGAGGAACAAAGATGTGAAAAATGCTCTTCTGAGAGTCATACATAGAAAA
 CTTTTTCCATGA (SEQ ID NO: 396)

AOLFR213 sequences:

45 MNSLGKLVSMILSAHVFCYSKFNCFGCTHSIPALGADPPGGMGLGNESSLMDFILLGFSHPRL
 EAVLFVFLFFYLLTLVGNFTIIISYLDPLHTPMYFFLSNLSLLDICFTTSLAPQTLVNLQRPKK
 TITYGGCVAQLYISLALGSTECILLADMALDRYIAVCKPLHYVVMNPRLCQQLASISWLSGLA
 SSLIHATFTLQPLCGNHRLDHFICEVPALLKLACVDTTVNELVLFVSVLVFVIPPALISISYFI
 TQAVLRIKSVEARHKAFSTCSSHLTVIIFYGTIIYVYLQPSDSYAQDQGKFISLFYTMVPTLNP
 IYTLRNKDMKEALRKLLSGKL (SEQ ID NO: 397)

50 ATGAATAGTTTGGGAAAGTTGGTCTCCATGATCCTCTCAGCTCATGTGTTCTGTTATTCTAA
 ATTTAATTGTTTTGGATGTACCCATTCCATTCTGCCTTAGGTGCGGATCCCCCTGGAGGG
 ATGGGATTGGGCAATGAGAGTTCCTAATGGATTTCACTCTTAGGCTTCTCAGACCACC
 CTCGTCTGGAGGCTGTTCTCTTTGTATTGTCTTTTCTTCTACCTCCTGACCTTGTGGGA
 55 AACTTACCATAATCATCATCTCATATCTGGATCCCCCTTTCATACCCCAATGTACTTTTT
 TCTCAGCAACCTCTCTTTACTGGACATCTGCTTCACTACTAGCCTTGCTCCTCAGACCTTAG

TTAACTTGCAAAGACCAAAGAAGACGATCACTTACGGTGGTTGTGTGGCGCAACTCTATAT
 TTCTCTGGCACTGGGCTCCACTGAATGTATCCTCTTGGCTGACATGGCCTTGGATCGGTAC
 ATTGCTGTCTGCAAACCCCTCCACTATGTAGTCATCATGAACCCACGGCTTTGCCAACAGC
 TGGCATCTATCTCCTGGCTCAGTGGTTTGGCTAGTTCCTAATCCATGCAACTTTTACCTTG
 5 CAATTGCCCTCTCTGTGGCAACCATAGGCTGGACCATTTTATTTGCGAAGTACCAGCTCTTCT
 CAAGTTGGCTTGTGTGGACCACTGTCAATGAATTGGTGTCTTTTGTGTTAGTGTCTGT
 TTGTTGTCAATCCACCAGCACTCATCTCCATCTCCTATGGCTTCATAACTCAAGCTGTGCTG
 AGGATCAAATCAGTAGAGGCAAGGCATAAAGCCTTCAGCACCTGCTCCTCCCACCTTACAG
 TGGTGATTATATTTCTATGGCACCATAATCTACGTGTACCTGCAACCTAGTGACAGCTATGC
 10 CCAGGACCAAGGGAAGTTTATCTCCCTCTTCTACACCATGGTGACCCCCACTTTAAATCCT
 ATCATCTATACTTTAAGGAACAAGGATATGAAAGAGGGCTCTGAGGAACTTCTCTCGGGA
 AAATTGTGA (SEQ ID NO: 398)

AOLFR214 sequences:

15 MDKSNSSVSEFVLLGLCSSQKLQLFYFCFFSVLYTVIVLGNLLILTVTSDTSLHSPMYFLLGN
 LSFVDICQASFATPKMIADFLSAHETISFSGCIAQIFHILFTGGEMVLLVSMA YDRYVAICKPLY
 YVVMISRRCTVLVMISWAVSLVHTLSQLSFTVNL PFCGPNVVD SFFCDLPRVTKLACLD SYHE
 ILIVVNSGILSLSTFSLLVSSYIILVT VWLKSSAAMAKAFSTLASHIAV VILFFGPCIFYVWPFTIS
 PLDKFLAIFYTVFPLNPIHYTLNRNMDKAAVRKIVNHYLRPRRISEMSLVVRTSFH (SEQ ID
 20 NO: 399)

ATGGATAAGTCCAATTCTTCAGTGGTGTCTGAATTTGTACTGTTGGGACTCTGTAGTTCTC
 AAAA ACTCCAGCTTTTCTATTTTGTCTCTCTGTGTGTATACAGTCATTGTGCTGGGA
 AATCTTCTCATTATCCTCACAGTGACTTCTGATACCAGCCTGCACTCCCCTATGTACTTTCT
 25 CTTGGGAAACCTTTTCTTTGTTGACATTGTGTCAGGCTTCTTTTGCTACCCCTAAAATGATTG
 CAGATTTTCTGAGTGCACACGAGACCATATCTTTCAGTGGCTGCATAGCCCAAATTTTCTTT
 ATTCACCTTTTACTGGAGGGGAGATGGTGTACTTGTTCGATGGCCTATGACAGGTATG
 TAGCCATATGCAAACCTTATACTATGTGGTCATCATGAGCCGAAGGACATGCACTGTCTT
 GGTAATGATCTCCTGGGCTGTGAGCTTGGTGCACACATTAAGCCAGTTATCATTTACTGTG
 30 AACCTGCCTTTTGTGGACCTAATGTAGTAGACAGCTTTTTTGTGATCTTCTCGAGTCAC
 CAAACTTGCCTGCCTGGACTCTTACATCATTGAAATACTAATTGTGGTCAATAGTGGAATT
 CTTTCCCTAAGCACTTTCTCTCTTGGTCAGCTCCTACATCATTATTCTTGTACAGTTTG
 GCTCAAGTCTTTCAGCTGCAATGGCAAAGGCATTTTCTACGCTGGCTTCCCATATTGCAGTA
 GTAATTATTCTTTGGACCTTGCATCTTCACTATGTGTGGCCCTTTACCATCTCTCCTTT
 35 GGATAAATTTCTTGCCATATTTTACACTGTTTACCCCCGTCCTAAACCCATTATTTATA
 CACTAAGGAATAGGGATATGAAGGCTGCCGTAAGGAAAATTGTGAACCATTACCTGAGGC
 CAAGGAGAATTTCTGAAATGTCACTAGTAGTGAGAACTTCCTTTCATTAA (SEQ ID NO:
 400)

AOLFR215 sequences:

40 MAHTNESMVSEFVLLGLSNSWGLQLFFFAIFSIVYVTSVLGNVLIIVISFDSHLNSPMYFLLSNL
 SFIDICQSNFATPKMLVDFFIERKTISFEGCMAQIFVLHSFVGSEMMLLVAMAYDRFIAICKPLH
 YSTIMNRRLCVIFVSISWAVGVLSVSHLAFTVDLPFCGPNEVD SFFCDLPLVIELACMDTYEM
 BIMTLTNSGLISLSCFLALIIISYTIILIGVRCRSSGSSKALSTLTAHITV VILFFGPCIFYIWPFSRL
 45 PVDKFLSVFYTVCTPLNPIIYSLRNEDVKAAMWKLNRNHHVNSWKN (SEQ ID NO: 401)

ATGGCTCACACAAATGAATCGATGGTGTCTGAGTTTGTACTTTTGGGACTCTCTAATTCCT
 GGGGACTTCAACTTTTCTTTTTCGCCATCTTCTCTATAGTCTATGTGACATCAGTGCTAGGC
 AATGTCTTAATTATTGTCAATTATTTCTTTTACTCCCATTTGAACTCTCCTATGTACTTCTTG
 50 CTCAGTAATCTTTCTTTCAATTGATATCTGTCACTAATTTGCCACCCCAAGATGCTTGT
 AGACTTTTTTATTGAGCGCAAGACTATCTCCTTTGAGGGTTGCATGGCCCAGATATTGCTT
 CTTACAGTTTTTGTGGGAGTGAGATGATGTTGCTTGTAGCTATGGCATATGACAGATTTA
 TAGCCATATGTAAGCCTCTGCACTACAGTACAATTATGAACCGGAGGCTCTGTGTAATTTT
 TGTGTCTATTTCTGGGCGGTGGGCGTTCTTCACTTCTGTGAGCCACTTGGCTTTTACAGTGG
 55 ACCTGCCATTCTGTGGTCCCAATGAGGTGGATAGCTTCTTTTGTGACCTTCCCTTGGTGATA
 GAGCTGGCTTGCATGGATACATATGAAATGGAAATTATGACCCTAACGAACAGTGGCCTG

ATATCATTGAGCTGTTTCCTGGCTTTAATTATTTCTACACCATCATTTTGATCGGTGTCCG
 ATGCAGGTCCCTCCAGTGGGTCATCTAAGGCTCTTTCTACATTAAGTGGCCACATCACAGTG
 GTCATTCTTTTCTTCGGGCTTGCATTTATTTCTATATATGGCCTTTTAGCAGACTTCCTGT
 GGACAAATTTCTTTCTGTGTTCTACACTGTTTGTACTCCCTTGTGAACCCCATCATCTACT
 5 CTTTGAGGAATGAAGATGTTAAAGCAGCCATGTGGAAGCTGAGAAACCATCATGTGAACT
 CCTGGAAAACTAG (SEQ ID NO: 402)

AOLFR216 sequences:

MDVGNKSTMSEFVLLGLSNSWELQMFVFFMVSLLYVATMVGNLIVTVIVDPHLHSPMYFLL
 10 TNLSIIDMSLASFATPKMITDYLTHKKTISFDGCLTQIFFLHLFTGTEILLMAMSFDRYIAICKPL
 HYASVISPVQCVLVAASWIMGVMHMSQVIFALTLPCGPEVDSFFCDLPVVFQLACVDTY
 VLGLFMISTSGHIALSCFVLFNSYVIVLVTVKHSSRGSSKALSTCTAHFIVVFLFFGPCIFYMW
 PLSSFLTDKILSVFYTIFTPTLNPITYTLRNQEVKIAMRKLKNRFLNFKAMPS (SEQ ID NO: 403)

15 ATGGATGTGGGCAATAAGTCTACCATGTCTGAATTTGTTTTGCTGGGGCTCTCTAATTCCT
 GGGAACTACAGATGTTTTCTTTATGGTGTTCATTGCTTTATGTGGCAACAATGGTGGG
 TAACAGCCTCATAGTCATCACAGTTATAGTGGACCCTCACCTACACTCTCTATGTATTTCC
 TGCTTACCAATCTTTCAATCATTGATATGTCTCTTGCTTCTTTGCCCCACCCCAAAGATGATT
 ACAGATTACCTAACAGGTCACAAAACCATCTCTTTTGATGGCTGCCCTTACCCAGATATTCT
 20 TTCTCCACCTTTTCACTGGAAGTGAATCATCTTACTCATGGCCATGTCCCTTGATAGGTAT
 ATTGCAATATGCAAGCCCTGCACTATGCTTCTGTCTATTAGTCCCCAGGTGTGTGTTGCTCT
 CGTGGTGGCTTCTGATTATGGGAGTTATGCATTCAATGAGTCAGGTCATATTTGCCCTC
 ACGTTACCAATCTGTGGTCCCTATGAGGTAGACAGCTTTTTCTGTGACCTTCTGTGGTGT
 CCAGTTGGCTTGTGTGGATACTTATGTTCTGGGCCTCTTTATGATCTCAACAAGTGGCATA
 25 ATTGCGTTGTCTGTTTTATTGTTTTATTTAATTCATATGTTATTGTCTGGTTACTGTGAA
 GCATCATTCTCCAGAGGATCATCTAAGGCCCTTTCTACTTGTACAGCTCATTTTATTGTTG
 TCTTCTTGTCTTTTGGGCCATGCATCTTCATCTACATGTGGCCACTAAGCAGCTTTCTCACA
 GACAAGATTCTGTCTGTGTTTTATACCATCTTTACTCCCACTCTGAACCCAATAATCTATAC
 TTTGAGGAATCAAGAAGTAAAGATAGCCATGAGGAAACTGAAAAATAGGTTTCTAAATTT
 30 TAATAAGGCAATGCCTTCATAG (SEQ ID NO: 404)

AOLFR217 sequences:

MLESFQKSEQMAWSNQSAVTEFILRGLSSSLELQIFYFLFFSIVYAATVLGNLLIVVTIASEPHLH
 SPTYFLLGNLSFIDMSLASFATPKMIADFLREHKAI SFEGCMTQMFFLHLLGGAIVLLISMSFD
 35 RYVAICKPLHYLTMSRRMCVGLVILSWIVGIFHALSQLAFTVNLPFCGPNEVDSFFCDLPVVIK
 LACVDTYILGVFMISTSGMIALVCFILLVISYTIILVTVRQRSSGGSSKALSTCSAHFTVVTLFFGP
 CTFIYVWPFTNFPIDKVLVSFYTTYTPLLNPVIYTVRNKDVKYSMRKLSSHIFKSRKTDHTP
 (SEQ ID NO: 405)

40 ATGCTAGAGTCCTTCCAGAAATCAGAGCAAATGGCCTGGAGCAATCAGTCTGCGGTAACC
 GAATTCATACTACGGGGTCTGTCCAGTTCTTTAGAACTCCAGATTTTCTACTTCCTGTTTT
 CTCCATAGTCTATGCAGCCACTGTGCTGGGGAACCTTCTTATTGTGGTCACCATGTCATCA
 GAGCCACACCTTCATTCCCCTACGTACTTCTGCTGGGCAATCTCTCCTTCATTGACATGTC
 CCTGGCCTCATTGGCCACCCCAAAATGATTGCAGACTTCCTTAGAGAACACAAAGCCATC
 45 TCTTTTGAAGGCTGCATGACCCAGATGTTCTTCTACATCTCTTAGGGGGTGCTGAGATTG
 TACTGCTGATCTCCATGTCCTTTGATAGGTACGTGGCTATCTGTAAGCCTCTACATTACCTA
 ACAATCATGAGCCGAAGAATGTGTGTTGGGCTTGTGATACTTCTGATTGTGCGGCATCT
 TCCATGCTCTGAGTCAGTTAGCATTTACAGTGAATCTGCCCTTCTGTGGACCCAATGAAGT
 AGACAGTTTCTTTTGTGACCTCCCTTTGGTGATTAAACTTGCTTGTGTGACACATATATTC
 50 TGGGGGTGTTGATGATCTCAACCAAGTGGCATGATTGCCCTGGTGTGCTTCATCCTCTTGGT
 GATCTCTTACACTATCATCTGGTCACCGTTCCGGCAGCGTTCCTCTGGTGGATCCTCCAAA
 GCCCTCTCCACGTGCAGTGCCCACTTTACTGTTGTGACCCCTTTCTTTGGCCCATGCATTT
 CATTATGTGTGGCCTTTACAAAATTTCCCAATAGACAAAGTACTCTCAGTATTTTATACCA
 TATACACTCCCCTCTTGAATCCAGTGATCTATACCGTTAGGAATAAAGATGTCAAGTATTC
 55 CATGAGGAAACTAAGCAGCCATATCTTTAAATCTAGGAAGACTGATCATACTCCTTAA
 (SEQ ID NO: 406)

AOLFR218 sequences:

METANYTKVTEFVLGTLSQTREVQLVLFVIFLSFYLFILPGNLIICTIRLDPHLTSPMYFLLANLA
 LLDIWYSSITAPKMLIDFFVERKIIISFGGCIQLFFLHFVGASEMFLIVMAYDRYAICRPLHYA
 5 TIMNRRLCCILVALSWMGGFIHSIIQVALIVRPFPCPNELDSYFCDITQVRIACANTFPEELVM
 ICSSGLISVVCFIALLMSYAFLLALLKKHSGSDENTNRAMSTCYSHITIVLVMFGPSIYIYARFDF
 SFSLDKVVSVFHTVIFPLLNPIIYTLRNKEVKAAMRKVVTKYLCEEK (SEQ ID NO: 407)

 ATGGAAACTGCAAATTACACCAAGGTGACAGAATTTGTTCTCACTGGCCTATCCCAGACTC
 10 GGGAGGTCCAACCTAGTCCTATTTGTTATATTTCTATCCTTCTATTTGTTTCATCCTACCAGGA
 AATATCCTTATCATTGCAACCATCAGGCTAGACCCCTCATCTGACTTCTCCTATGTATTTCCT
 GTTGGCTAAATCTGGCCCTCCTTGATATTTGGTACTCTTCCATTACAGCCCCTAAAATGCTCA
 TAGACTTCTTTGTGGAGAGGAAGATAATTTCTTTGGTGGATGCATTGCACAGCTCTTCTT
 CTTACACTTTGTTGGGGCTTCGGAGATGTTCTTGCTCATAGTGATGGCCTATGACCGCTAT
 15 GCTGCTATCTGCCGACCCCTCCACTATGCTACCATCATGAATCGACGCTCTGCTGTATCCT
 GGTGGCTCTCTCCTGGATGGGGGGCTTCATTCTATAATACAGGTGGCTCTCATTGTT
 CGACTTCCTTTCTGTGGGGCCCAATGAGTTAGACAGTTACTTCTGTGACATCACACAGGTTG
 TCCGGATTGCCTGTGCCAACACCTTCCCAGAGGAGTTAGTGATGATCTGTAGTAGTGGTCT
 GATCTCTGTGGTGTGTTTCATTGCTCTGTTAATGTCCTATGCCTTCCTTCTGGCCTTGCTCA
 20 AGAAACATTGAGGCTCAGATGAGAATACCAACAGGGCCATGTCCACCTGATTTCCCAAT
 TACCATTTGTGGTGCTAATGTTTGGGCCATCCATCTACATTTATGCTCGCCCAATTGACTCAT
 TTTCCCTAGATAAAGTGGTGTCTGTGTTTCATACTGTAATATTCCCTTTACTTAATCCCATT
 ATTTACACATTGAGAAACAAGGAAGTAAAGGCAGCCATGAGGAAGGTGGTCACCAAATAT
 ATTTTGTGTGAAGAGAAGTGA (SEQ ID NO: 408).
 25

AOLFR219 sequences:

MLTSLTDLCPFPIQVAEIKSLPKSMNETNHSRVTEFVLLGLSSSRELQPFLFTFSLLYLAILLGNF
 LIILVTSDSRLHTPMYFLLANLSFIDVCVASFATPKMIADFLVERKTSISFADCLAQIFFVHLFTGS
 30 EMVLLVSMA YDRYVAICKPLHYMTVMSRRVCVVLVLISWVFGFIHTTSQLAFTVNLPCGPN
 KVDSEFCDLPLVTKLACIDTYVVSLLIVADSGFLSLSSFLLLVSYSYTVILVTVNRNRSASMAKAR
 STLTAHITVTVLFFGPCIFYVWPFSSYSVDKVLAVFYTIFTLILNPVIYTLRNKEVKAAMSKLKS
 RYLKPSQVSVVRNVLFLETK (SEQ ID NO: 409).

 ATGCTCACITTCATTAAGTATCTCTGTTTCTCTCCTATTCAGGTAGCTGAAATTAAGTCCCT
 35 TCCAAAATCGATGAATGAGACAAATCATTCTCGGGTGACAGAATTTGTGTTGCTGGGACTG
 TCTAGTTCAAGGGAGCTCCAACCTTTCTTGTTTCTTACATTTTCACTACTTTATCTAGCAAT
 TCTGTTGGGCAACTTTCTCATCATCCTCACTGTGACCTCAGATTCCCGCCTTCACACCCCCA
 TGTACTTTCTGCTTGCAAACCTGTCAATTTATAGACGTATGTGTTGCCTCTTTTGCTACCCCT
 AAAATGATTGCAGACTTTCTGGTTGAGCGCAAGACTATTTCTTTGATGCCTGCCTGGCCCC
 40 AGATTTTCTTTGTTCACTCTTCACTGGCAGTGAAATGGTGCTCCTAGTTTCCATGGCCTAT
 GACCGTTATGTTGCTATATGCAAACCTCTCCACTACATGACAGTCATGAGCCGTCGTGTAT
 GTGTTGTGCTCGTCTCATTTTCATGGTTTGTGGGCTTCATCCATACTACCAGCCAGTTGGCA
 TTCACTGTTAATCTGCCATTTTGTGGTCTAATAAGGTAGACAGTTTTTCTGTGACCTTCC
 TCTAGTGACCAAGTTAGCCTGCATAGACACTTATGTTGTCAGCTTACTAATAGTTGCAGAT
 45 AGTGGCTTTCTTTCTGAGTTCTTTCTCCTCTTGTTGTCTCCTACACTGTAATACTTGT
 ACAGTTAGGAATCGCTCCTCTGCAAGCATGGCGAAGGCCCGCTCCACATTGACTGCTCACA
 TCACTGTGGTCACTTTATTCTTTGGACCATGCATTTTCATCTATGTGTGGCCCTTCAGCAGT
 TACTCAGTTGACAAAGTCCTTGCTGTATTCTACACCATCTTCACGCTTATTTTAAACCTGT
 AATCTACACGCTAAGAAACAAGAGTGAAGGCAGCTATGTCAAACTGAAGAGTCGGTA
 50 TCTGAAGCCTAGTCAGGTTTCTGTAGTCATAAGAAATGTTCTTTTCTAGAAACAAAGTAA
 (SEQ ID NO: 410).

AOLFR220 sequences:

MKQYSVGNQHSNYRSLFLPFLCSQMTQLTASGNQTMVTEFLFSMFPHAHRGGLLFFIPLLLIYG
 55 FILTGNLIMFVIQVGMALHTPLYFFISVLSFLEICYTTTTPKMLSCLISEQKSISVAGCLLQMYFF
 HSLGITESCVLTA MAIDRYAICNPLRYPTMIPKLCIQLTVGSCFCGFLVLPEIAWISTLPFCGS

NQIHQIFCDFTPVLSLACTDTFLVVTVDATHAAEIVASFLVIALSYIRIIVILGMHSAEGHHKAFST
CAAHLA VLLFFGSVAVMYLRFSATYSVFWDTAIAVTFVILAPFFNPITYSLKNKDMKEAIGRLF
HYQKRAGWAGK (SEQ ID NO: 411).

- 5 ATGAAGCAATATTCAGTGGGTAATCAACATTCCAATTATAGGAGTCTCTTGTTCCTTTTCT
GTGTTACAGATGACACAGTTGACGGCCAGTGGGAATCAGACAATGGTGACTGAGTTCCT
CTTCTCTATGTTCCCGCATGCGCACAGAGGTGGCCTCTTATTCTTTATTCCCTTGCTTCTCA
TCTACGGATTTATCCTAACTGGAAACCTAATAATGTTCAATTGTCATCCAGGTGGGCATGGC
CCTGCACACCCCTTTGTATTTCTTTATCAGTGTCTCTCTCTCTGGAGATCTGCTATACCA
10 CAACCACCATCCCCAAGATGCTGTCTGCCTAATCAGTGAGCAGAAGAGCATTTCCTGGG
TGGCTGCCTCCTGCAGATGTACTTTTCCACTCACTTGGTATCACAGAAAGCTGTGTCTG
ACAGCAATGGCCATTGACAGGTACATAGCTATCTGCAATCCACTCCGTTACCCAACCATCA
TGATTCCCAAACCTTTGTATCCAGCTGACAGTTGGATCCTGCTTTTGTGGCTTCTCTCTGTG
CTTCTGAGATTGCATGGATTTCCACCTTGCCTTTCTGTGGCTCCAACCAGATCCACCAGAT
15 ATTTCTGTGATTTACACCTGTGCTGAGCTTGGCCTGCACAGATACATTCTTAGTGGTCATT
GTGGATGCCATCCATGCAGCGGAAATTGTAGCCTCCTTCTGCTCATTGCTCTATCCTACA
TCCGGATTATTATAGTGATTCTGGGAATGCACTCAGCTGAAGGTCATCACAAGGCCTTTTC
CACCTGTGCTGCTCACCTTGTGTCTTGTCTATTTTTTGGCAGTGTGGCTGTCTGTATT
TGAGATTCTCAGCCACCTACTCAGTGTTTTGGGACACAGCAATTGCTGTCACTTTTGTATC
20 CTGTGCTCCCTTTTCAACCCATCATCTATAGCCTGAAAAACAAGGACATGAAAGAGGCTA
TTGGAAGGCTTTTCCACTATCAGAAGAGGGCTGGTTGGGCTGGGAAATAG (SEQ ID NO:
412).

AOLFR221 sequences:

- 25 MRNLSGGHVVEFVLVGFPPTPPLQLLLFVLFVLYLLTLENALIVFTIWLAPSLHRPMYFFLGH
LSFLELWYINVTPRLLAFLTQDGRVSYVGCMTQLYFFIALACTECVLLAVMAYDRYLAICGP
LLYPSLMPSSLATRLAAASWGSFGFSSMMKLLFISQLSYCGPNINHFCDISPLNLTCSDKEQA
ELVDFLLALVMILLPLLA VVSSYTAIAAILRIPTSRGRHKAFSTCAAHLA VVVYIYSSLTFTYAR
PRAMYTFNHNKIIISVLYTIVPFFNPAYICLRNKEVKEAFRKTVMGRCHYPRDVQD (SEQ ID
30 NO: 413).

- ATGAGAAATTTGAGTGGAGGCCATGTGCGAGGAGTTTGTCTTGGTGGGTTTCCCTACCACGC
CTCCCTCCAGCTGCTCCTCTTTGTCTTTTTTTTGAATTTACCTTCTGACATTGTTGGAGA
ATGCACTTATTGTCTTCACAATATGGCTTGCTCCAAGCCTTCATCGTCCCATGTACTTTTC
35 CTGGCCATCTCTCTTTCTGGAGCTATGGTACATCAATGTCACCATTCTCGGCTCTTGGC
AGCCTTTCTTACCAGGATGGTAGAGTCTCCTACGTAGGTTGCATGACCCAACTGTACTTC
TTTATTGCCTTAGCCTGTACTGAATGTGTGCTGTTGGCAGTTATGGCCTATGATCGCTACCT
GGCCATCTGTGGACCCCTCCTTTACCCTAGTCTCATGCCTTCCAGTCTGGCCACTCGCCTTG
CTGCTGCCTCTTGGGGCAGTGGCTTCTTCAGCTCCATGATGAAGCTTCTTTTATTTCCCAA
40 TTGCTCTACTGTGGACCCAACATTATCAACCACTTTTTCTGTGATATTTCCCACTACTCAA
CCTCACCTGCTCTGACAAGGAGCAAGCAGAGCTAGTAGACTTCCTTCTGGCCCTGGTGATG
ATTCTACTCCCTCTATTGGCTGTGGTTTCATCATACACTGCCATCATTGCAGCCATCCTGAG
GATCCCTACGTCCAGGGGACGCCACAAAGCCTTTTCCACTTGTGCCGCTCATCTGGCAGTG
GTTGTTATCTACTACTCTCCTCACTCTCTTCACTATGCACGGCCCCGGGCCATGTACACCTT
45 CAACCACAACAAGATTATCTCTGTGCTCTACACTATCATTGTACCATTCTTCAACCCAGCCA
TCTACTGCCTGAGGAACAAGGAGGTGAAGGAGGCCTTCAGGAAGACAGTGATGGGCAGAT
GTCACTATCCTAGGGATGTTTCAGGACTGA (SEQ ID NO: 414).

AOLFR222 sequences:

- 50 MGQTNVTSWRDFVFLGFSSSGELQLLLFALFLSLYLVTLSNVFIILAIRLDSHLHTPMYLFLSFL
SFSETCYTLGIIPRMLSLAGGDQAI SYVGCAAQMFSSASWACTNCFLLAAMGFDRYVAICAPL
HYASHMNP TLCAQLVITSFLTGYLFGLMTLVIFHLSFSSHEIQHFCDTPPVL SLACGDTGPS
ELRIFILSLVLLVSFFFTISYAYILAILRIPSAEGQKKAFTSCASHLTVVIIHYGCASFVYLRPK
ASYSLERDQLIAMTYTVVTPLLNPVYSLRTRAIQTALRNAFRGRLLGKG (SEQ ID NO: 415).

55

ATGGGGCAGACCAACGTAACCTCCTGGAGGGATTTTGTCTTCCTGGGCTTCTCCAGTTCTG
 GGGAGTTGCAGCTCCTTCTCTTTGCCTTGTCTCTCTGTATCTAGTCACTCTGACCAGC
 AATGTCTTCATTATCATAGCCATCAGGCTGGATAGCCATCTGCACACCCCATGTACCTCTT
 CCTTTCTCTCTATCCTTCTCTGAGACCTGCTACACTTTGGGCATCATCCCTAGAATGCTCT
 5 CTGGCCTGGCTGGGGGGGACCAGGCTATCTCCTATGTGGGCTGTGCTGCCAGATGTTCTT
 TTCTGCCTCATGGGCCTGTACTAACTGCTTCTTCTGGCTGCCATGGGCTTTGACAGATATG
 TGGCCATCTGTGCTCCACTCCACTATGCCAGCCACATGAATCCTACCCTCTGTGCCAGCT
 GGTCATTACTTCTTCTGACTGGATACCTCTTTGGACTGGGAATGACACTAGTTATTTTCC
 ACCTCTCATTTCTGCAGCTCCCATGAAATCCAGCACTTTTTTTGTGACACGCCACCTGTGCTG
 10 AGCCTAGCCTGTGGAGATACAGGCCCGAGTGAGCTGAGGATCTTTATCCTCAGTCTTTTGG
 TCCTCTTGGTCTCCTTCTTCTTCATCACCATCTCCTACGCCTACATCTTGGCAGCAATACTG
 AGGATCCCCTCTGCTGAGGGGCAGAAGAAGGCCCTTCTCCACTTGTGCCTCGCACCTTACAG
 TGGTCATTATTATTATGGCTGTGCTTCTTCTCGTGTACCTGAGGCCCAAAGCCAGCTACTCT
 CTTGAGAGAGATCAGCTTATTGCCATGACCTATACCTGTAGTGACCCCCCTCCTTAATCCCA
 15 TTGTTTATAGTCTAAGGACTAGGGCTATACAGACAGCTCTGAGGAATGCTTTCAGAGGGAG
 ATTGCTGGGTAAAGGATGA (SEQ ID NO: 416).

AOLFR223 sequences:

MEAANESSEGISFVLLGLTTPGQQRPLFVLFLLLYVASLLGNGLIVAAIQASPALHAPMYFLLA
 20 HLSFADLCFASVTVPKMLANLLAHDHSISLAGCLTQMYFFALGVTDSCLLAAMAYDCYVAIR
 HPLPYATRMSRAMCAALVGMALVSHVHSLLYILLMARLSFCASHQVPHFFCDHQPLRLRLSC
 SDTHIQLLIFTEGAADVVTPLLLASYGAIAAVLQLPSASGRRLRAVSTCGSHLAVVSLFYGT
 VIAVYFQATSREAEWGRVATVMYTVVTPMLNPIIYSLWNRDVQALRALLIGRRISASDS
 (SEQ ID NO: 417).

25 ATGGAGGCTGCCAATGAGTCTTCAGAGGGAATCTCATTGTTTTATTGGGACTGACAACAA
 GTCCTGGACAGCAGCGGCCTCTCTTTGTGCTGTTCTTGTCTTGTATGTGGCCAGCCTCCTG
 GGTAATGGACTCATTGTGGCTGCCATCCAGGCCAGTCCAGCCCTTCATGCACCCATGTACT
 TCCTGCTGGCCACCTGTCCTTTGCTGACCTCTGTTTCGCCTCCGTCACTGTGCCCAAGATG
 30 TTGGCCAACTTGTTGGCCCATGACCACTCCATCTCGCTGGCTGGCTGCCTGACCCAAATGT
 ACTTCTTCTTTGCCCTGGGGGTAAGTATAGCTGTCTTCTGGCGGCCATGGCCTATGACTG
 CTACGTGGCCATCCGGCACCCCTCCCCTATGCCACGAGGATGTCCCGGGCCATGTGCGCA
 GCCCTGGTGGGAATGGCATGGCTGGTGTCCACGTCCACTCCCTCCTGTATATCCTGCTCA
 TGGCTCGCTTGTCTTCTGTGCTTCCACCAAGTGCCCCACTTCTTCTGTGACCAACAGCCT
 35 CTCTTAAGGCTCTCGTGTCTGTACACCCACCATCCAGCTGCTCATCTTACCGAGGGCG
 CCGCAGTGGTGGTCACTCCCTTCTGCTCATCTCGCTCCTATGGGGCCATCGCAGCTGC
 CGTGCTCCAGCTGCCCTCAGCCTCTGGGAGGCTCCGGGCTGTGTCCACCTGTGGCTCCCAC
 CTGGCTGTGGTGAACCTCTTCTATGGGACAGTCATTGCAGTCTACTTCCAGGCCACATCCC
 GACGCGAGGCAGAGTGGGGCCGTGTGGCCACTGTATGTACACTGTAGTACCCCCATGC
 40 TGAACCCCATCATCTACAGCCTCTGGAATCGCGATGTACAGGGGGCACTCCGAGCCCTTCT
 CATTGGGCGAAGGATCTCAGCTAGTGACTCCTGA (SEQ ID NO: 418).

AOLFR224 sequences:

MGSFNSTSFEDGFILVGFSWDPQLEPILFVFIFYSLTFLGNTIIIALSWLDLRLHTPMYFFLSHL
 45 LDLCFTTSTVPQLLINLCGVDRITTRGGCVAQLFIYALGSTECVLLVVMADFDRYA AVCRPLHY
 MAIMHPLHCQTLAIAWSWAGFVNSLIQTGLAMAMPLCGHRLNHFFCEMPVFLKLACADTEGT
 EAKMFVARVIVVAVPAALILGSYVHIAHAVLRVKSTAGRRKAFGTGSHLLVVFLFYGSAIYT
 YLQSIHNYSEREGKFVALFYTIITPILNPLIYTLRNKDKGALWKVLWRGRDSG (SEQ ID NO:
 419).

50 ATGGGAAGTTTCAACACCAGTTTTGAAGATGGCTTCATTTTGGTGGGATTCTCAGATTGGC
 CGCAACTGGAGCCCATCCTGTTTGTCTTTATTTTATTTTCTACTCCCTAACTCTCTTTGGC
 AACACCATCATCATCGCTCTCTCCTGGCTAGACCTTCGGCTGCACACACCTATGTACTTCTT
 TCTCTCTCATCTGTCCCTCCTGGACCTCTGCTTCAACACCAGCACCGTGCCCCAGCTCCTGA
 55 TCAACCTTTGCGGGGTGGACCGCACCATCACCGTGGAGGGTGTGTGGCTCAGCTCAT
 CTACCTAGCCCTGGGCTCCACAGAGTGTGTGCTCCTGGTGGTGTGGCCTTTGACCGCTAT

GCTGCTGTCTGTGCTCCACTCCACTACATGGCCATCATGCACCCCCATCTCTGCCAGACCCCT
 GGCTATCGCCTCCTGGGGTGC GG GTTTCGTGAACCTCTCTGATCCAGACAGGTCTCGCAATG
 GCCATGCCTCTCTGTGGCCATCGACTGAATCACTTCTTCTGTGAGATGCCTGTATTTCTGAA
 GTTGGCTTGTGCGGACACAGAAGGAACAGAGGCCAAGATGTTTGTGGCCCGAGTCATAGT
 5 CGTGGCTGTTCTCTGCAGCACTTATTCTAGGCTCCTATGTGCACATTGCTCATGCAGTGCTG
 AGGGTGAAGTCAACGGCTGGGCGCAGAAAGGCTTTTGGGACTTGTGGGTCCCACCTCCTA
 GTAGTTTTCCTTTTTTATGGCTCAGCCATCTACACATATCTCCAATCCATCCACAATTATTC
 TGAGCGTGAGGGAAAATTTGTTGCCCTTTTTTATACTATAATTACCCCCATTTCTCAATCCTC
 TCATTTATACACTAAGAAACAAGGACGTGAAGGGGGCTCTGTGGAAAGTACTATGGAGGG
 10 GCAGGGACTCAGGGTAG (SEQ ID NO: 420).

AOLFR225 sequences:

MENYNQSTDFILLGLFPPSIDLFFFILIVFIFLMALIGNLSMILLIFLDTHLHTPMYFLLSQLSLID
 LNYISTIVPKMASDFLHGNKSISFTGCGIQSFFFLALGGAEALLASMA YDRYAICFPLHYLRM
 15 SKRVCVLMITGWSWIGSINACAHTVYVLHIPYCRSRRAINHFFCDVPAMVTLACMDTWVYEGTV
 FLSATIFLVFPFIGISCSYGQVLFVAVYHMKSAEGRKKAYLTCSTHLTVVTFYYAPFVYTYLRPRS
 LRSPTEDKVLAVFYTILTPMLNPIIYSLRNKEVMGALTRVSQRICSVKM (SEQ ID NO: 421).

ATGGA AAAATTACAATCAAACATCAACTGATTTTCATCTTATTGGGGCTGTTTCCACCATCAA
 20 TAATTGACCTTTTCTTCTTCTCATTCTCATTGTTTTTCATTTTCCTGATGGCTCTAATTGGAAACC
 TGTCCATGATTCTTCTCATCTTCTTGGACACCCATCTCCACACACCCATGTATTTCTACTG
 AGTCAGCTCTCCCTCATTGACCTAAATTACATCTCCACCATTTGTTCTAAGATGGCATCTGA
 TTTTCTGCATGGAAACAAGTCTATCTCCTTCACTGGGTGTGGGATTCAGAGTTTCTTCTTCT
 TGGCATTAGGAGGTGCAGAAGCACTACTTTTGGCATCTATGGCCTATGATCGTTACATTGC
 25 TATTTGCTTTCTCTCCACTATCTCATCCGCATGAGCAAAAGAGTGTGTGTGCTGATGATA
 ACAGGGTCTTGGATCATAGGCTCGATCAATGCTTGTGCTCACACTGTATATGTACTCCATA
 TTCCTTATTGCCGATCCAGGGCCATCAATCATTTCTTCTGTGATGTCCAGCAATGGTGACT
 CTGGCCTGCATGGACACCTGGGTCTATGAGGGCACAGTGT TTTTGAGTGCCACCATCTTTC
 TCGTGT TTTCCCTTCAATTGGTATTTTCATGTTCTCTATGGCCAGGTTCTCTTTGCTGTCTACCAC
 30 ATGAAATCTGCAGAAGGGAGGAAGAAAGCCTATTTGACCTGCAGCACCCACCTCACTGTA
 GTAAC TTTCTACTATGCACCTTTTGTCTACACTTATCTACGTCCAAGATCCCTGCGATCTCC
 AACAGAGGACAAGGTTCTGGCTGTCTTCTACACCATCCTCACCCCAATGCTCAACCCCATC
 ATCTATAGCCTGAGGAACAAGGAGGTGATGGGGGCCCTGACACGAGTGAGTCAGAGAATC
 TGCTCTGTGAAAATGTAG (SEQ ID NO: 422).

35

AOLFR226 sequences:

MEWRNHSGRVSEFVLLGFPAPAPLQVLLFALLLAYVLVTENTLIIMAIRNHSTLHKPMYFFL
 ANMSFLEIWYVTVTIPKMLAGFVGSQDHDGQLISFEGCMTQLYFFLGLGCTECVLLAVMAYD
 RYMAICYPLHYPVIVSGRLCVQMAAGSWAGGFGISMVKVFLISGLSYCGPNIINHFFCDVSPLL
 40 NLSCTDMSTAELTDFILAIFILLGPLSVTGASYVAITGAVMHISSAAGRYKAFSTCASHLTVVIF
 YAASIFIYARPKALS AFDTNKLVS VLYAVIVPLLNPIIYCLRNQEVKRALCCTLHLYQHQPDP
 KKASRNV (SEQ ID NO: 423).

ATGGAGTGGCGGAACCATAGTGGGAGAGTGAGTGAGTTTGTGTTGCTGGGCTTCCCTGCT
 45 CCTGCGCCACTACAGGTACTATTGTTTGCCCTTTTGCTGCTGGCCTATGTGTTGGTGCTGAC
 TGAGAACACACTCATCATTATGGCAATTAGGAACCATTTACCTCCACAAACCCATGTAC
 TTTTTCTAGCTAATATGTCCTTTCTGGAGATCTGGTATGTCACTGTCACTATTCCCAAGAT
 GCTTGCTGGCTTTGTTGGATCCAAACAGGATCATGGACAGCTAATCTCCTTTGAGGGATGC
 ATGACACAGCTCTACTTTTCTTGGCTTGGGCTGCACTGAGTGTGCTCTTCTCGTGTAT
 50 GGCCTATGATCGCTATATGGCCATCTGCTATCCTCTCCACTACCCAGTCATTGTCACTGGCC
 GGCTGTGTGTGCAGATGGCTGCTGGCTCTTGGGCTGGAGGTTTGGCATCTCCATGGTCAA
 AGTTTTTCTTATTTCTGGCCTCTCTTACTGTGGCCCCAACATCATCAACCACTTTTTCTGTG
 ATGTCTCTCCATTGCTCAACCTCTCATGCACTGATATGTCCACAGCAGAGCTTACAGATTTT
 ATCCTGGCCATTTTTATTCTTCTAGGGCCACTCTCTGTCACTGGGGCCTCCTATGTGGCCAT
 55 TACTGGTGTGTGATGCACATATCTCGGCTGCTGGACGCTATAAGGCCTTTTCCACCTGT
 GCCTCTCATCTCACTGTTGTGATAATCTTCTATGCAGCCAGTATCTTCATCTATGCTCGGCC

AAAGGCACTCTCAGCTTTTGACACCAACAAGTTGGTCTCTGTACTGTATGCTGTCATTGTA
CCATTGCTCAATCCCATCATTTACTGCCTGCGCAATCAAGAGGTCAAGAGAGCCCTATGCT
GTACTCTGCACCTGTACCAGCACCAGGATCCTGACCCCAAGAAAGCTAGCAGAAATGTATA
G (SEQ ID NO: 424).

5

AOLFR227 sequences:

MEPQNTSTVTNFQLLGFQNLLEWQALLFVIFLLIYCLTIIGNVVITTVVSQGLRLHSPMYMFLQH
LSFLEVWYTSTTVPLLLANLLSWGQAISFSACMAQLYFFVFLGATECFLLAFMAYDRYLAJCSF
LRYPFLMHRGLCARLVVSWCTGVSTGFLHSMMSRLDFCGRNQINHFFCDLPPLMQLSCSRV
YITEVTIFILSIAVLCICFFLTLPYVVFIVSSILRIPSTSGRRKTFSTCGSHLAVVTLYYGTMISMIV
CPSPHLLPEINKIISVFYTVVTPLLNPVIYSLRNKDFKEAVRKVMRRKCGILWSTSKRKF
LY (SEQ ID NO: 425).

10

ATGGAGCCCCAAAATACCTCCACTGTGACTAACTTTCAGCTGTTAGGATTCCAGAACCTTC
15 TTGAATGGCAGGCCCTGCTCTTTGTCAATTTTCTGCTCATCTACTGCCTGACCATTATAGGG
AATGTTGTATCATCACCCTGGTGAGCCAGGCCCTGCGACTGCACTCCCCTATGTACATGT
TCCTCCAGCATCTCTCCTTCTGGAGGTCTGGTACACGTCCACCACTGTGCCCTTCTCCTA
GCCAACCTGCTGTCTGGGGCCAAGCCATCTCCTTCTCTGCTGCATGGCACAGCTCTACT
TCTTCGTATTCTCGGCGCCACCGAGTGCTTTCTCCTGGCCTTCATGGCCTATGACCGTTAC
20 CTGGCCATCTGCAGCCCACTCCGCTACCCCTTTCTCATGCATCGTGGGCTATGTGCCAGGTT
GGTGGTGGTCTCATGGTGCACAGGGGTCAGCACAGGCTTTCTGCATTCCATGATGATTCC
AGGTTGGACTTCTGTGGGCGCAATCAGATTAACCATTTCTTCTGCGACCTCCCGCCACTCA
TGCAGCTCTCCTGTTCCAGAGTTTATATCACCGAGGTGACCATCTTCATCCTGTCAATTGCC
GTGCTGTGCATTTGTTTTTTCTGACACTGGGGCCCTATGTTTTTATTGTGTCTCCATATT
25 GAGAATCCCTTCCACCTCTGGCCGGAGAAAGACCTTTTCCACATGTGGCTCCCACCTGGCT
GTTGTCACTCTCTACTACGGGACCATGATCTCCATGTATGTGTGTCCCAGTCCCCACCTGTT
GCCTGAAATCAACAAGATCATTTCTGTCTCTACACTGTGGTACACCACTGCTGAACCCA
GTTATCTACAGCTTGAGGAACAAAGACTTCAAAGAAGCTGTTAGAAAGGTCATGAGAAGG
AAATGTGGTATTCTATGGAGTACAAGTAAAAGGAAGTTCCTTTATTAG (SEQ ID NO: 426).

30

AOLFR229 sequences:

MFYVNQIPFQLYHISFVYPTELWSRAIIPCMPTLSFWVCSATPVSPGFFALILLVFVTSIASNVVK
IILHIDSRLHTPMYFLLSQLSLRDILYISTIVPKMLVDQVMSQRAISFAGCTAQHFLYLTLAGAE
FFLLGLMSCDRYVAICNPLHYPDLMRSKICWLIVAAAWLGGSIDGFLLPVTMOPFPFCASREIN
35 HFFCEVPALLKLSCTDTSAYETAMYVCCIMMLLIPFSVISGSYTRILITVYRMSEABGRRKAVAT
CSSHMVVVSLFYGAAMYTYVLPHSYHTPEQDKAVSAFYTILTPMLNPLIYSLRNKDVGTALQK
VVGRCVSSGKVTTT (SEQ ID NO: 427).

35

ATGTTTTATGTAAATCAGATACCTTTCCAACCTTATCATATCTCTTTCTGTGACCTACAGA
40 GCTATGGAGCAGAGCAATTATTCCTGTATGCCGACTTTATCCTTCTGGGTTTGTTACGA
ACGCCCGTTTCCCCTGGCTTCTTTGCCCTCATTCTCCTGGTCTTTGTGACCTCCATAGCCAG
CAACGTGGTCAAGATCATTTCTATCCACATAGACTCCCGCCTCCACACCCCATGTACTTC
CTGCTCAGCCAGCTCTCCCTCAGGGACATCCTGTATATTTCCACCATTGTGCCCAAAATGCT
GGTCGACCAGGTGATGAGCCAGAGAGCCATTTCTTTGCTGGATGCACTGCCCAACACTTC
45 CTCTACTTGACCTTAGCAGGGGCTGAGTTCTTCTCCTAGGACTCATGTCTGTGATCGCTA
CGTAGCCATCTGCAACCCCTCTGCACTATCCTGACCTCATGAGCCGCAAGATCTGCTGGTTG
ATTGTGGCGCCAGCCTGGCTGGGAGGGTCTATCGATGGTTTCTTGCTCACCCTGTCACCA
TGCAAGTCCCCTTCTGTGCCTCTCGGGAGATCAACCACTTCTTCTGCGAGGTGCTGCCCTT
CTGAAGCTCTCCTGCACGGACACATCAGCCTACGAGACAGCCATGTATGTCTGCTGTATTA
50 TGATGCTCCTCATCCCTTTCTCTGTGATCTCGGGCTCTTACACAAGAATTCTCATTACTGTT
TATAGGATGAGCGAGGCAGAGGGGAGGCGAAAGGCTGTGGCCACCTGCTCCTCACACATG
GTGGTTGTGACCTCTTCTATGGGGCTGCCATGTACACATACGTGCTGCCTCATTCTTACCA
CACCCTGAGCAGGACAAAGCTGTATCTGCCTTCTACACCATCCTCACTCCCATGCTCAAT
CCAATCATTTACAGCCTTAGGAACAAGGATGTACAGGGGGCCCTACAGAAGGTTGTTGGG
55 AGGTGTGTGCTCCTCAGGAAAGGTAACCACTTTCTAA (SEQ ID NO: 428).

55

AOLFR230 sequences:

MGMEGLLQNSTNFVLTLGLTHPAFPGLLFAIVFSIFVVAITANLVMILLIHMD SRLHTPMYFLLS
 QLSIMDTTYICITVPKMLQDLLSKDKTISFLGCAVQIFLYLTLIGGEFFLLGLMAYDRYVAVCNP
 LRYPLLMNRRVCLFMVVGSWVVGSLDGFM LTPVTMSFFPCR SREINHFFCEIPAVLKL SCDTDS
 5 LYETLMYACCVLM LLLPLSVISVSYTHILLTVHRMNSAEGRRKAFATCSSHIMVVS VFYGA AFY
 TNVLPHSYHTPEKDKVVS AFYTILTPMLNPLIYSLRNKDVA AALRKVLGR CGSSQSIRVATVIR
 KG (SEQ ID NO: 429).

ATGGGCATGGAGGGTCTTCTCCAGAACTCCACTAACTTCGTCCTCACAGGCCTCATCACCC
 10 ATCCTGCCTTCCCCGGGCTTCTCTTTGCAATAGTCTTCTCCATCTTTGTGGTGGCTATAACA
 GCCAACTTGGTCATGATTCTGCTCATCCACATGGACTCCCGCCTCCACACACCCATGTACTT
 CTTGCTCAGCCAGCTCTCCATCATGGATACCATCTACATCTGTATCACTGTCCCCAAGATGC
 TCCAGGACCTCCTGTCCAAGGACAAGACCATTTCTTCTGCTGGGCTGTGCAGTTCAGATCTT
 CCTTACCTGACCCTGATTGGAGGGGAATTCTTCTGCTGGGTCTCATGGCCTATGACCGC
 15 TATGTGGCTGTGTGCAACCTCTACGGTACCCTCTCCTCATGAACCGCAGGGTTTGCTTATT
 CATGGTGGTCCGGCTCCTGGGTGGTGGTTCCTTGGATGGGTTCATGCTGACTCCTGTCACT
 ATGAGTTTCCCCTTCTGTAGATCCCGAGAGATCAATCACTTTTTCTGTGAGATCCCGAGCCGT
 GCTGAAGTTGTCTTGACACAGACACGTCACTCTATGAGACCTGATGTATGCCTGCTGCGTG
 CTGATGCTGCTTATCCCTCTATCTGTCTCTGTCTCCTACACGCACATCCTCCTGACTGT
 20 CCACAGGATGAACTCTGCTGAGGGCCGCGCAAAGCCTTTGCTACGTGTTCTCCACATT
 ATGGTGGTGAGCGTTTTCTACGGGGCAGCCTTCTACACCAACGTGCTGCCCCACTCCTACC
 AACTCCAGAGAAAGATAAAGTGGTGTCTGCCTTCTACACCATCCTACCCCCATGCTCAA
 CCCACTCATCTACAGCTTGAGGAATAAAGATGTGGCTGCAGCTCTGAGGAAAGTACTAGG
 GAGATGTGGTTCTCCAGAGCATCAGGGTGGCGACTGTGATCAGGAAGGGCTAG (SEQ ID
 25 NO: 430).

AOLFR231 sequences:

MERANHSVSEFILLGLSKSQNLQILFFLGFSVVFVGIVLGNLLILVTVTFD SILHTPMYFLLSNL
 SCIDMILASFATPKMIVDFLRERKTISWWGCYSQMFFMHLGGSEMMLLVAMAIDRYVAICKP
 30 LHYMTIMSPRVL TGLLLSSYAVGFVHSSQMAFM LTLPCGPNVIDSFFCDLPLV K LACKD TYI
 LQLLVIADSGLLSLVCFLLLVSYGVIFSVRYRAASRSSKAFSTLSAHITVVT LFFAPCVFIYVW
 PFSRYSVDKILSVFYTIFTPLLNPIYTLRNQEVKAAIKRLCI (SEQ ID NO: 431).

ATGGAAAGAGCAAACCATTCA GTGGTATCGGAATTTATTTTGTGGGACTTTCCAAATCTC
 35 AAAATCTTCAGATTTTATTCTTCTTGGGATTCTCTGTGGTCTTCGTGGGGATTGTGTTAGGA
 AACCTGCTCATCTTGGTGACTGTGACCTTTGATTGCTCCTTCACACACCAATGTATTTCT
 GCTTAGCAACCTCTCCTGCATTGATATGATCCTGGCTTCTTTTGTACCCCTAAGATGATTG
 TAGATTCTCCTCCGAGAACGTAAGACCATCATGTTGGGGATGTTATTCCAGATGTTCTT
 TATGCACCTCCTGGGTGGGAGTGAGATGATTGCTTGTAGCCATGGCAATAGACAGGTAT
 40 GTTGCCATATGCAAACCCCTCCATTACATGACCATCATGAGCCACGGGTGCTCACTGGGC
 TACTGTTATCCTCCTATGCAGTTGGATTTGTGCACTCATCTAGTCAAATGGCTTTTATGTTG
 ACTTTGCCCTTCTGTGGTCCCAATGTTATAGACAGCTTTTTCTGTGACCTTCCCCTTGTGAT
 TAAACTTGCTGCAAGGACACCTACATCCTACAGCTCCTGGTCATTGCTGACAGTGGGCTC
 CTGTCACTGGTCTGCTTCTCCTCTTGTCTCTCTATGGAGTCATAATATCTCAGTTAG
 45 GTACCGTGCTGCTAGTCGATCCTCTAAGGCTTCTCCACTCTCTCAGCTCACATCACAGTTG
 TGACTCTGTTCTTTGCTCCGTGTGTCTTTATCTACGTCTGGCCCTTCAGCAGATACTCGGTA
 GATAAAATTCTTTCTGTGTTTACACAATTTTACACCTCTCTTAAATCCTATTATTATAC
 ATTAAGAAATCAAGAGGTAAAGCAGCCATTAAAAAAGACTCTGCATATAA (SEQ ID NO:
 432).

50

AOLFR232 sequences:

MDNITWMASHTGWSDFILMGLFRQSKHPMANITWMANHTGWSDFILLGLFRQSKHPALLCV
 VIFVVFLMALSGNAVILLIHCD AHLHTPMYFFISQLSLMDMAYISVTPKMLLDQVMGVN KIS
 APEGCMQMFFYVTLAGSEFFLLATMAYDRYVAICHPLRYPVLMNHRVCLFLSSGCWFLGSVD
 55 GFTFTPTMTFPFRGSREIHFFCEVPAVLNLSCSDTSLYEIFMYLCCVLM LLLPVV ISSSYLLILL

TIHGMNSAEGRRKKAFATCSSHLTVVILFYGAAIYTYMLPSSYHTPEKDDMMVSVFYTILTPVVNP
LIYSLRNKDVGMALKKMLTVEPAFQKAME (SEQ ID NO: 433).

5 ATGGACAACATCACCTGGATGGCCAGCCACACTGGATGGTCGGATTTTCATCCTGATGGGAC
TCTTCAGACAATCCAAACATCCAATGGCCAATATCACCTGGATGGCCAACCACACTGGATG
GTCGGATTTTCATCCTGTTGGGACTCTTCAGACAATCCAAACATCCAGCACTACTTTGTGTG
GTCATTTTTGTGGTTTTCTGATGGCGTTGTCTGGAAATGCTGTCCTGATCCTTCTGATACA
CTGTGACGCCCCACCTCCACACCCCCATGTACTTTTTTCATCAGTCAATTGTCTCTCATGGACA
TGGCGTACATTTCTGTCACTGTGCCAAGATGCTCCTGGACCAGGTCATGGGTGTGAATAA
10 GATCTCAGCCCCGAGTGTGGGATGCAGATGTTCTTCTACGTGACACTAGCAGGTTTCAGAA
TTTTTCCTTCTAGCCACCATGGCCTATGACCGCTACGTGGCCATCTGCCATCCTCTCCGTTA
CCCTGTCTCATGAACCATAGGGTGTGTCTTCTCTGTCATCAGGCTGCTGGTTTCTGGGCT
CAGTGGATGGCTTCACATTCACCTCCCATCACCATGACCTTCCCCTTCCGTGGATCCCCGGA
GATTCATCATTTCTTCTGTGAAGTTCCTGCTGTATTGAATCTCTCCTGCTCAGACACCTCAC
15 TCTATGAGATTTTCATGTACTTGTGCTGTGTCCTCATGCTCCTCATCCCTGTGGTGATCATT
TCAAGCTCCTATTTACTCATCTCCTCACCATCCACGGGATGAACCTCAGCAGAGGGCCGGA
AAAAGGCCCTTTGCCACCTGCTCCTCCCACCTGACTGTGGTCATCCTCTTCTATGGGGCTGCC
ATCTACACCTACATGCTCCCCAGCTCCTACCACACCCCTGAGAAGGACATGATGGTATCTG
TCTTCTATACCATCCTCACTCCAGTGGTGAACCCCTTTAATCTATAGTCTTAGGAATAAGGAT
20 GTCATGGGGGCTCTGAAGAAAATGTAAACAGTGGAACTGCCTTTCAAAAAGCTATGGAG
TAG (SEQ ID NO: 434).

AOLFR233 sequences:

25 MANITRMANHTGKLDFFILMGLFRRSKHPALLSVVIFVFLKALSGNAVLILLIHCD AHLHSPMY
FFISQLSLMDMAYISVTVPKMLLDQVMGVNKVSAPECGMQMFLYLTLAGSEFFLLATMAYDR
YVAICHPLRYPVLMNHRVCLFLASGCWFLGSDGFMLTPITMSFPFCRSWEIHFFCEVPAVTI
LSCSDTSLYETLMYLCCVLMLLIPVTIHSYLLILLTVHRMNSAEGRRKKAFATCSSHLTVVILFY
GAAVYTYMLPSSYHTPEKDDMMVSVFYTILTPVLNPLIYSLRNKDVGMALKKMLTVRFVL
(SEQ ID NO: 435).
30 ATGGCCAACATCACCAGGATGGCCAACCACACTGGAAAGTTGGATTTTCATCCTCATGGGAC
TCTTCAGACGATCCAAACATCCAGCTCTACTTAGTGTGGTCATCTTTGTGGTTTTCTGAAG
GCGTTGTCTGGAAATGCTGTCCTGATCCTTCTGATACACTGTGACGCCCACCTCCACAGCC
CCATGTACTTTTTTCATCAGTCAATTGTCTCTCATGGACATGGCGTACATTTCTGTCACTGTG
35 CCAAGATGCTCCTGGACCAGGTCATGGGTGTGAATAAGGTCTCAGCCCCGAGTGTGGG
ATGCAGATGTTCTCTATCTGACACTAGCAGGTTTCGGAATTTTTCTTCTAGCCACCATGGC
CTATGACCGCTACGTGGCCATCTGCCATCCTCTCCGTTACCCTGTCTCATGAACCATAGG
GTCTGTCTTTTCTGGCATCGGGCTGTGGTTCTTGGGCTCAGTGGATGGCTTCATGCTCAC
TCCCACCATGAGCTTCCCCTTCTGCTGATCCTGGGAGATTCATCATTCTTCTGTGAAG
40 TCCCTGCTGTAAACGATCCTGTCTGCTCAGACACCTCACTCTATGAGACCCCTCATGTACCTA
TGCTGTGTCTCATGCTCCTCATCCCTGTGACGATCATTTCAGCTCCTATTTACTCATCCT
CCTCACCGTCCACAGGATGAACCTCAGCAGAGGGCCGGAAGGCCTTTGCCACCTGCTC
CTCCACCTGACTGTGGTCATCCTCTTCTATGGGGCTGCCGTCTACACCTACATGCTCCCCA
GCTCCTACCACACCCCTGAGAAGGACATGATGGTATCTGTCTTCTATACCATCCTCACTCC
45 GGTGCTGAACCCCTTTAATCTATAGTCTTAGGAATAAGGATGTCATGGGGGCTCTGAAGAAA
ATGTTAACTGTGAGATTCTGCTCTTAG (SEQ ID NO: 436).

AOLFR234 sequences:

50 MPNSTTVMEFLLMRFSDVWTLQILHSASFFMLYLVTLMGNILIVTVTCDSSLHMPMYFFLRN
LSILDACYISVTVPTSCVNSLLDSTTISKAGCVAQVFLVFFVYVELLFTMAHDRVAVACQPL
HYPVIVNSRICQMTLASLLSGLVYAGMHTGSTFQLPFCRSNVIHQFFCDIPSLLKLSCSDTFSNE
VMIVVSALGVGGGCFIFIRSYIHIFSTVLGFPRGADRTKAFSTCIPHILVVSFLSSCSSVYLRRP
AIPAATQDLILSGFYSIMPPLFNPIIYSLRNKQIKVAIKKIMKRIFYSENV (SEQ ID NO: 437).
55 ATGCCCAATTCAACCACCGTGATGGAATTTCTCCTCATGAGGTTTTCTGATGTGTGGACAC
TACAGATTTTACATTCTGCATCCTTCTTTATGTTGTATTTGGTAACTCTAATGGGAAACATC

CTCATTGTGACCGTCACCACCTGTGACAGCAGCCTTCACATGCCCATGTACTTCTTCCTCAG
 GAATCTGTCTATCTTGGATGCCTGCTACATTTCTGTTACAGTCCCTACCTCATGTGTCAATT
 CCTACTGGACAGCACCACCATTTCTAAGGCGGGATGTGTAGCTCAGGTCTTCCTCGTGGT
 TTTTTTGTATATGTGGAGCTTCTGTTTCTCACCATTATGGCTCATGACCGCTATGTGGCTG
 5 TCTGCCAGCCACTTCACTACCCTGTGATCGTGAACCTCTCGAATCTGCATCCAGATGACACT
 GGCTCCCTACTCAGTGGTCTTGTCTATGCAGGCATGCACACTGGCAGCACATTCCAGCTG
 CCCTTCTGTCCGTCCAACGTTATTCATCAATTCTTCTGTGACATCCCCTCTCTGCTGAAGCT
 CTCTTGCTCTGACACCTTCAGCAATGAGGTCATGATTGTTGTCTCTGCTCTGGGGGTAGGT
 GGCGGCTGTTTCATCTTTATCATCAGGTCTTACATTACATCTTTTCGACCGTGCTCGGGTT
 10 TCCAAGAGGAGCAGACAGAAACAAAGGCCTTTTCCACCTGCATCCCTCACATCCTGGTGGTG
 TCAGTCTTCTCAGTTCATGCTCTTCTGTGTACCTCAGGCCACCTGCGATACCTGCAGCCAC
 CCAGGATCTGATCCTTTCTGGTTTTTATTCCATAATGCCTCCCCTCTTTAACCTATTATTTA
 CAGTCTTAGAAATAAGCAAATAAAGGTGGCCATCAAGAAAATCATGAAGAGAATTTTTTA
 TTCAGAAAATGTGTAA (SEQ ID NO: 438).

15

AOLFR235 sequences:

MDGVNDSSLQGFVLMGISDHPQLEMIFFIALLFSYLLTLLGNSTHILLSRLEARLHTPMYFFLSNL
 SSLLAFATSSVPQMLINLWGPCKTISYGGCITQLYVFLWLGAECILLVVMADFDRYVAVCRPL
 RYTAIMNPQLCWLLAVIACLGGLGNSVIQSTFTLQLPLCGHRRVEGFLCEVPAMIKLACGDTSL
 20 NQAVLNGVCTFTFAVPLSIIVISYCLIAQAVLKIRSAEGRRKAFNTCLSHLLVFLFYGSASYGY
 LLPAKNSKQDQKFISLFYSLVTPMVNPLIYTLRNMEVKALRRLLGKGREVG (SEQ ID NO:
 439).

ATGGACGGGGTGAATGATAGCTCCTTGCAGGGCTTTGTTCTGATGGGCATATCAGACCATC
 25 CCCAGCTGGAGATGATCTTTTTTATAGCCATCCTCTTCTCCTATTTGCTGACCCTACTTGGG
 AACTCAACCATCATCTTGCTTTCCCGCTGGAGGCCCGGCTCCATACACCCATGTACTTCTT
 CCTCAGCAACCTCTCCTCCTTGGACCTTGCTTTCGCTACTAGTTCAGTCCCCCAAATGCTGA
 TCAATTTATGGGGACCAGGCAAGACCATCAGCTATGGTGGCTGCATAACCCAGCTCTATGT
 CTTCTTTGGCTGGGGGCCACCGAGTGCATCCTGCTGGTGGTGATGGCATTGACCGCTAC
 30 GTGGCAGTGTGCCGGCCCCCTCCGCTACACCGCCATCATGAACCCCAAGCTCTGCTGGCTGC
 TGGCTGTGATTGCCTGCCTGGGTGGCTTGGGCAACTCTGTGATCCAGTCAACATTCACTCT
 GCAGCTCCCATTTGTGTGGGCACCGGAGGGTGGAGGGATTCTCTGCGAGGTGCCTGCCAT
 GATCAAACTGGCCTGTGGCGACACAAGTCTCAACCAAGGCTGTGCTCAATGGTGTCTGCACC
 TTCTTCACTGCAGTCCCACTAAGCATCATCGTGATCTCCTACTGCCTCATTGCTCAGGCAGT
 35 GCTGAAAATCCGCTCTGCAGAGGGGAGGCGAAAGGCGTTCAATACGTGCCTCTCCCATCT
 GCTGGTGGTGTCTCTCTATGGCTCAGCCAGCTATGGGTATCTGCTTCCGCGCAAGAAC
 AGCAAAACAGGACCAGGGCAAGTTCATTTCCCTGTTCTACTCGTTGGTCACACCCATGGTGA
 ATCCCCTCATCTACACGCTGCGGAACATGGAAGTGAAGGGCGCACTGAGGAGGTTGCTGG
 GGAAAGGAAGAGAAGTTGGCTGA (SEQ ID NO: 440).

40

AOLFR236 sequences:

MTSQERDTAIYSINVSFVAKGMTSRVCEKMTMTTENPNQTVVSHFFLEGLRYTAKHSSLFFL
 LFLLIYSITVAGNLLILLTVGSDSHLSLPMYHFLGHLSDLACLSTVTPKVMAGLLTLDGKVIS
 FEGCAVQLYCFHFLASTECLYTVMAYDRYLAICQLHPVAMNRRMCAEMAGITWAIGATH
 45 AAIHTSLTFRLLYCGPCHIAFFCDIPPVLKLACTDTTINELVMLASIGIVAAGCLLIVISYIFIVA
 AVLRIRTAQGRQRAFSPCTAQLTGVLVYVPPVCYILQPRSSEAGAGAPAVFYTIVTPMLNPFY
 TLRNKEVKHALQRLLCSSFRESTAGSPPP (SEQ ID NO: 441).

ATGACATCTCAGGAAAGGGATACAGCTATTTATTCCATTAATGTCAAGTTTGTGCAAAGG
 50 GGATGACTAGCCGCTCTGTGTGTGAGAAGATGACCATGACAACGGAGAACCCCAACCAGA
 CTGTGGTGAGCCACTTCTTCTGGAGGGTTTGAGGTACACCGCTAAACATTCTAGCCTCTT
 CTTCCTCCTCTTCTCCTCATCTACAGCATCACTGTGGCTGGGAATCTCCTCATCCTCCTAA
 CTGTGGGCTCTGACTCTCAGCTCAGCTTACCACTGTACCACTTCTGGGGCAGCTCTCCTTC
 CTGGATGCCTGTTTGTCTACAGTGACAGTACCCCAAGGTCATGGCAGGCCTGCTGACTCTGG
 55 ATGGGAAGGTGATCTCCTTTGAGGGCTGTGCCGTACAGCTTTATTGCTTCCACTTTCTGGC
 CAGCACTGAGTGCTTCTGTACACAGTCATGGCCTATGACCGCTATCTGGCTATCTGTCAA

CCCCTGCACTACCCAGTGGCCATGAACAGAAGGATGTGTGCAGAAATGGCTGGAATCACC
 TGGGCCATAGGTGCCACGCACGCTGCAATCCACACCTCCCTCACCTTCCGCCTGCTCTACT
 GTGGGCCTTGCCACATTGCCTACTTCTTCTGCGACATACCCCCTGTCCTAAAGCTCGCCTGT
 ACAGACACCACCATTAAATGAGCTAGTCATGCTTGCCAGCATTGGCATCGTGGCTGCAGGCT
 5 GCCTCATCCTCATCGTTATTTCTACATCTTCATCGTGGCAGCTGTGTTGCGCATCCGCACA
 GCCCAGGGCCGCGCAGCGGGCCTTCTCCCCCTGCACTGCCAGCTCACTGGGGTGCTCCTGT
 ACTACGTGCCACCTGTCTGTATCTACCTGCAGCCTCGCTCCAGTGAGGCAGGAGCTGGGGC
 CCCTGCTGTCTTCTACACAATCGTAACTCCAATGCTCAACCCATTCAATTTACACTTTGCGGA
 ACAAGGAGGTGAAGCATGCTCTGCAAAGGCTTTTGTGCAGCAGCTTCCGAGAGTCTACAG
 10 CAGGCAGCCCACCCCATAG (SEQ ID NO: 442).

AOLFR237 sequences:

MDQRNYTRVKEFTFLGITQSRELSQVLFITFLVYMTTLMGNFLIMVTVTCEHLHTPMYFLL
 RNLSDICFSSITAPKVLIDLLSETKTISFSGCVTQMFFFHLLGGADVFSLSVMAFDRIYAIKPL
 15 HYMTMSRGRCTGLIVGFLGGGLVHSIAQISLLPLPVCNPNVLDTFYCDVPQVLKLACTDTFT
 LELLMISNGLVSWFVFFLLISYTVILMMLRSHTGEGRRKAISTCTSHITVVTLHFVPCIVVYA
 RPFALPTDAISVTFITVISPLNPIIYTLRNQEMKLMRKLKRRLGQSERILIQ (SEQ ID NO:
 443).

20 ATGGATCAGAGAAATTACACCAGAGTGAAAGAATTTACCTTCCTGGGAATTACTCAGTCCC
 GAGAACTGAGCCAGGTCTTATTTACCTTCCTGTTTTTGGTGTACATGACAACTCTAATGGG
 AAACCTCCTCATCATGGTTACAGTTACCTGTGAATCTCACCTTCATACGCCCATGTACTCC
 TGCTCCGCAACCTGTCTATTCTTGACATCTGCTTTTCTCCATCACAGCTCCTAAGGTCCTG
 ATAGATCTTCTATCAGAGACAAAAACCATCTCCTTCAGTGGCTGTGTCACTCAAATGTTCT
 25 TCTTCCACCTTCTGGGGGGAGCAGACGTTTTTCTCTCTGTGTATGGCGTTTGACCGCTAT
 ATAGCCATCTCCAAGCCCTGCACTATATGACCATCATGAGTAGGGGGCGATGCACAGGCC
 TCATCGTGGGCTTCCTGGGTGGGGGGCTGTCCACTCCATAGCGCAGATTTCTCTATTGCT
 CCCACTCCCTGTCTGTGGACCCAATGTTCTTGACACTTTCTACTGCGATGTCCCCCAGGTCC
 TCAAACCTTGCTGCACTGACACCTTCACTCTGGAGCTCCTGATGATTTCAAATAATGGGTT
 30 AGTCAGTTGGTTTGTATTCTTCTTCTCCTCATATCTTACACGGTCATCTTGATGATGCTGA
 GGTCTCACACTGGGGAAGGCAGGAGGAAAGCCATCTCCACCTGCACCTCCACATCACCG
 TGGTGACCCTGCATTTCTGTGCCCTGCATCTATGTCTATGCCCCGCCCTTCACTGCCCTCCC
 ACAGACACTGCCATCTCTGTACCTTCACTGTATCTCCCTTTGCTCAATCCTATAATTTA
 CACGCTGAGGAATCAGGAAATGAAGTTGGCCATGAGGAAACTGAAGAGACGGCTAGGAC
 35 AATCAGAAAGGATTTTAATTCAATAA (SEQ ID NO: 444).

AOLFR238 sequences:

MAPENFTRVTEFILTGVSSCPQLPLFLVFLVLYVLTLMAGNLGITLTSVDSRLQTPMYFFLRHL
 AIINLGNSTVIAPKMLMNFVKKKTTSFYECATQLGGFLFIVSEVMMLAVMAYDRYVAICNP
 40 LLYMVVVSRRCLLLVSLTYLYGFSTAIVVSPCIFSVSYCSSNIINHFCYDIAPLLALSCSDTYPE
 TTVFISAATNLFFSMITVLVSFNIIVLSILRIRSPEGRKKAFTSCASHMIAVTVFYGTMLFMYLQP
 QTNHSLDTDKMASVFYTLVIPMLNPLIYSLRNNDVNVALKKFMENPCYSFKSM (SEQ ID NO:
 445).

45 ATGGCTCCTGAAAATTTACCAGGGTCACTGAGTTTATTCTCACAGGTGTCTCTAGCTGTC
 CAGAGCTCCAGATTCCCCTCTTCTGGTCTTCTAGTGCTCTATGTGCTGACCATGGCAGG
 GAACCTGGGCATCATCACCTCACCAGTGTGACTCTCGACTTCAAACCCCATGTACTTTT
 TCCTGAGACATCTAGCTATCATCAATCTTGGCAACTCTACTGTCATTGCCCTAAAATGCTG
 ATGAACTTTTAGTAAAGAAGAAACTACCTCATTCTATGAATGTGCCACCAACTGGGAG
 50 GGTTCTTGTCTTTATTGTATCGGAGGTAATGATGCTGGCTGTGATGGCCTATGACCGCTA
 TGTGGCCATTTGTAACCTCTGCTCTACATGGTGGTGGTGTCTCGCGGGCTCTGCCTCCTGC
 TGGTGTCCCTCACGTACCTCTATGGCTTTTCTACAGCTATTGTGGTTTCACTTGTATATTC
 TCTGTGCTTATGCTCTTCTAATATAATCAATCATTTTTACTGTGATATTGCACCTCTGTT
 AGCATTATCTTGTCTGTATACCTACATACCAAGAAACAATAGTCTTTATATCTGCAGCAACA
 55 AATTTGTTTTTTTCCATGATTACAGTTCTAGTATCTTATTTCAATATTGTTTTGTCCATTCTA
 AGGATACGTTTACCAGAAGGAAGGAAAAAGCCTTTTCCACCTGCGCTTCGCATATGATA

GCAGTCACGGTTTTCTATGGGACAATGCTATTTATGTATTTGCAGCCCCAAACCAACCACT
 CACTGGATACTGATAAGATGGCTTCTGTGTTTTACACATTGGTGATTCTATGCTGAATCC
 CTTGATCTACAGCCTGAGGAATAATGATGTAAATGTTGCCTTAAAGAAATTCATGGAAAAAT
 CCATGTTACTCCTTTAAATCAATGTAA (SEQ ID NO: 446).

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AOLFR239 sequences:

MDPQNYSLVSEFVLHGLCTSRHLQNFFFIFFGVYVAIMLGNLLLVTVISDPCLHSSPMYFLLG
 NLAFLDMWLASFATPKMIRDFLSDQKLISFGGCMQAIFLHFTGGAEMVLLVSMAYDRYVAIC
 KPLHYMTLMSWQT CIRLVLASWVVG FVHSISQVAFVNL PYCGPNEVDSFFCDLPLVIKLACM
 10 DTYVLGHMISDSGLLSLSCFLLLISYTVILLAIRQRAAGSTSKALSTCSAHIMVVTLFFGPCIFV
 YVRPFSRFSVDKLLSVFYTIFTPLLNPIIYTLRNEEMKAAMKKLQNRRTVFQ (SEQ ID NO: 447).

ATGGACCCACAGAACTATTCCTTGGTGTCAGAAATTTGTGTTGCATGGACTCTGCACTTCAC
 GACATCTTCAAAAATTTTTCTTTATATTTTTCTTTGGGGTCTATGTGGCCATTATGCTGGGT
 15 AACCTTCTCATTTTGGTCACTGTAATTTCTGATCCCTGCCTGCACTCCTCCCTATGTACTT
 CCTGCTGGGGAACCTAGCTTTCCTGGACATGTGGCTGGCCTCATTGCCACTCCCAAGATG
 ATCAGGGATTTCCTTAGTGATCAAAAACCTCATCTCCTTTGGAGGATGTATGGCTCAAATCT
 TCTTCTGCACTTTACTGGTGGGGCTGAGATGGTGCTCCTGGTTTCCATGGCCTATGACAG
 ATATGTGGCCATATGCAAACCTTGCATTACATGACTTTGATGAGTTGGCAGACTTGCATC
 20 AGGCTGGTGCTGGCTTCATGGGTGCTTGGATTTGTGCACTCCATCAGTCAAGTGGCTTTCA
 CTGTAAATTTGCCTTACTGTGGCCCCAATGAGGTAGACAGCTTCTTCTGTGACCTCCCTCTG
 GTGATCAAACTTGCCCTGCATGGACACCTATGTCTTGGGTATAATTATGATCTCAGACAGTG
 GGTGCTTTTCTTGAGCTGTTTTCTGCTCCTCCTGATCTCCTACACCGTGATCCTCCTCGCT
 ATCAGACAGCGTGCTGCCGGTAGCACATCCAAAGCACTCTCCACTTGCTCTGCACATATCA
 25 TGGTAGTGACGCTGTTCTTTGGCCCTTGCAATTTTTGTTTATGTGCGGCCTTTCAGTAGGTTT
 TCTGTGGACAAGCTGCTGTCTGTGTTTTATACCATTTTTACTCCACTCCTGAACCCCATAT
 CTACACATTGAGAAATGAGGAGATGAAAGCAGCTATGAAGAACTGCAAAACCGACGGGT
 GACTTTTCAATGA (SEQ ID NO: 448).

30 **AOLFR240 sequences:**

MAGENHTTLPEFLLLGFSDLKALQGPLFWVVLVYLVTLGNLIILLTQVSPALHSPMYFFLR
 QLSVVELFYTTDIVPRTLNLGSPHPQAISFQGCQAQMYVFIVLGISECCLLTAMAYDRYVAIC
 QPLRYSTLLSPRACLAMVGSSWLTGIIATTHASLIFSLPFRSHPIIPHFLCDILPVLRLASAGKHR
 SEISVMTATIVFIMPFSILVTSYRILGAILAMASTQSRRKVFSTCSSHLLVVSLEFFGTASITYRQP
 35 AGSSVTTDRVLSLFYTVIIPMLNPIIYTLRNDVRRALRHLVKRQRPS (SEQ ID NO: 449).

ATGGCTGGGGAAAACCATACTACACTGCCTGAATTCCTCCTTCTGGGATTCTCTGACCTCA
 AGGCCCTGCAGGGCCCCCTGTTCTGGGTGGTGCTTCTGGTCTACCTGGTCACCTTGCTGGG
 40 TAACTCCCTGATCATCCTCCTCACACAGGTCAGCCCTGCCCTGCACTCCCCCATGTACTTCT
 TCCTGCGCCAACTCTCAGTGGTGGAGCTCTTCTACACCACTGACATCGTGCCAGGACCT
 GGCCAACTCTGGGCTCCCCGCATCCCCAGGCCATCTCTTCCAGGGCTGTGCAGCCCAGATG
 TACGTCTTCATTGTCCTGGGCATCTCGGAGTGCTGCTGCTCACGGCCATGGCCTATGACC
 GATATGTTGCCATCTGCCAGCCCCCTACGCTATTCCACCCTCTTGAGCCCACGGGCTGCTT
 GGCCATGGTGGGGTCTCCTGGCTCACAGGCATCATCACGGCCACCACCCATGCCTCCCTC
 45 ATCTTCTCTCTACCTTTTCGCAGCCACCCGATCATCCCGCACTTTCTCTGTGACATCCTGCC
 AGTACTGAGGCTGGCAAGTGCTGGGAAGCACAGGAGCGAGATCTCCGTGATGACAGCCAC
 CATAGTCTTCATTATGATCCCCCTTCTCTCTGATTGTCACTCTTACATCCGCATCCTGGGTG
 CCATCCTAGCAATGGCCTCCACCCAGAGCCGCCGCAAGGTCTTCTCCACCTGCTCCTCCCA
 TCTGCTCGTGGTCTCTCTCTTTTGAACAGCCAGCATCACCTACATCCGGCCGCGAGGCA
 50 GGCTCCTCTGTTACCACAGACCGCGTCTCAGTCTCTTCTACACAGTCATCACACCCATGCT
 CAACCCCATCATCTACACCTTCGGAACAAGGACGTGAGGAGGGCCCTGCGACACTTGGT -
 GAAGAGGCAGCGCCCTCACCTGA (SEQ ID NO: 450).

AOLFR241 sequences:

MPQILFTYLNMFYFFPPLQLAENLTMVTEFLLLGFSGLGEIQLALFVVFLLYLVLSGNVTHIS
 55 VIHLDKSLHTPMYFFLGILSTSETFYTFVILPKMLINLLSVARTISFNCCALQMFFFLGFAITNCLL

LGVMGYDRYAAICHPLHYPTLMSWQVCGKLAACAIGGFLASLTVVNLVFSLPFCSANKVNH
YFCDISAVILLACTNTDVNEFVIFCGVLVLPFLFICVSYLCILRTLKIPSAEGRRKAFSTCAS
HLSVVIVHYGCASFYLRPTANYVSNKDRLVTVTYTIVTPLLNPMVYSLRNKDVQLAIRKVLG
KKGSLKLYN (SEQ ID NO: 451).

5 ATGCCCCAAATTCTTATATTCACATACCTGAATATGTTTTACTTCTTTCCCCCTTTGCAGAT
CTTGGCAGAAAACCTCACCATGGTCACCGAATTCCTGTTGCTGGGTTTTTCCAGCCCTGGT
GAAATTCAGCTGGCCCTCTTTGTAGTTTTCTTTTTCTGTATCTAGTCATTCTTAGTGGCAA
10 TGTCACCATTATCAGTGTACATCCACCTGGATAAAAGCCTCCACACACCAATGTACTTCTTCC
TTGGCATTCTCTCAACATCTGAGACCTTCTACACCTTTGTCAATTCTACCCAAGATGCTCATC
AATCTACTTTCTGTGGCCAGGACAATCTCCTTCAACTGTTGTGCTCTTCAAATGTTCTTCTT
CCTTGGTTTTGCCATTACCAACTGCCTGCTATTGGGTGTGATGGGTTATGATCGCTATGCTG
CCATTTGTCAACCTCTGCATTACCCCACTCTTATGAGCTGGCAGGTGTGTGGAAAACCTGGC
15 AGCTGCCTGTGCAATTGGTGGCTTCTTGGCCTCTCTTACAGTAGTAAATTTAGTTTTAGCC
TCCCTTTTTGTAGCGCCAACAAAGTCAATCATTACTTCTGTGACATCTCAGCAGTCATTCTT
CTGGCTGTACCAACACAGATGTTAACGAATTTGTGATATTCATTGTGGAGTTCTTGTAC
TTGTGGTTCCCTTTCTGTTTATCTGTGTTTCTTATCTCTGCATTCTGAGGACTATCCTGAAG
ATTCCCTCAGCTGAGGGCAGACGAAAGCGTTTTCCACCTGCGCCTCTCACCTCAGTGTG
TTATTGTTCAATTATGGCTGTGCTTCTTCTATCTACCTGAGGCCTACAGCAAACTATGTGTCC
20 AACAAAGACAGGCTGGTGACGGTGACATACAGATTGTCACTCCATTACTAAACCCCATG
GTTTATAGCCTCAGAAACAAGGATGTCCAACCTGCTATCAGAAAAGTGTGGGCAAGAAA
GGTCTCTAAAACTATATAATTGA (SEQ ID NO: 452).

AOLFR242 sequences:

25 MNTTLFHPYSFLLLGPGLSMHLWVGPFPAVFLTAVLGNITLFVIQTDSSLHHPMFYFLAILS
SIDPGLSTSTIPKMLGTFWFTLREISFEGCLTQMFFIHLCTGMESAVLVAMAYDCYVAICDPLCY
TLVLTNKVVSVMALAIPLRPLVFVIPFVLFILRLPFCGHQIIPHTYGEHMGILRLSCASIRVNIY
LCAISILVFDIIAIVISYVQILCAVFLSSHARLKAFSTCGSHVCVMLTFYMPAFFSFMTHFRGR
NIPHFIIHLLANFYVVIPALNSVIYGVRTKQIRAQVLKMFFNK (SEQ ID NO: 453).

30 ATGAATACCACTCTATTTTCATCCTTACTCTTTCCTTCTTCTGGGAATTCCTGGGCTGGAAAG
TATGCATCTCTGGGTTGGTTTTCTTCTTCTTCTGCTGTGTTCTGACAGCTGTCCTTGGGAATA
TCACCATCCTTTTGTGATTCAGACTGACAGTAGTCTCCATCATCCCATGTTCTACTTCTCTG
GCCATTCTGTCACTATTGACCCGGGCCTGTCTACATCCACCATCCCTAAAAATGCTTGGCAC
35 CTTCTGGTTTACCCTGAGAGAAATCTCCTTTGAAGGATGCCTTACCCAGATGTTCTTTCATCC
ACCTGTGCACTGGCATGGAATCAGCTGTGCTTGTGGCCATGGCCTATGATTGCTATGTGGC
CATCTGTGACCCCTTTTGTCTACACGTTGGTGCTGACAAACAAGGTGGTGTCAAGTTATGGCA
CTGGCCATCTTTCTGAGACCCCTTAGTCTTTGTCTATACCCTTTGTTCTATTTATCCTAAGGCT
TCCATTTTGTGGACACCAAATTATTCCTCATACTTATGGTGAGCACATGGGCATTGCCCGC
40 CTGTCTGTGCCAGCATCAGGGTTAACATCATCTATGGCTTATGTGCCATCTCTATCCTGGT
CTTTGACATCATAGCAATTGTCAATTTCTATGTACAGATCCTTTGTGCTGTATTTCTACTCT
CTTCACATGATGCACGACTCAAGGCATTACAGCACCTGTGGCTCTCATGTGTGTGTCATGTT
GACTTTCTATATGCCTGCATTTTTCTCATTATGACCCATAGGTTTGGTCGGAATATACCTC
ACTTTATCCACATTCTTCTGGCTAATTTCTATGTAGTCATTCCACCTGCTCTCAACTCTGTA
45 ATTTATGGTGTGAGAACCAACAGATTAGAGCACAAAGTGCTGAAAATGTTTTCAATAAA
AA (SEQ ID NO: 454).

AOLFR243 sequences:

MEQVNKTVVREFVVLGFSSRLRLQQLLFVIFLLLYLFTLGTNAIISTIVLDRALHTPMYFFLAIL
50 SCSEICYTFVIVPKMLVDLLSQKKTISFLGCAIQMFSFLFFGSSHSFLLAAMGYDRYMAICNPLR
YSVLMGHGVCMLMAAACACGFTVSLVTTSLVFHLPFHSSNQLHFFCDISPVLKLASQHSF
SQLVIFMLGVFALVIPLLLVSYRIISAILKIPSSVGRYKTFSTCASHLIVTVHYSCASFYLRPK
TNYTSSQDILISVSYTILTPLFNPMIYSLRNKEFKSALRRRTIGQTFYPLS (SEQ ID NO: 455).

55 ATGGAGCAAGTCAATAAGACTGTGGTGAGAGAGTTCGTCGTCCTCGGCTTCTCATCCCTGG
CCAGGCTGCAGCAGCTGCTCTTGTATCTTCTGCTCCTCTACCTGTTCACTCTGGGCACC

AATGCAATCATCATTTCCACCATTTGTGCTGGACAGAGCCCTTCATACTCCCATGTACTTCTT
 CCTTGCCATCCTTTCTTGCTCTGAGATTTGCTATACCTTTGTCAATTGTACCAAGATGCTGG
 TTGACCTGCTGTCCAGAAGAAGACCATTTCTTTCTGGGCTGTGCCATCCAAATGTTTTCC
 TTCCTCTTCTTTGGCTCCTCTCACTCCTTCTGCTGGCAGCCATGGGCTATGATCGCTATAT
 5 GGCCATCTGTAAACCACTGCGCTACTCAGTGCTCATGGGACATGGGGTGTGTATGGGACTA
 ATGGCTGCTGCCTGTGCCTGTGGCTTCACTGTCTCCCTGGTCACCACCTCCCTAGTATTTCA
 TCTGCCCTTCCACTCCTCCAACCAGCTCCATCACTTCTTCTGTGACATCTCCCTGTCTTA
 AACTGGCATCTCAGCACTCCGGCTTCAGTCAGCTGGTCATATTCATGCTTGGTGTATTTGC
 CTTGGTCATTCTCTGCTACTTATCTAGTCTCTACATCCGCATCATCTCTGCCATTCTAA
 10 AAATCCCTTCCCTCGTTGGAAGATACAAGACCTTCTCCACCTGTGCCTCCCATCTCATTGTG
 GTAACCTGTTCACTACAGTTGTGCCTCTTTCATCTACTTAAGGCCCAAGACTAATTACACTTC
 AAGCCAAGACACCCTAATATCTGTGTACATACCATCCTTACCCCATTTGTTCAATCCAATG
 ATTTATAGTCTGAGAAATAAGGAATTCAAATCAGCCCTACGAAGAACAATCGGCCAACT
 TTCTATCCTCTTAGTTAA (SEQ ID NO: 456).

15

AOLFR244 sequences:

MWQEYFYFLNVFFPLKVCCLTINSHVILLPWECYHLIWKILPYIGTTVGSMEEYNTSSTDFTF
 MGLFNRKETSGLFAIHSIIFFTALMANGVMIFLIQTDRLHTPMYFLLSHLSLIDMMYISTIVPKM
 LVNYLLDQRTISFVGCTAQHFLYTLVGAEFFLLGLMAYDRYVAICNPLRYPVLMSSRRVCWMI
 20 IAGSWFGGSLDGFLLPITMSFPFCNSREINHFFCEAPAVLKLACADTALYETVMYVCCVLMML
 IPFSVVLASYARILTTVQCMSSVEGRKKAFATCSSHMTTVVSLFYGAAMYTYMLPHSYHKPAQ
 DKVLSVFYITLTPMLNPLIYSLRNKDVGTALKRALGRFKGPQRVSGGVF (SEQ ID NO: 457).

25

ATGTGGCAAGAATACTATTTTTTAAATGTTTTCTTCCCACTTTTAAAAGTTTGCTGCCTAAC
 AATTAATTCACATGTTGTTATTTTACTGCCCTGGGAATGCTATCATCTTATTTGGAAGATAT
 TACCTTATATCGGCACAACCTGTAGGATCAATGGAAGAGTACAACACATCCTCTACAGACTT
 CACTTTCATGGGGCTGTTCAACAGAAAGGAAACCTCAGGTCTTATTTTTGCCATCATCTCT
 ATCATCTTCTTCAACCGCACTGATGGCCAATGGGGTTATGATCTTCTGATCCAAACAGATT
 TGCGCCTTCATACACCCATGTACTTCTCCTCAGCCACCTTCTCTTAATTGACATGATGTAT
 30 ATTTCCACTATTGTGCCTAAGATGCTGGTTAATTACCTGCTGGATCAAAGGACCATTTCTT
 TGTGGGGTGCACAGCTCAACACTTCTCTACCTTACCCTTGTGGGAGCTGAATTCTTCTCTG
 CTGGGCCTCATGGCCTATGACCGCTATGTGGCCATTGCAACCCCTCTGAGATACCCCTGTCC
 TCATGAGCCGCGGGTCTGTTGGATGATTATAGCAGGTTCTGTTTGGGGGCTCTTTGGA
 TGGCTTCTCTCTAACCCCATCACCATGAGCTTCTCTTCTGCAATTCCCGGGAGATTAACC
 35 ACTTCTTCTGTGAGGCACCAGCAGTCTGAAGTTGGCATGTGCAGACACAGCCCTCTACGA
 GACAGTGATGTATGTGTGCTGTGTTTGTGCTGCTGATTCTTCTCTGTAGTCTTGTCTT
 CCTATGCCCCGAATCCTGACTACAGTTCAGTGATGAGCTCAGTGGAGGGCAGGAAGAAGG
 CATTTGCCACTTGCTCATCCCATGACTGTGGTGTCTTGTCTACGGGGGCTGCCATGTAC
 ACCTACATGCTGCCACATTCTTACCACAAGCCAGCCAGGACAAAGTCTCTCTGTGTTTT
 40 ACACCATTCTCACACCCATGCTGAACCCCTCATCTACAGCCTTAGAAACAAGGATGTGAC
 TGGAGCTCTGAAGAGGGCCTTGGGGAGGTTCAAGGGTCTCAAAGGGTGTGAGGAGGTGT
 CTTTTGA (SEQ ID NO: 458).

AOLFR245 sequences:

MDLKNGLSVTEFILLGFFGRWELQIFFVTFSLIYGATVMGNILIMVTVTCRSTLHSPLYFLLGN
 LSFLDMCLSTATTPKMIIDLLTDHKTISVWGCVTQMFFMHFFGGAEMTLLIIMAFDRYVAICKP
 LHYRTIMSHKLLKGFAILSWIIGFLHSISQIVLTMNLPFCGHNVINNIFCDLPLVIKLACIETYTLE
 LFVIADSGLLSFTCFILLVSYIVILVSPKKSSHGLSKALSTLSAHIIIVTLFFGPCIFYVWPFSLL
 50 ASNKTLAVFYTVITPLLNPSTYTLRNKKMQEAIKRLRFQYVSSAQNF (SEQ ID NO: 459).

55

ATGGATCTTAAAAATGGATCTCTAGTGACCGAGTTTATTTTACTAGGATTTTTTGGACGAT
 GGGAACCTTCAAATTTTCTTCTTTGTGACATTTTCCCTGATCTACGGTGCTACTGTGATGGGA
 AACATTCTCATTATGGTCACAGTGACATGTAGGTCAACCCCTTCTTCTCCCTGTACTTTCT
 CCTTGAAATCTCTCTTTTTTGGACATGTGTCTCTCCACTGCCACAACACCAAGATGATCA
 TAGATTTGCTCACTGACCACAAGACCATCTCTGTGTGGGGCTGCGTGACCCAGATGTTCTT
 CATGCACTTCTTTGGGGGTGCTGAGATGACTCTTCTGATAATCATGGCCTTTGACAGGTAT

GTAGCCATATGTAAACCCCTGCACTATAGGACAATCATGAGCCACAAGCTGCTAAAGGGG
 TTTGCGATACTTTTCATGGATAATTGGTTTTTACACTCCATAAGCCAGATAGTTTTAAACAAT
 GAACCTTGCCTTTCTGTGGCCACAATGTCATAAAACAACATATTTTGTGATCTTCCCCTTGTGA
 TCAAGCTTGGCTTGCATTGAAACATACACCTGGAATTATTTGTCATTGCTGACAGCGGGCT
 5 GCTCTCTTTACCTGTTTCATCCTCTTGCTTGTTCCTTACATTGTCATCCTGGTCAGTGTACC
 AAAAAAATCATCACATGGGCTCTCCAAGGCGCTGTCCACATTGTCTGCCACATCATTGTG
 GTCACCTCTGTTCTTGGACCTTGTATTTTATCTATGTTTGGCCATTGATAGTTTGGCAAG
 CAATAAAACTCTTGGCGTATTTTATACAGTTATCACACCCTTACTGAATCCGAGTATTTATA
 10 CCTGAGAAATAAGAAAATGCAAGAGGCCATAAGAAAATTACGGTTCCAATATGTTAGTT
 CTGCACAGAATTTCTAG (SEQ ID NO: 460).

AOLFR246 sequences:

MSPENQSSVSEFLLLGLPIRPEQQA VFFTLFLGMYLTTVLGNLLIMLLIQLDShLHTPMYFFLSH
 LALTDISFSSVTPKMLMDMRKYKSYLYEBCISQMYFFIFFDLDSFLITSMAYDRYVAICHPL
 15 HYTVIMREELCVFLVAVSWILSCASSLSHTLLRLSFCANTIPHVFCDLAALLKLSCSDIFLNE
 LVMFTVGVVVITLPMCLVSYGYIGATILRVPSTKGIHKALSTCGSHLSVVSLLYGSIFGQYLF
 PTVSSSIDKDVIVALMYTVVTPMLNPFYSLRNRDMKEALGKLFSRATFFSW (SEQ ID NO:
 461).

ATGAGCCCTGAGAACCAGAGCAGCGTGTCCGAGTTCCTCCTTCTGGGCCTCCCCATCCGGC
 CAGAGCAGCAGGCTGTGTTCTTACCCTGTTCTGGGCATGTACCTGACCACGGTGTCTGGG
 GAACCTGCTCATCATGCTGCTCATCCAGCTGGACTCTACCTTACACCCCCATGTACTTCT
 TCCTCAGCCACTGGCTCTCACTGACATCTCCTTTTCATCTGCTCACTGTCCCTAAGATGCTG
 ATGGACATGCGGACTAAGTACAAATCGATCCTCTATGAGGAATGCATTTCTCAGATGTATT
 25 TTTTATAATTTTACTGACCTGGACAGCTTCCTTATTACATCAATGGCATATGACCGATAT
 GTTGCCATATGTCACCCTCTCCACTACACTGTCATCATGAGGGAAGAGCTCTGTGTCTTCTT
 AGTGGCTGTATCTTGGATTCTGTCTTGTGCCAGCTCCCTCTCTCACACCCTTCTCCTGACCC
 GGCTGTCTTTCTGTGCTGCGAACACCATCCCCATGTCTTCTGTGACCTTGTGCCCCTGCTC
 AAGCTGTCTGCTCAGATATCTTCTCAATGAGCTGGTCATGTTACAGTAGGGGTGGTGG
 30 TCATTACCTGCCATTATGTGTATCCTGGTATCATATGGCTACATTGGGGCCACCATCCTG
 AGGGTCCCTTCAACCAAAGGGATCCACAAAGCATTGTCCACATGTGGCTCCCATCTCTCTG
 TGGTGTCTCTATTATGGGTCAATATTTGGCCAGTACCTTTTCCCGACTGTAAGCAGTCTCT
 ATTGACAAGGATGTCAATTGTGGCTCTCATGTACACGGTGGTACACCCATGTTGAACCCCT
 TTATCTACAGCCTTAGGAACAGGGCATGAAAGARGCCCTTGGGAAACTCTTCACTAGAG
 35 CAACATTTTCTCCTTGGTGACATCTGACTTTTTTAAAAAATTAG (SEQ ID NO: 462).

AOLFR247 sequences:

MGQHNLTVLTEFILMELTRPELQIPLFGVFLVYILITVVGNLTMILTKLDSHLHTPMYFSIRHL
 ASVDLGNSTVICPKVLANFVVDRNTISYYACAAQLAFLMFISEFFLSAMAYDRYVAICNPILL
 40 YYVIMSQRLLCHVLVGIQYLYSTFQALMFTIKIFLTFCGSNVISHFYCDDVPLLPMLCSNAQEIE
 LLSILFSVFNLISSFLIVLSYMLILLAICQMHSABGRKKAFSTCGSHLTVVVVFYGSLLFMYMQ
 PNSTHFFDTDKMASVFYTLVIPMLNPLIYSLRNEEVKNIFYKLFEN (SEQ ID NO: 463).

ATGGGCCAACACAATCTAACAGTGCTAACTGAATTCATTCTGATGGAACCTACAAGGCGGC
 45 CTGAGCTGCAGATTCCCCTTTTTGGAGTCTTCTCGTCATCTACCTAATCACAGTGGTGGGC
 AACCTAACTATGATCATTTTGACCAAAGTGGACTCCCACTTACATACACCTATGTACTTTTC
 TATCAGACATTTGGCTTCTGTTGATCTTGGTAATTCTACTGTCAATTTGTCCCAAGGTGCTGG
 CAAATTTTGTGTGGATCGAAATACTATTTCCTATTATGCATGTGCTGCACAGCTGGCATTCT
 TTCCTTATGTTTATTATCAGTGAATTTTTCATCCTGTCAGCCATGGCCTATGACCGCTATGT
 50 GGCCATTTGTAACCCCTCTGCTCTATTATGTTATTATGTCTCAGCGACTGTGTCATGTACTGG
 TGGGCATTCAATATCTCTACAGCACATTTAGGCTCTGATGTTCACTATTAAGATTTTACA
 TTGACCTTCTGTGGCTCTAATGTGTCATCAGTCATTTTACTGTGATGATGTTCTCTTGTCTACC
 TATGCTTTGCTCAAATGCACAGGAAATAGAATTGTTGAGCATACTATTTTCTGTATTTAATT
 TGATCTCCTCTTCTGATAGTCTTAGTGTCTACATGTTGATTTTGTAGCTATATGTCAA
 55 ATGCATTCTGCAGAGGGCAGGAAAAAGGCTTTCTCCACATGTGGTTCCCATTGACAGTGG
 TGGTTGTGTTCTATGGGTCTCTACTCTTCATGTACATGCAGCCCAATCCCACTCACTTCTTT

GATACTGATAAAATGGCTTCTGTGTTTTACACTTTAGTAATCCCCATGCTTAACCCCTTTGAT
TTACAGCTTAAGAAACGAAGAGGTGAAAAATGCCTTCTATAAGCTCTTTGAGAATTGA
(SEQ ID NO: 464).

5 **AOLFR248 sequences:**

MPCMPALPTGGLLPHQHTMMEIANVSSPEVFLVLLGFSTRPSLETVLFIVVLSFYMVLSILGNGI
IILVSHTDVHLHTPMYFFLANLPFLDMSFTTSIVPQLLANLWGPQKTISYGGCVVQFYISHWL
ATECVLLATMSYDRYAAICRPLHYTVIMHPQLCLGLALASWLGLTSMVGSITLMLPLCG
NNCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFLVPLGLILVSYGHIARAVLKIRSAEGR
10 RKAFTNCSSHVAVVSLFYGSIFMYLQPAKSTSHEQKFIALFYTVVTPALNPLIYTLRNTEVKS
ALRHMVLENC CGSAGKLAQI (SEQ ID NO: 465).

ATGCCCTGTATGCCCTGTGCTCTTCCACAGGTGGCCTTTTGCCCCACCCCCAGCATACAAT
GATGGAAATAGCCAATGTGAGTTCTCCAGAACTCTTGTCTCCTGGGCTTCTCCACACGA
15 CCCTCACTAGAACTGTCTCTTCATAGTTGTCTTGAGTTTTTACATGGTATCGATCTTGGG
CAATGGCATCATCTTCTGGTCTCCCATACAGATGTGCACCTCCACACACCTATGTACTTCT
TTCTTGCCAACTCCCCTTCTGGACATGAGCTTCACCACGAGCATTGTCCACAGCTCCTG
GCTAACCTCTGGGGACCACAGAAAACCATAAGCTATGGAGGGTGTGTGGTCCAGTTCTAT
ATCTCCCATTTGGCTGGGGGCAACCGAGTGTGTCTGCTGGCCACCATGTCTATGACCGCT
20 ACGCTGCCATCTGCAGGCCACTCCATTACACTGTCTATGCATCCACAGCTTTGCCTTGG
GCTAGCTTTGGCCTCCTGGCTGGGGGTCTGACCACCAGCATGGTGGGCTCCACGCTCACC
ATGCTCCTACCGCTGTGTGGGAACAATTGCATCGACCACTTCTTTGCGAGATGCCCTCA
TTATGCAACTGGCTTGTGTGGATACCAGCCTCAATGAGATGGAGATGTACCTGGCCAGCTT
TGCTTTGTGTCTGCTGCTCTGGGGCTCATCTGGTCTCTTACGGCCACATTGCCCGGGCCG
25 TGTTGAAGATCAGGTCAGCAGAAGGGCGGAGAAAGGCATTCAACACCTGTCTTCCCACG
TGGCTGTGGTGTCTCTGTTTTACGGGAGCATCATCTTCATGTATCTCCAGCCAGCCAAGAG
CACCTCCCATGAGCAGGGCAAGTTCATAGCTCTGTTCTACACCGTAGTCACTCCTGCGCTG
AACCCACTTATTTACACCCTGAGGAACACGGAGGTGAAGAGCGCCCTCCGGCACATGGTA
TTAGAGAACTGCTGTGGCTCTGCAGGCAAGCTGGCGCAAATTTAG (SEQ ID NO: 466).

30

AOLFR249 sequences:

MKSQIEKSDLKYRAILLQKVTRMFLFWVLLVLSRLLVVMGRGNSTEVTEFHLLGFGVQHEF
QHVLFIVLLIYVTSIGNIGMILLIKTDSRLQTPMYFFPQHAFVDICYTSAITPKMLQSFTEN
NLITFRGCVIQFLVYATFATSDCYLLAIMAMDCYVAICKPLRYPMIMSQT VYIQLVAGSYIIGSI
35 NASVHTGFTFSLFCKSNKINHFFCDGLPILALSCSNIDINILDVVFVGFDLMFTLVIFSYIYM
VTILKMSSTAGRKKSFTCASHLTA VTIIFYGTLSYMYLQPQSNNSQENMKVASIFYGTVIPMLN
PLIYSLRNKEGK (SEQ ID NO: 467).

ATGAAAAGTCAAATTGAAAAAAGTGACTTAAATATAGAGCCATTTTATTGCAAAAAGTC
40 ACAAGGATGTTCTGCTTTTCTGGGTCTTCTCTTGGTCTTTCTAGACTTTTGGTAGTCAT
GGGTCGAGGAAACAGCACTGAAGTGACTGAATTCCATCTTCTGGGATTTGGTGTCCAACAC
GAATTTAGCATGTCCTTTTCTTGTACTTCTTCTTATCTATGTGACCTCCCTGATAGGAAA
TATTGGAATGATCTTACTCATCAAGACCGATTCCAGACTTCAAACACCCATGTACTTTTTC
CACAACATTTGGCTTTTGTGTGATATCTGTTATACTTCTGCTATCACTCCCAAGATGCTCCAA
45 AGCTTCACAGAAGAAAATAATTTGATAACATTTGCGGGGCTGTGTGATACAATTCTTAGTTT
ATGCAACATTTGCAACCAGTGACTGTTACCTCCTAGCTATTATGGCAATGGATTGTTATGT
TGCCATCTGTAAGCCCCTTCGCTATCCCATGATCATGTCCCAAACAGTCTACATCCAACCTCG
TAGCTGGCTCATATATTATAGGCTCAATAAATGCCTCTGTACATACAGGTTTACATTTTCA
CTGTCCTTCTGCAAGTCTAATAAAATCAATCACTTTTCTGTGATGGTCTCCCAATTCTTGC
50 CCTTTCATGCTCCAACATTGACATCAACATCATTCTAGATGTTGTCTTTGTGGGATTTGACT
TGATGTTCACTGAGTTGGTCATCATCTTTTCTACATCTACATTATGGTCACCATCCTGAAG
ATGCTTCTACTGCTGGGAGGAAAAATCCTTCTCCACATGTGCTCCACCTGACAGCAG
TAACCATTTTCTATGGGACACTCTCTTACATGTACTTACAGCCTCAGTCTAATAATTCTCAG
GAGAATATGAAAGTAGCCTCTATATTTATGGCACTGTTATTCCCATGTTGAATCCTTTAAT
55 CTATAGCTTGAGAAATAAGGAAGGAAAAATAA (SEQ ID NO: 468).

AOLFR250 sequences:

MENQSSISEFFLRGISAPPEQQQSLFGIFLCMYLVLTGNLLIILAIGSDLHLHTPMYFFLANLSFV
 DMGLTSSVTVKMLVNIQTRHHTISYTGCLTQMYFFLMFGDLDSFFLAAMAYDRYVAICHPLCY
 STVMRPQVCALMLALCWVLTNIVALHTHTFLMARLSFCVTGEIAHFFCDITPVLKLSGSDTHINE
 5 MMVFVLGGTVLIVPFLCIVTSYIHVPAILRVTRGGVGKAFSTCSSHL CVV CVFYGTLFSAYLC
 PPSIASEEKDIAAAAMYTIVTPMLNPFYSLRNKDMKGALKRFLSHRSIVSS (SEQ ID NO: 469).

ATGGAAAACCAATCCAGCATTCTGAATTTTCTCCTCCGAGGAATATCAGCGCCTCCAGAGC
 AACAGCAGTCCCTCTTCGGAATTTTCTGTGTATGTATCTTGTCACCTTGACTGGGAACCTG
 10 CTCATCATCTGGCCATTGGCTCTGACCTGCACCTCCACACCCCATGTACTTTTTCTTGCC
 CAACCTGTCTTTGTTGACATGGGTTTAACGTCCTCCACAGTTACCAAGATGCTGGTGAAT
 ATACAGACTCGGCATCACACCATCTCCTATACGGGTTGCCTCACGCAAATGTATTTCTTTCT
 GATGTTTGGTGATCTAGACAGCTTCTTCTGGCTGCCATGGCGTATGACCGCTATGTGGCC
 ATTTGCCACCCCTCTGCTACTCCACAGTCATGAGGCCCAAGTCTGTGCCCTAATGCTTGC
 15 ATTGTGCTGGGTCTCACC AATATCGTTGCCCTGACTCACACGTTCTCATGGCTCGGTTGT
 CCTTCTGTGTGACTGGGGAAATTGCTCACTTTTTCTGTGACATCACTCCTGTCTGAAGCTG
 TCATGTTCTGACACCCACATCAACGAGATGATGGTTTTGTCTTGGGAGGCACCGTACTCA
 TCGTCCCCCTTTTATGCATTGTCACTCTACATCCACATGTGCCAGCTATCCTGAGGGTC
 CGAACCCGTGGTGGGGTGGGCAAGGCCTTTTCCACCTGCAGTTCCACCTCTGCGTTGTTT
 20 GTGTGTTCTATGGGACCCTCTCAGTGCCTACCTGTGTCTCCTCCCTCCATTGCCTCTGAAGAG
 AAGGACATTGCAGCAGCTGCAATGTACACCATAGTGAAGTCCCATGTTGAACCCCTTTATCT
 ATAGCCTAAGGAACAAGGACATGAAGGGGGCCCTAAAGAGGCTCTCAGTCACAGGAGTA
 TTGTTTCTCTTAG (SEQ ID NO: 470).

25 **AOLFR251 sequences:**

MEGNKTIWTDITLPRFQVGPAL EILL CGLFSAFYTLTLLGNGVIFGHCILDCKLHTPMYFFLSHLA
 IVDISYASNYVPKMLTNLMNQESTISFFPCIMQTFLYLAFHVECLILVMSYDRYADICHPLRY
 NILMSWRVCTVLAVASWVFSLLALVPLVLILRPFPGPHEINHFEILSVLKLACADTWLNQV
 30 VIFAACVFILVGPLCLVLVSYLRLAAILRJQSGEGRRKAFSTCSSHL CVV GLFFGSAIVTYMAPK
 SRHPPEQKQVLSLFYSLFNPMLNPLIYSLRNAEVKGALRRALRKERLT (SEQ ID NO: 471).

ATGGAAGGCAACAAGACATGGATCACAGACATCACCTTGCCGCGATTCCAGGTTGGTCCA
 GCACTGGAGATTCTCCTCTGTGGACTTTTCTCTGCCTTCTATACACTCACCTGCTGGGGAA
 TGGGGTCATCTTTGGGATTATCTGCCTGGACTGTAAGCTTCACACACCCATGTACTTCTTCC
 35 TCTCACACCTGGCCATTGTTGACATATCCTATGCTTCCAATATGTCCCAAGATGCTGACG
 AATCTTATGAACCAGGAAAGCACCATCTCCTTTTTTCCATGCATAATGCAGACATTCTTGT
 ATTTGGCTTTTGCTCACGTAGAGTGTCTGATTTTGGTGGTGATGTCCTATGATCGCTATGCG
 GACATCTGCCACCCCTTACGTTACAATATCCTCATGAGCTGGAGAGTGTGCCTGCTGCTGG
 CTGTGGCTTCTGGGTGTTTCACTTCTCCTGGCTCTGGTCCCTTTAGTTCTCATCCTGAGG
 40 CTGCCCTTCTGCGGGCCTCATGAAATCAACCACTTCTGTGAAATCCTGTCTGTCTCAAGTT
 GGCCTGTGCTGACACCTGGCTCAACCAGGTGGTCACTTTTGCAGCCTGCGTGTTCATCCTG
 GTGGGGCCACTCTGCCTGGTGTGCTGCTCCTACTTGCGCATCTGGCCGCCATCTTGAGGA
 TCCAGTCTGGGGAGGGCCGAGAAAGGCCTTCTCCACCTGCTCCTCCACCTTTGCGTGGT
 GGGACTCTTCTTTGGCAGCGCCATTGTCAAGTACATGGCCCCCAAGTCCCGCCATCCTGAG
 45 GAGCAGCAGAAAGTTCTTTCCCTGTTTTACAGCCTTTTCAATCCAATGCTGAACCCCTGA
 TATATAGCCTAAGGAATGCAGAGGTCAAGGGCGCCCTGAGGAGGGCACTGAGGAAGGAG
 AGGCTGACGTGA (SEQ ID NO: 472).

AOLFR252 sequences:

50 MRLANQTLGGDFFLLGIFSQISHPGRCLLIFSIFLMAVSWNITLILLIHIDSSLHTPMYFFINQLSL
 IDLTYISVTVPKMLVNQLAKDKTISVLGCGTQMYFYLLQGGAECCLLAAMAYDRYVAICHPLR
 YSVLMSHRVCLLLASGCWFVGSVDGFMLTPIAMSFPFCRSHEIQHFFCEVPAVLKLSGSDTSLY
 KIFMYLCCVIMLLIPVTVISVSYIILTIHKMNSVEGRKKAFTTCSHITVVSIFYGAAIYNYML
 PSSYQTPEKDDMMSSFFYTILTPVLNPIYSFRNKDVTRALKKMLSVQKPPY (SEQ ID NO: 473).

55

ATGCGGCTGGCCAAACCAGACCCTGGGTGGTGACTTTTTCTGTTGGGAATCTTCAGCCAGA
TCTCACACCCTGGCCGCTCTGCTTGCTTATCTTCAGTATATTTTATGATGGCTGTGCTTGG
AATATTACATTGATACTTCTGATCCACATTGACTCTCTGCTACTCCCATGTACTTCTT
TATAAACAGCTCTCACTCATAGACTTGACATATATTTCTGTCACTGTCCCCAAAATGCTG
5 GTGAACCAGCTGGCCAAAGACAAGACCATCTCGGTCTTGGGTGTGGCACCCAGATGTAC
TTCTACCTGCAGTTGGGAGGTGCAGAGTGCTGCCTTCTAGCCGCCATGGCCTATGACCGCT
ATGTGGCTATCTGCCATCCTCTCCGTTACTCTGTGCTCATGAGCCATAGGGTATGTCTCCTC
CTGGCATCAGGCTGCTGGTTTGTGGGCTCAGTGGATGGCTTCATGCTCACTCCCATCGCCA
TGAGCTTCCCCTTCTGCAGATCCCATGAGATTCAGCACTTCTTCTGTGAGGTCCCTGCTGTT
10 TTGAAGCTCTCTTGCTCAGACACCTCACTTTACAAGATTTTCATGTACTTGTGCTGTGTCAT
CATGCTCCTGATACCTGTGACGGTCACTTTCAGTGCTTACTACTATATCATCCTCACCATCC
ATAAGATGAACTCAGTTGAGGGTCGGAAGGCTTCACCACCTGCTCCTCCCACATTAC
AGTGGTCAGCCTCTTCTATGGAGCTGCTATTTACAACATACATGCTCCCCAGCTCCTACCAA
ACTCCTGAGAAAGATATGATGTCATCCTTTTTCTACACTATCCTTACACCTGTCTTGAATCC
15 TATCATTTACAGTTTCAGGAATAAGGATGTCACAAGGGCTTTGAAAAAATGCTGAGCGT
GCAGAAACCTCCATATTAA (SEQ ID NO: 474).

AOLFR253 sequences:

MTFFSSGGNCEPVMCSGNQTSQNQTASTDFLTGLFAESKHAALLYTVTFLLFLMALTGNALL
20 ILLIHSEPR LHTPMYFFISQLALMDLMLYLCVTPKMLVGQVTGDDTISPSGCGIQMFHLLTAG
AEVFLLAAMAYDRYAAVCRPLHYPLLMNQVRVQLLVSAWVLGMVDGLLLTPITMSFFCQS
RKLSFFCETPALKLSCSDVSLYKMLTYLCCILMLLTPIMVISSSYTLHLHIRMNSAAGRKA
LATCSSHMIIVLLFGASFYTYMLRSSYHTAEQDMMVSAFYTIFTPLNPLIYSLRNKDVTRAL
RSMMQSRMNQEK (SEQ ID NO: 475).

25

ATGACTTTTTTTTCTCAGGGGGAAACTGTGAGCCAGTCATGTGCTCAGGGAATCAGACTT
CTCAGAATCAAACAGCAAGCACTGATTTACCCTCACGGGACTCTTGTGAGAGCAAGCA
TGCTGCCCTCCTCTACACCGTGACCTTCTTCTTCTTCTGATGGCCCTCACTGGGAATGCCC
TCCTCATCCTCCTCATCCACTCAGAGCCCCGCCTCCACACCCCATGTACTTCTTCATCAGC
30 CAGCTCGCGCTCATGGATCTCATGTACCTATGCGTGACTGTGCCAAGATGCTTGTGGGCC
AGGTCACCTGGAGATGATACCATTTCCCGCTCAGGCTGTGGGATCCAGATGTTCTTCCACCT
GACCCTGGCTGGAGCTGAGGTTTTCTCCTGGCTGCCATGGCCTATGACCGATATGCTGCT
GTTTGCAGACCTCTCCATTACCCACTGCTGATGAACCAGAGGGTGTGCCAGCTCCTGGTGT
CAGCCTGCTGGGTTTTGGGAATGGTTGATGGTTTGTGCTCACCCCCATTACCATGAGCTT
35 CCCCTTTTGCCAGTCTAGGAAAATCCTGAGTTTTTCTGTGAGACTCCTGCCCTGCTGAAGC
TCTCCTGCTCTGACGTCTCCCTCTATAAGATGCTCACGTACCTGTGCTGCATCCTCATGCTT
CTCACCCCCATCATGGTCATCTCCAGCTCATACACCTCATCCTGCATCTCATCCACAGGAT
GAATTCTGCCGCCGGCCGCAGGAAGGCCTTGGCCACCTGCTCCTCCCACATGATCATAGTG
CTGCTGCTCTTCCGTGCTTCTTCTACACCTACATGCTCCGGAGTTCCTACCACACAGCTGA
40 GCAGGACATGATGGTGTCTGCCCTTTACACCATCTTCACTCCTGTGCTGAACCCCTCATTT
ACAGTCTCCGCAACAAAGATGTCACCAAGGCTCTGAGGAGCATGATGCAGTCAAGAATGA
ACCAAGAAAAGTAG (SEQ ID NO: 476).

AOLFR254 sequences:

MTNTSSSDFTLLGLLVNSEAAGIVFTVILAVFLGAVTANLVMIFLIQVDSRLHTPMYFLLSQLSI
45 MDTLFICTTVPKLLADMVSKEKHSFVACGIQFLYLTMIQSEFFLLGLMAYDCYVAVCNPLRYP
VLMNRKKCLLLAAGAWFGGSLDGFLLPITMNVPCGSRSSINHHFCEIPAVLKLACADTSLYET
LMYICCVLMLLPISHSSTSYSLILLTHRMPSAEGRRKAFTTCSHLTVVSIFYGAIFYTYVLPQS
FHTPEQDKVVSIFYTIVTPMLNPLIYSLRNKDVIGAFKKVFACSSAQKVATSDA (SEQ ID NO:
50 477).

ATGACGAACACATCATCCTCTGACTTCACCCTCCTGGGGCTTCTGGTGAACAGTGAGGCTG
CCGGGATTGTATTTACAGTGATCCTTGCTGTTTTCTTGGGGGCCGTGACTGCAAATTTGGT
CATGATATTCTTGATTGAGGTGGACTCTCGCCTCCACACCCCATGTACTTTCTGCTCAGTC
55 AGCTGTCCATCATGGACACCCTTTTCATCTGTACCACTGTCCCAAACTCCTGGCAGACAT
GGTTTCTAAAGAGAAGATCATTTCTTTGTGGCCTGTGGCATCCAGATCTTCTCTACCTG

ACCATGATTGGTTCTGAGTTCTTCCTCCTGGGCCTCATGGCCTATGACTGCTACGTGGCTGT
 CTGTAACCTCTGAGATACCCAGTCCTGATGAACCGCAAGAAGTGTCTTTTGGCTGGCTGCT
 GGTGCTGGTTTGGGGGCTCCCTCGATGGCTTTCTGCTCACTCCCATCACCATGAATGTCC
 CTTACTGTGGCTCCCGAAGTATCAACCATTTTTTCTGTGAGATCCCAGCAGTTCTGAAACT
 5 GGCCTGTGCAGACACGTCCTTGTATGAAACTCTGATGTACATCTGCTGTGCTCATGTTG
 CTCATCCCCATCTCTATCATCTCCACTTCTACTCCCTCATCTTGTTAACCATCCACCGCAT
 GCCCTCTGCTGAAGGTCGCAAAAAGGCCTTACCACCTTGTTCTCCCACTTGACTGTAGTT
 AGCATCTTCTATGGGGCTGCCTTCTACACATACGTGCTGCCCCAGTCCTTCCACACCCCCG
 AGCAGGACAAAGTAGTGTGACGCTTCTATACCATTGTACGCCCCATGCTTAATCCTCTCAT
 10 CTACAGCCTCAGAAACAAGGACGTCATAGGGGCATTTAAAAAGGTATTGTCATGTTGCTCA
 TCTGCTCAGAAAGTAGCAACAAGTGATGCTTAG (SEQ ID NO: 478).

AOLFR255 sequences:

MEQSNYSVYADFILLGLFSNARFPWLLFALLLVFLTSLASNVVKIILIHDSRLHTPMYFLLSQLS
 15 LRDILYISTIVPKMLVDQVMSQRAISFAGCTAQHFLYLTLAGAEFFLLGLMSYDRYVAICNPLH
 YPVLMSRKICWLIVAAAWLGGSIDGFLTPVTMQPFCASREINHFFCEVPALLKLSCTDTSAY
 ETAMYVCCIMMLLIPFSVISGSYTRILITVYRMSEAEGRGKAVATCSSHMVVVSLFYGAAMYT
 YVLPHSYHTPEQDKAVSAFYTLTPMLNPLIYSLRNKDVGTALQKVVGRCVSSGKVTTF (SEQ
 ID NO: 479).
 20
 ATGGAGCAGAGCAATTATTCCGTGTATGCCGACTTTATCCTTCTGGGTTTGTTCAGCAACG
 CCCGTTTCCCCTGGCTTCTCTTGGCCCTCATTCCTGCTCTTTTGACCTCCATAGCCAGC
 AACGTGGTCAAGATCATTCTCATCCACATAGACTCCCGCCTCCACACCCCCATGTACTTCTT
 GCTCAGCCAGCTCTCCCTCAGGGACATCCTGTATATTTCCACCATTGTGCCCAAAATGCTG
 25 GTCGACCAGGTGATGAGCCAGAGAGCCATTTCTTTGCTGGATGCACTGCCCAACACTTCC
 TCTACTTGACCTTAGCAGGGGCTGAGTTCTTCTCCTAGGACTCATGTCCTATGATCGCTAC
 GTAGCCATCTGCAACCTCTGCACTATCCTGTCTCATGAGCCGCAAGATCTGCTGGTTGA
 TTGTGGCGGCAGCCTGGCTGGGAGGGTCTATCGATGGTTTCTTGCTACCCCCGTCACCAT
 GCAGTTCCCCTTCTGTGCCTCTCGGGAGATCAACCACTTCTTCTGCGAGGTGCCTGCCCTTC
 30 TGAAGCTCTCCTGCACGGACACATCAGCCTACGAGACAGCCATGTATGTCTGCTGTATTAT
 GATGCTCCTCATCCCTTTCTCTGTCTATCTCGGGCTCTTACACAAGAATTCTCATTACTGTTT
 ATAGGATGAGCGAGGCAGAGGGGAGGGGAAAGGCTGTGGCCACCTGCTCCTCATGATGG
 TGGTTGTGACGCTCTTCTATGGGGCTGCCATGTACACATACGTGCTGCCTCATCTTACCAC
 ACCCTGAGCAGGACAAAGCTGTATCTGCCTTCTACACCATCCTTACTCCCATGCTCAATC
 35 CACTCATTTACAGCCTTAGGAACAAGGATGTACAGGGGCCCTACAGAAGGTTGTGGGGA
 GGTGTGTCTCTCAGGAAAGGTAACCACTTTCTAA (SEQ ID NO: 480).

AOLFR256 sequences:

MGGKQPWVTEFILVGFQVGPALAILLCGLFSVFYTLTLLGNGVIFGHIICLDSKLHTPMYFFLSHL
 40 AIIDMSYASNNVPMKMLANLMNQKSTISFVPCIMQTFLYLAFVTECLILVMSYDRYVAICHPF
 QYTVMSWRVCTILASTCWHSFLMALVHITHLRPPFCGPQKINHFIQIMSVFKLACAGPRLNQ
 VVLYAGSAFIVEGPLCLELVSNLHILSRHLEDPMGRAADRLTLPAPSHLCMVGLLFGSTMVM
 YMAPKSRHPBEEQKVLSLFYSLFNPMLNPLIYSLRNAEVKGALKRVLWKQRSK (SEQ ID NO:
 481).
 45
 ATGGGAGGCAAGCAGCCCTGGGTACAGAAATTCATCCTGGTGGGATTCCAGGTTGGTCCA
 GCACTGGCGATTCTCCTCTGTGGACTCTTCTGTCTTCTATACACTCACCCCTGCTGGGGAA
 TGGGGTCATCTTTGGGATTATCTGCCTGGACTCTAAGCTTCACACACCCATGTACTTCTTCC
 TCTCACACCTGGCCATCATTGACATGTCTATGCTTCCAACAATGTTCCCAAGATGTTGGC
 50 AAACCTAATGAACCAGAAAAGCACCATCTCCTTTGTTCCATGCATAATGCAGACTTTTTTG
 TATTTGGCTTTTGTGTTACAGAGTGCCTGATTTTGGTGGTGATGTCCTATGATAGGTATGT
 GGCCATCTGCCACCCCTTCCAGTACACTGTATGAGCTGGAGAGTGTGCACGATCCTG
 GCCTCAACATGCTGGATAATTAGCTTTCTCATGGCTCTGGTCCATATAACTCATATTCTGAG
 GCCGCCTTTTTGTGGCCCAAAAAGATCAACCACTTTATCTGTCAAATCATGTCCGTATTCA
 55 AATTGGCCTGTGCTGGCCCTAGGCTCAACCAGGTGGTCTATATGCGGGTTCTGCGTTTCAT
 CGTAGAGGGGCCGCTCTGCCTGGAGCTGGTCTCCAACCTGCACATCCTGTGCGGCCATCTT

5 GAGGATCCAGTAATGGGGAGGGCCGCGACCGACTTACTCTTCCTGCTCCTTCCACCTTT
GCATGGTGGGACTCCTTTTGGCAGCACCATGGTCATGTACATGGCCCCCAAGTCCCGCCA
CCCTGAGGAGCAGCAGAAGGTCTTTCCCTGTTTTACAGCCTTTTCAACCCGATGCTGAAC
CCCTTGATCTACAGCCTGAGGAACGCAGAGGTCAAGGTGCCCTGAAAAGAGTGTTGTGG
AAACAGAGATCAAAGTGA (SEQ ID NO: 482).

AOLFR257 sequences:

10 MESNQTWITEVILLGFQVDPALFLFGLFLLFYSLTLMGNGIILGLIYLD SRLHTPMYVFLSHL
AIVDMSYASSTVPMKMLANLVMHKKVISFAPCILQTFLYLAFATECLILVMMCYDRYVAICHPL
QYTLIMNWRVCTVLASTCWIFSLLALVHTLLRLPFCGPQKINHFFCQIMSVFKLACADTRLN
QVVLFAGSFILVGPLCLVLVSYLHILVAILRIQSGEGRRKAFSTCSSHL CVVGLFFGSAIVMYM
APKSSHSQERRKILSLFYSLFNPILNPLIYSLRNAEVKGALKRVLWKQRSM (SEQ ID NO: 483).

15 ATGGAAAGCAATCAGACCTGGATCACAGAAGTCATCCTGTTGGGATTCCAGGTGGACCCA
GCTCTGGAGTTGTTCTCTTTGGGTTTTCTTGCTATTCTACAGCTTAACCCTGATGGGAAA
TGGGATTATCCTGGGGCTCATCTACTTGGACTCTAGACTGCACACACCCATGTATGTCTTC
CTGTCACACCTGGCCATTGTGGACATGTCCTATGCCTCGAGTACTGTCCCTAAGATGCTAG
CAAATCTTGTGATGCACAAAAAGTCATCTCCTTTGCTCCTTGACATACTTCAGACTTTTTTG
TATTTGGCGTTTGCTATTACAGAGTGCTGATTTTGGTGATGATGTGCTATGATCGGTATG
20 TGGCAATCTGTACCCCTTGCAATACACCCCTATTATGAAGTGGAGAGTGTGCACTGTCCT
GGCCTCAACTTGCTGGATATTAGCTTTCTCTTGGCTCTGGTCCATATTACTCTTATTCTGA
GGCTGCCCTTTTTGTGGCCCAACAAAGATCAACCACTTTTTCTGTCAAATCATGTCCGTATTC
AAATTGGCCTGTGCTGACACTAGGCTCAACCAGGTGGTCCTATTTGCGGGTTCTGCGTTCA
TCTTAGTGGGGCCGCTCTGCCTGGTGCTGGTCTCCTACTTGCACATCCTGGTGGCCATCTTG
25 AGGATCCAGTCTGGGGAGGGCCGCGAGAAAGGCCTTCTCTACCTGCTCCTCCACCTCTGCG
TGGTGGGGCTTTTCTTTGGCAGCGCCATTGTCATGTACATGGCCCCCAAGTCAAGCCATTC
TCAAGAACGGAGGAAGATCCTTTCCCTGTTTTACAGCCTTTTCAACCCGATCCTGAACCCC
CTCATCTACAGCCTTAGGAATGCAGAGGTGAAAGGGGCTCTAAAGAGAGTCCCTTTGAAAA
CAGAGATCAATGTGA (SEQ ID NO: 484).

30

AOLFR259 sequences:

MGDNQSRVTEFILVGFQLSVEMEVLFWIFSLLYLFSLLANGMILGLICLDPRLRTPMYFFLSHL
AVIDIYYASSNLLNMLENLVKHKKTISFISCIMQMALYLFAAAVCMILVMSYDRFVAICHPL
HYTVIMNWRVCTVLATTSWACGFSLLALINLILLRLPFCGPQEVNHFFGEILSVLKLACADTWIN
35 EIFVFAGGVFVLVGPLSLMLISYMRILLAILKIQSKEGRKKAFTSCSSHL CVVGLYFGMAMVVY
LVPDINSQRQKQKILTLFYSLFNPLNPLIYSLRNAQVKGALYRALQKKRTM (SEQ ID NO:
485).

40 ATGGGGGACAACCAATCAGGGTCAAGAATTCATCCTGGTTGGATTCCAGCTCAGTGTG
GAGATGGAAGTGCTCCTCTTCTGGATCTTCTCCCTGTTATATCTCTTCAGCCTGCTGGCAAA
TGGCATGATCTTGGGGCTCATCTGTCTGGATCCCAGACTGCGCACCCCATGTACTTCTTCC
TGTCACACTTGGCCGTCATTGACATATACTATGCTTCCAGCAATTTGCTCAACATGCTGGA
AAACCTAGTGAAACACAAAAAACTATCTCGTTTCATCTCTTGCAATTATGCAGATGGCCTTG
TATTTGACTTTTGCTGCTGCAGTGTGCATGATTTTGGTGGTGATGTCCTATGACAGATTTGT
45 GCGCATCTGCCATCCCCTGCATTACACTGTCATCATGAACTGGAGAGTGTGCACAGTACTG
GCTATTACTTCTGGGCATGTGGATTTTCCCTGGCCCTCATAAATCTAATTCTCCTTCTAAG
GCTGCCCTTCTGTGGGCCCCAGGAGGTGAACCACTTCTTCGGTGAAATTCTGTCTGTCTC
AAACTGGCCTGTGCAGACACCTGGATTAATGAAATTTTGTCTTTGCTGGTGGTGTGTTTG
TCTTAGTGGGGCCCCCTTTCTTGATGCTGATCTCCTACATGCGCATCCTCTTGGCCATCCTG
50 AAGATCCAGTCAAAGGAGGGCCGCAAAAAAGCCTTTTCCACCTGCTCCTCCACCTCTGTG
TGGTTGGGCTTTACTTTGGCATGGCCATGGTGGTTTACCTGGTCCCAGACAACAGTCAACG
ACAGAAGCAGCAGAAAAATTCTCACCTGTTTTACAGCCTTTTCAACCCATTGCTGAACCCC
CTCATCTACAGCCTGCGGAATGCTCAAGTGAAGGGTGCCCTATACAGAGCACTGCAGAAA
AAGAGGACCATGTGA (SEQ ID NO: 486).

55

AOLFR24B sequences:

MPSINDTHFYPPFFLLGLDGLDTHIWFSPFCIVYLIAIVGNMTILFVIKTEHSLHQPMFYFLAM
 LSMIDLGLSTSTIPKMLGIFWFNLQEISFGGCLLQMFFIHMFTGMETVLLVVMAYDRFVAICNP
 LQYTMILTNKTISILASVVVGRNLVLVTPFVFLRLPFCGHNTVPHTYCEHRGLAGLACAPIKIN
 5 IYGLMVISYIIVDVLIASSYVLILRAVFRLPQDVRKAFNTCGSHVCVMLCFYTPAFFSFMTH
 RFGQNIPHYIHILLANLYVVVPPALNPVIYGVRTKQIREQIVKIFVQKE (SEQ ID NO: 487)

ATGCCTTCTATCAATGACACCCACTTCTATCCCCCTTCTTCTCCTGCTAGGAATACCAGG
 ACTGGACACTTTACATATCTGGATTCTTTCCCATCTGTATTGTGTACCTGATTGCCATTG
 10 TGGGAATATGACCACTTCTTTGTGATCAAACTGAACATAGTCTACACCAGCCCATGTT
 CTACTTCTGGCCATGTTGTCTATGATTGATCTGGGTCTGTCCACATCCACTATCCCCAAAA
 TGCTAGGAATCTTCTGGTTCAACCTCCAAGAGATCAGCTTTGGGGGATGCCTTCTTCAGAT
 GTTCTTTATTACATGTTTACAGGCATGGAGACTGTTCTGTTGGTGGTCATGGCTTATGACC
 GCTTTGTTGCCATCTGCAACCCTCTCCAGTACACCATGATCCTCACCATAAAAACCATCAG
 15 TATCCTAGCTTCTGTGGTTGTTGGAAGAAATTTAGTTCTTGTAACCCCATTTGTGTTTCTCA
 TTCTGCGTCTGCCATTCTGTGGGCATAACATCGTACCTCACACATACTGTGAGCACAGGGG
 TCTGGCCGGGTTGGCCTGTGCACCCATTAAGATCAACATAATCTATGGGCTCATGGTGATT
 TCTTATATTATTGTGGATGTGATCTTAATTGCCTCTTCCTATGTGCTTATCCTTAGAGCTGT
 TTTTCGCCCTTCCCTCTCAAGATGTCCGACTAAAGGCCTTCAATACCTGTGGTCTCTCATCT
 20 GTGTTATGCTGTGCTTTTACACACCACTAATTTTCTTTTATGACACATCGTTTGGCCAA
 AACATTCCCCATATCCATATTTCTTTGGCTAACCTGTATGTGGTTGTCCCACCTGCCCT
 TAACCTGTCAATTTATGGAGTCAGGACCAAGCAGATCCGAGAGCAAATTGTGAAAATATTT
 GTACAGAAAGAATAA (SEQ ID NO: 488)

AOLFR33B sequences:

MLHTNNTQFHPSTFLVVGVPGLVDVHVWIGFPFFAVYLTALLGNIIILFVIQTEQSLHQPMFYFL
 AMLAGTDLGLSTATIPKMLGIFWFNLGEIAFGACITQMYTHICTGLESVVLTVTGIDRYIAICNP
 LRYSMILTINKVAILGIVIVRTL VFVTPFVFLRLPFCGVRIIPHTYCEHMGGLAKLACASINVY
 GLIAFSVGYIDISVIGFSYVQILRAVFHLPADWARKALSTCGSHVCVMLAFYLPALFSFMTHRF
 30 GHNIPHYIHILLANLYVVFPALNSVIYGVKTKQIREQVLRILNPKSFWHFDPKRIFHNNSVRQ
 (SEQ ID NO: 489)

ATGCTTCATACCAACAATACACAGTTTACCCTTCCACCTTCTCCTCGTAGTGGGGGTCCCAG
 GGCTGGAAGATGTGCATGTATGGATTGGCTTCCCCTTCTTTGCGGTGTATCTAACAGCCCT
 35 TCTAGGGAACATCATTATCCTGTTTGTGATACAGACTGAACAGAGCCTCCACCAACCCATG
 TTTTACTTCTAGCCATGTTGGCCGGCACTGATCTGGGCTTGTCTACAGCAACCATCCCCA
 AGATGCTGGGAATTTTCTGGTTTAACTTGGAGAGATTGCATTTGGTGCCTGCATCACACA
 GATGTATACCATTCATATATGCACTGGCCTGGAGTCTGTGGTACTGACAGTCACGGGCATA
 GATCGCTATATTGCCATCTGCAACCCCTGAGATATAGCATGATCCTTACCAACAAGGTAA
 40 TAGCCATTCTGGGCATAGTCATCATTGTCAGGACTTTGGTATTTGTGACTCCATTACATTT
 CTCACCTGAGATTGCCTTTCTGTGGTGTCCGATTATCCCTCATACCTATTGTGAACACAT
 GGGCTTGGCAAAGTTAGCTTGTGCCAGTATTAATGTTATATATGGAATTGATTGCCTTCTCA
 GTGGGATACATTGACATTTCTGTGATTGGATTTTCTATGTCCAGATCCTCCGAGCTGTCTT
 CCATCTCCCAGCCTGGGATGCCCGGCTTAAGGCACTCAGCACATGTGGCTCTCACGTCTGT
 45 GTTATGTTGGCTTTCTACCTGCCAGCCCTCTTTCTCTCATGACACACCGCTTTGGCCACAA
 CATCCCTCATTACATCCACATTCTTCTGGCCAATCTGTATGTGGTTTTTCCCCTGCTCTTA
 ACTCTGTTATCTATGGGGTCAAAACAAAACAGATACGAGAGCAGGTACTTAGGATACTCA
 ACCCTAAAAGCTTTTGGCATTTTGACCCCAAGAGGATCTTCCACAACAATTAGTTAGACA
 ATAA (SEQ ID NO: 490)

50

AOLFR112B sequences:

MKNKTVLTFEILLGLTDVPELQVAVFTFLFLAYLLSILGNLTILTLTLLDSHLQTPMYFFLRNFSF
 LEISFTNIFIPRVLISITGNKSISFAGCFQYFFAMFLGATEFYLLAAMSVDYVAICKPLHYTTI
 MSSRICIQLIFCSWLGLMAIIPITITLMSQQDFCASNRLNHYFCDYEPLELSCSDTSLIEKVVFL
 55 VASVTLVVTLVLVILSYAFIHKTLKLPQAQRTKAFSTCSSHMIVISLSYGSCMFMYINPSAKEG
 DTFNKGVALITSVAPLLNPFYTLRNQVQKQPFKDMVKKLLNL (SEQ ID NO: 491)

ATGAAAAATAAAACCGTGTTAACTGAGTTTATCCTTCTGGGTCTAACAGATGTCCCTGAAC
 TCCAGGTGGCAGTTTTACCTTTCTTTCTGCGTATTTACTCAGCATCCTTGGAATCTG
 ACTATCCTCATCCTCACCTTGCTGGACTCCACCTTCAGACTCCCATGTATTTCTTTCTCCG
 5 GAACTTCTCCTTCTTGAAAATTTCTTTCACAAACATCTTCATTCCAAGGGTCTGATTAGCA
 TCACAACAGGGAACAAGAGTATCAGCTTTGCTGGCTGCTTCACTCAGTATTTCTTTGCCAT
 GTTCTTGGGGCTACAGAGTTTTACCTTCTGGCTGCCATGTCCTATGACCGCTATGTGGCC
 ATCTGCAAACCTCTGCATTACACCACCATCATGAGCAGCAGAATCTGCATCCAGCTGATTT
 TCTGCTCTTGGCTGGGTGGGCTAATGGCTATTATACCAACAATCACCTGATGAGTCAGCA
 10 GGACTTTTGTGCATCCAACAGACTGAATCATTACTTCTGTGACTATGAGCCTCTTCTGGAA
 CTCTCATGTTTCAGACACAAGCCTCATAGAGAAGGTGTCTTTCTTGTGGCATCTGTGACCC
 TGGTGGTCACTCTGGTGCTAGTGATTCTCTCCTATGCATTCAATTATCAAGACTATTCTGAAG
 CTCCCCTCTGCCCAACAAGGACAAAAGCCTTTTCCACATGTTCTTCCACATGATTGTCAT
 CTCCCCTCTTTACGGAAGCTGCATGTTTATGTACATTAAATCCCTCTGCAAAAGAAGGGGAT
 15 ACATTCAACAAGGGAGTAGCTCTACTCATTACTTCAGTTGCTCCTTTGTTGAACCCCTTTAT
 TTACACCCTAAGGAACCAACAGGTAAAACAACCCTTCAAGGATATGGTCAAAAAGCTTCT
 GAATCTTTAA (SEQ ID NO: 492)

AOLFR130B sequences:

20 MEGKNQAPSEFIILGFDHLNELQYLLFTIFFLTYICTLGGNVFIIVVTIADSHLHTPMYYFLGNL
 ALIDICYTTTNVPMQMMVHLLSEKKIISYGGCVTQLFAFIFFVGSECLLLAAMAYDRYIAICKPLR
 YSFIMNKALCSWLAASCWTCGFLNSVLHTVLTFHLPFCGNNQINYYFCDIPPLLLSCGDTSLNE
 LALLSIGILISWTFPLCILSYLYIISTILRIRSEGRHKAFSTCASHLLIVILYYGSAIFTYVRPISSYS
 LEKDRLISVLYSVVTPMLNPVIYTLRNKDIKEAVKAIGRKWQPPVFSSDI (SEQ ID NO: 493)
 25
 ATGGAAGGAAAGAATCAAACAGCTCCATCTGAATTCATCATCTTGGGGTTCGACCACCTGA
 ATGAATTGCAGTATTTACTCTTCACCATCTTCTTTCTGACCTACATATGCACCTTAGGAGGC
 AATGTTTTTATCATTGTGGTGACCATAGCTGATTCCCACCTACACACACCCATGTATTATTT
 30 CCTAGGAAATCTTGCCCTTATTGACATCTGCTACACTACTACTAATGTCCCCCAGATGATG
 GTGCATCTTCTGTGAGAGAAGAAAATCATTTCCTATGGAGGCTGTGTGACCCAGCTCTTTG
 CATTCATTTTCTTTGTTGGCTCAGAGTGTCTCCTCCTGGCAGCAATGGCATATGATCGATAT
 ATTGCTATCTGTAAGCCGTTAAGGTACTCATTTATTATGAACAAGGCCCTGTGCAGCTGGT
 TAGCAGCCTCATGCTGGACATGTGGGTTTCTCAACTCAGTGTTGCACACCGTTCTGACCTT
 CCACCTGCCCTTCTGTGGTAACAATCAGATCAATTATTTCTTCTGTGACATACCTCCCTTGC
 35 TCATCTTGTCTTGTGGTGATACTTCCCTCAATGAAGTGGCTTTGCTGTCCATTGGGATCCTC
 ATAAGCTGGACTCCTTTCTGTGCATCATCCTTTCTACCTTTACATCATCTCCACCATCCT
 GAGGATCCGTTCTCTGAGGGGAGGCACAAAGCCTTTTCCACCTGTGCCTCCACCTGCTC
 ATTGTTATTCTCTATTATGGCAGTGCTATCTTCACGTATGTGAGGCCCATCTCATCTTACTC
 TCTAGAGAAAGATAGATTGATCTCAGTGCTGTATAGTGTGTGCACACCCATGCTGAATCCT
 40 GTAATTTATACGCTAAGGAATAAGGACATCAAAGAGGCTGTGAAGGCCATAGGGAGAAAG
 TGGCAGCCACCAGTTTTCTTCTGATATATAA (SEQ ID NO: 494)

AOLFR142B sequences:

45 MARKDMAHINCTQATEFILVGLTDHQELKMPLFVLFLSIYLFVVGNLGLILLIRADTSLNTPM
 YFFLSNLAFFVDFCYSSVITPKMLGNFLYKQNVISFDACATQLGCFLTFMISESLLLASMAYDRY
 VAICNPILLYMVVMTPGICILVAVPYSYSELMALFHTILTFRLSYCHSNIVNHFYCDMDPLRL
 TCSDRTRFKQLWIFACAGIMFISSLLIVFVSYMFIIAISLRMHSAEGRQKAFSTCGSHMLAVTIFYG
 TLIFMYLQPSSSHALDTDKMASVFYTVIIPMLNPLYSLQNKKEVKEALKKIINKN (SEQ ID NO:
 495)
 50
 ATGGCCAGAAAAGATATGGCTCACATCAATTGCACCCAGGCGACAGAGTTTATTCTTGTGG
 GCCTCACAGACCATCAGGAGTTGAAGATGCCCTCTTTGTGCTATTCTTATCCATCTACCTC
 TTCACAGTGGTAGGCAACTTGGGTTTGATCCTACTCATTAGAGCGGATACAAGTCTCAACA
 CACCAAGTACTTCTTTCTTAGCAACCTAGCTTTTGTGGATTCTGTTACTCTTCTGTCATT
 55 ACACCCAAATGCTTGGGAATTTCTTGTACAAACAAAATGTTATATCCTTTGATGCTAGTG
 CTACTCAACTGGGCTGCTTTCTCACCTTCATGATATCAGAATCCTTGCTACTGGCTTCCATG

GCCTATGACCGATATGTGGCCATTTGTAACCCTCTATTGTATATGGTTGTAATGACTCCAG
 GAATCTGCATTCAACTTGTAGCAGTTCCTTATAGCTATAGCTTCCTAATGGCACTATTTTAC
 ACCATCCTCACCTTCCGCTCTCCTATTGCCACTCCAACATTGTCAACCATTCTATTGTGA
 TGACATGCCTCTCCTCAGGCTAACTTGCTCAGACACTCGCTTCAAACAGCTCTGGATCTTT
 5 GCCTGTGCTGGTATCATGTTCAATTTCTCCCTTCTGATTGCTTTGTCTCCTACATGTTTCATC
 ATTTCTGCCATCCTGAGGATGCATTGAGCTGAGGGAAGACAGAAGGCTTTCTCGACGTGTG
 GCTCTCACATGCTGGCAGTCACCATATTCTATGGGACCCTCATTTTTATGTACTTACAGCCT
 AGCTCTAGCCATGCCCTGGACACAGACAAGATGGCCTCTGTCTTCTACACAGTGATCATTC
 CCATGTTGAATCCCTTAATCTATAGCCTCCAGAATAAGGAGGTGAAAGAAGCTCTGAAGA
 10 AAATCATTATCAATAAAAACTAG (SEQ ID NO: 496)

AOLFR171C sequences:

MAEVNIYVTVFILKGITNRPELQAPCFGVFLVIYLVTVLGNLGLITLIKIDTRLHTPMYYFLSHL
 AFVDLCYSSAITPKMMVNFVVERNIPFHACATQLGCFLTFMITECFLLASMAFYDCYVAICSPL
 15 HYSTLMSRRVCIQLVAVPYTYSFLVALFHTVTTFRITYCGPNLNHFYCDLPLFALSCSDTHMK
 EILIFAFAGFDMISSSIVLTSYIFIAAILRIRSTQGQHKALSTCGSHMVTVTIFYGTLIFMYLQPKS
 NHSLDITDKMASVFYTVVIPMLNPLIYSLRNKEVKDASKKALDKGCENLQILFLKIRKLY (SEQ
 ID NO: 497)

ATGGCTGAAGTTAATATCATTTATGTCACTGTATTCACTCTGAAAGGAATTACCAACCGGC
 CAGAGCTTCAGGCCCCGTGCTTTGGGGTGTTTTTAGTTATCTATCTGGTCACAGTGCTGGG
 CAATCTTGGGTTGATTACTTTAATCAAGATTGATACTCGACTCCACACACCTATGTAATATT
 TCCTCAGCCACCTGGCCTTTGTTGACCTTTGTTACTCTCTGCTATTACACCGAAGATGATG
 GTGAATTTTGTGTTGGGAACGCAACACCATTCCTTTCCATGCTTGTGCAACCCAACTGGGTT
 25 GTTTTCTCACCTTCATGATCACTGAGTGTTTCTTCTAGCCTCCATGGCCTACGATTGCTAT
 GTCGCCATCTGTAGTCCCCTGCATTATTCAACACTGATGTCAAGAAGAGTCTGCATTCAAC
 TGGTGGCAGTTCATATATATACAGCTTCTGGTGGCCTCTTCCACACCGTTATCACTTTC
 CGTCTGACTTACTGTGGCCCAAACCTAATTAACCATTTCTATTGTGATGACCTCCCCCTTCTT
 AGCTCTGTCTGCTCAGACACACATGAAGGAAATTCTGATATTTGCCTTTGCTGGCTTT
 30 GATATGATCTCTTCTCTTCCATTGTCTCACCTCCTACATCTTTATTATTGCCGCTATCCTA
 AGGATCCGCTCTACTCAGGGGCAACACAAAGCCATTTCCACCTGTGGCTCCCATATGGTGA
 CTGTCACTATTTCTATGGCACACTGATCTTTATGTACCTACAGCCCAAATCAAATCACTCC
 TTGGACACAGACAAGATGGCTTCTGTATTTTACACAGTGTTGATCCCCATGTTAAACCCCC
 TAATCTATAGCTAAGGAACAAAGAAAGTGAAAGATGCCTCAAAGAAAGCCTTGGATAAAG
 35 GTTGTGAAAACCTTACAGATATTAACATTTTTTAAAAATAAGAAAACCTTTATTAA (SEQ ID NO:
 498)

AOLFR225B sequences:

MKNRMTMFGFILLGLTNQPELQVMIFIFLFLTYMLSILGNLTITLTLDDPHLQTPMYFFLRNFSF
 40 LEISFTSIFIPRFLTSMITGNKVISFAGCLTQYFFAIFLGATEFYLLASMSYDRYVAICKPLHYLTI
 MSSRVCIQLVFCSWLGGFLAILPPIILMTQVDFCVSNILNHYYCDYGPLVELACSDTSLELMVI
 LLAVVTLMVTLVLVLSYTYIIRTLRIPSAQQRKAFSTCSSHMIVISLSYGSCMFMYINPSAKE
 GGAFNKGIAVLITSVTPLLNPFITYTLRNQVQKQAFKDSVKKIVKL (SEQ ID NO: 499)

ATGAAAAACAGAACCATGTTTGGTGAGTTTATTCTACTGGGCCTTACAAATCAACCTGAAC
 TCCAAGTGATGATATTCATCTTTCTGTTCCCTCACCTACATGCTAAGTATCCTAGGAAATCTG
 ACTATTATCACCTCACCTTACTAGACCCCCACCTCCAGACCCCCATGTATTTCTTCTCCG
 GAATTTCTCCTTCTTAGAAATTTCCCTTCACATCCATTTTATTCCCAGATTTCTGACCAGCA
 TGACAACAGGAAATAAAGTTATCAGCTTTGCTGGCTGCTTGACTCAGTATTTTTTGTCTAT
 50 ATTTCTTGGAGCTACCGAGTTTACCTCCTGGCCTCCATGTCTTATGATCGTTATGTGGCCA
 TCTGCAAAACCTTGCAATTACCTGACTATTATGAGCAGCAGAGTCTGCATACAAGTATGTT
 CTGCTCCTGGTGGGGGATTCTAGCAATCTTACCAACATCATCCTGATGACCCAGGTA
 GATTTCTGTGCTCCAACATTCTGAATCACTATTACTGTGACTATGGGCCTCTCGTGAGCT
 TGCTGCTCAGACACAAGCCTCTTAGAACTGATGGTCATCCTCTTGGCCGTTGTGACTCTC
 55 ATGGTTACTCTGGTGTGGTGACACTTTCTTACACATACATTATCAGGACTATTCTGAGGA
 TCCCTTCTGCCAGCAAAGGACAAAGGCCTTTTCCACTGTCTCCTCCACATGATTGTCTCATC

TCCCTCTCTTATGGCAGCTGCATGTTTATGTACATTAATCCTTCTGCAAAAGAAGGAGGTG
 CTTTCAACAAAGGAATAGCTGTACTCATTACTTCGGTTACTCCCTTACTGAATCCCTTCATA
 TATACTTTAAGAAATCAGCAAGTGAAACAAGCTTTCAAGGACTCAGTCAAAAAGATTGTG
 AAACITTTAA (SEQ ID NO: 500)

5

AOLFR274B sequences:

MEFVFLAYPSCPBLHLSFLGVSLVYGLIITGNILIVVSIHTETCLCTSMYYFLGSLSGIEICYTAV
 VVPHILANTLQSEKTITLLGCATQMAFFIALGSADCFLLAAMAYDRYVAICHPLQYPLLMTLTL
 CVHLVVASVISGLFSLQLVAFIFSLPFCQAQGIEHFFCDVPPVMHVVCAQSHIHEQSVLVAAIL
 10 AIAVPFLLITTSYTFIVAALLKIHSAAGRHRAFSTCSSHLTVVLLQYGCCAFMYLCPSSSYNPKQ
 DRFISLVYTLGTPLLNPLIYALRNSEMKGAVGRVLTRNCLSQNS (SEQ ID NO: 501)

ATGGAATTTGTGTTCTCGGCCTATCCCTCCTGCCCAGAACTGCATATTCTGTCTTCTTGG
 GGTCAGCCTGGTTTATGGTTGATCATCACTGGGAACATTCTCATTGTGGTGTCCATTAC
 15 ACAGAAACCTGTCTATGCACATCCATGTACTATTTCTGGGCAGCCTTTCTGGGATTGAAA
 TATGCTACACTGCAGTGGTGGTGGCCCATATCCTGGCCAACACCCTACAGTCAGAGAAGAC
 CATCACTCTCCTGGGCTGTGCCACCCAGATGGCTTTCTTCATTGCACTGGGCAGTGCTGAT
 TGCTTCCTCTTGGCTGCCATGGCCTATGACCGCTATGTGGCCATTTGCCACCCGTTGCAGTA
 CCCTCTCCTCATGACATTGACTCTTTGTGTCCACTTGGTTGTGGCATCAGTCATCAGTGGTC
 20 TGTTCTCTGTCTTAACTGGTGGCCTTCATCTTCTCTCTGCCATTCTGCCAGGCTCAGGGC
 ATTGAGCACTTCTTTGTGATGTGCCACCAGTCATGCATGTTGTTGTGTCTCAGAGTCACAT
 TCATGAGCAGTCAGTGCTGGTGGCAGCCATACTAGCCATTGCTGTGCCTTTCTTCCTCATC
 ACCACCTCCTACACCTTCATAGTGCTGCTCTGCTCAAGATCCACTCGGCTGCTGGCCGCC
 ACCGGGCTTCTCCACCTGCTCTTCCACCTCACTGTGGTGTGCTGCAGTATGGCTGCTGT
 25 GCCTTCATGTACCTGTGCCCCAGCTCCAGCTACAACCCCAAGCAAGATCGGTTTCATCTCAC
 TGGTGTACACATTGGGAACCCCACTGCTCAACCCCACTTATCTATGCCCTGAGGAACAGTGA
 GATGAAAGGGGCCGTAGGGAGAGTTCTTACCAGGAACTGCCTTTCCAGAACAGCTAG
 (SEQ ID NO: 502)

30 **AOLFR276B sequences:**

MGGFGTNISSITSFTLTGFPEMKGLEHWLAALLLLLYAISFLGNILILFIKEEQSLHQPMYYFLS
 LFSVNDLGVSFSTLPTVLAAVCFHAPETTFDACLAQMFFIHFSSWTEFGILLAMSFHDHYVAICNP
 LRYATVLTDRVAHNGISIVRSFCMVFLPFLKRLPFCASVVLASVCLHADLRLPWGDT
 TINSMYGLFIVISAFGVDSSLILLSYVLILHSVLAIASRGERLKTILNTCVSHIYAVLIFYVPMVSVS
 35 MVHRFRGRAPEYVHKFMSLCTSNALPNYLFHQD (SEQ ID NO: 503)

ATGGGGGGCTTTGGGACTAACATCTCAAGTACTACCAGCTTCACTCTAACAGGCTTCCCTG
 AGATGAAGGGTCTGGAGCACTGGCTGGCTGCCCTTCTGCTGCTGCTTTATGCTATTTCCCT
 CCTGGGCAACATCCTCATCTCTTTATCATAAAGGAAGAGCAGAGCTTGCACCAGCCAATG
 40 TACTACTTCTGTCTCTTTTCTGTTAATGACCTGGGTGTGTCTTTTCTACATTGCCCACT
 GTACTGGCTGCTGTGTGTTTTCATGCCCCAGAGACAACCTTTGATGCCTGCCTGGCCCA
 TGTTCTTCATCCACTTTTCTCCTGGACAGAGTTTGGCATCCTACTGGCCATGAGTTTTGAC
 CACTATGTGGCCATCTGTAACCCGCTGCGCTATGCCACAGTGCTCACTGATGTCCGTGTGG
 CCCACAATGGCATATCCATTGTCATCCGCAGCTTCTGCATGGTATTCCCACTTCCCTTCTC
 45 CTGAAGAGACTGCCTTTCTGTAAGGCCAGTGTGGTACTGGCCATTCTACTGTCTGCATG
 CAGACCTGATTGGCTGCCCTGGGGAGACACTACCATCAACAGCATGTATGGCCTGTTTCAT
 TGTCATCTCTGCCTTTGGTGTAGATTCACTGCTCATCCTCCTCTCCTATGTGCTCATTTAC
 ATTCTGTGCTGGCCATTGCCTCCAGGGGTGAGAGGCTTAAGACACTCAACACATGTGTGTC
 ACATATCTATGCAGTGCTGATCTTCTATGTGCCTATGGTTAGTGTGTCCATGGTTCATCGAT
 50 TTGGGAGGCATGCTCCTGAATATGTGCACAAGTTCATGTCTCTTTGTACCTCCAATGCTCT
 ACCCAATTATCTATTCCATCAAGACTAA (SEQ ID NO: 504)

AOLFR311B sequences:

MDWENCSSLTDFLLGITNNPEMKVTLFAVFLAVYIINFSANLGMIVLIRMDYQLHTPMYFFLS
 55 HLSFCDLCYSTATGPKMLVDLLAKNKSIPFYGCALQFLVFCIFADSECLLSVMAFDYKAIINP
 LLYTVNMSSRVCYLLLTGVYLVGIADALIHMTLAFRLCFCGSNEINHFFCDIPPLLLLSRSDTQV

NELVLFTVFGFIELSTISGVFISYCYILSVLEIHSABGRFKALSTCTSHLSAVAIFQGTLLFMYFRP
SSSYSLDQDKMTSLFYTLVVPMLNPLIYSLRNKDVKEALKKLKNILF (SEQ ID NO: 505)

5 ATGGACTGGGAAAATTGCTCCTCATTAAGTATTTTTTCTCTTGGGAATTACCAATAACCC
AGAGATGAAAGTGACCCTATTTGCTGTATTCTTGGCTGTTTATATCATTAAATTTCTCAGCAA
ATCTTGGAATGATAGTTTTAATCAGAATGGATTACCAACTTCACACACCAATGTATTTCTT
CCTCAGTCATCTGTCTTTCTGTGATCTCTGCTATTCTACTGCAACTGGGCCCAAGATGCTGG
TAGATCTACTTGCCAAGAACAAGTCAATACCCCTCTATGGCTGTGCTCTGCAATTCTTGGT
CTTCTGTATCTTTGCAGATTCTGAGTGTCTACTGCTGTGAGTGATGGCCTTTGATCGGTACA
10 AGGCCATCATCAACCCCTGCTCTATACAGTCAACATGTCTAGCAGAGTGTGCTATCTACT
CTTGACTGGGGTTTATCTGGTGGGAATAGCAGATGCTTTGATACATATGACACTGGCCTTC
CGCCTATGCTTCTGTGGGTCTAATGAGATTAATCATTTCTTCTGTGATATCCCTCCTCTCTT
ATTACTCTCTCGCTCAGATACACAGGTCAATGAGTTAGTGTATTTCACCGTCTTTGGTTTTA
TTGAACTGAGTACCATTTCAAGGAGTTTTCAATTTCTTATTGTTATATCATCTATCAGTCTTG
15 GAGATACACTCTGCTGAGGGGAGGTTCAAAGCTCTCTACATGCACTTCCCACTTATCTG
CGGTTGCAATTTCCAGGGAAGTCTGCTCTTTATGTATTTCCGGCCAAGTTCTTCTATTCT
CTAGATCAAGATAAAAATGACCTCATTGTTTACACCCCTGTGGTTCCCATGTTGAACCCOCT
GATTTATAGCCTGAGGAACAAGGATGTGAAAGAGGCCCTGAAAAAACTGAAAAATAAAAT
TTTATTTTAA (SEQ ID NO: 506)

20

AOLFR314 sequences:

MEVKNCMVTEFILLGIPHTGLEMTLFLVLPFYACTLLGNVSILVAVMSSARLHTPMYFFLG
NLSVFDMGFSSVTCPKMLLYLMGLSRLISYKDCVCQLFFFHFLGSIECFLFTVMA YDRFTAICY
PLRYTVIMNPRICVALAVGTWLLGCHSSILSTLFTLPYCGPNVDHFFCDIPALLPLACADTSL
25 AQRVSFTNVGLISLVCFLILLSYTRITISILSIRTTEGRRRAFSTCSAHLAILCAYGPITVYLQPT
PNPMLGTVVQILMNLVGPMLNPLIYTLRNKEVKTALKTILHRTGHVPES (SEQ ID NO: 507)

30 ATGGAGGTGAAGAACTGCTGCATGGTGACAGAGTTCATCCTTTTGGGAATCCCACACACA
GAGGGGCTGGAGATGACACTTTTGTCTTATCTTGGCCTTCTATGCCTGCACTCTACTGGG
AAATGTGTCTATCCTTGTGTGCTGTTATGTCTTCTGCTCGCCTTCACACACCTATGTATTTCT
TCCTGGGAAACTTGTCTGTGTTTGACATGGGTTTCTCCTCAGTGACTTGTCCCAAAATGCT
GCTCTACCTTATGGGGCTGAGCCGACTCATCTCCTACAAAGACTGTGTCTGCCAGCTTTTCT
TCTTCCATTTCTCGGGAGCATTGAGTGCTTCTTGTGTTACGGTGATGGCCTATGACCGCTTC
ACTGCCATCTGTATCCTCTGCGATACACAGTCATCATGAACCCAAGGATCTGTGTGGCCC
35 TGGCTGTGGGCACATGGCTGTTAGGGTGCAATTCATTCCAGTATCTTGACCTCCCTCACCTTC
ACCTTGCCATACTGTGGTCCCAATGAAGTGGATCACTTCTTCTGTGACATTCCAGCACTGTT
GCCCTTGGCCTGTGCTGACACATCCTTAGCCAGAGGGTGAGCTTCAACCAACGTTGGCCTC
ATATCTCTTGTCTGCTTTCTGCTAATCTTTTATCTTACACTAGAATCACAATATCTATCTT
AAGCATCTGTAACACTGAGGGCCGTCGCCCTTCTCCACCTGCAGTGCTCATCCTCATT
40 GCCATCCTCTGTGCCTATGGGCCCATCATCACTGTCTACCTGCAGCCACACCCCAACCCCA
TGCTGGGAACCGTGGTACAAATTCTCATGAATCTGGTAGGACCAATGCTGAACCCCTTTGAT
CTATACCTTGAGGAATAAGGAAGTAAAAACAGCCCTGAAAACAATATTGCACAGGACAGG
CCATGTTCTGAGAGTTAG (SEQ ID NO: 508)

45 **AOLFR324B sequences:**

MPIANDTQFHTSSFLLLGIPGLEDVHIWIGFPFFSVYLIALLGNAAIFFVIQTEQSLHEPMYYCLA
MLDSIDLSTLSTATIPKMLGIFWFNIKEISFGGYLSQMFFIHFFTVMESIVLVAMAFDRYIAICKPL
WYTMILTSKIISLIAGI AVLRSLYMVPLVFLLLRLPFCGHRIPHTYCEHMGARLACASIKVNIM
FGLGSISLLLLDVLLILSHIRLYAVFCLPSWEARLKALNTCGSHIGVILAFSTPAFFSFFTHCFGH
50 DIPQYIHIFLANLYVVVPPTLNPVTYGVRTKHIRETVLRIFFKTDH (SEQ ID NO: 509)

ATGCCTATAGCTAACGACACCCAGTTCATCTTCTTCACTTCTACTGCTGGGTATCCCAGG
GCTAGAAGATGTGCACATCTGGATTGGATTCCCTTTTTTCTCTGTGTATCTTATTGCACTCC
TGGGAAATGCTGCTATCTTCTTTGTGATCCAAACTGAGCAGAGTCTCCATGAGCCCATGTA
55 CTA CTACTGCCTGGCCATGTTGGATTCCATTGACCTGAGCTTGTCTACGGCCACCATTCCTCAAA
ATGCTGGGCATCTTCTGGTTCAATATCAAGGAAATATCTTTTGGAGGCTACCTTTCTCAGA

TGTTCTTCATCCATTTCTTCACTGTCATGGAGAGCATCGTATTGGTGGCCATGGCCTTTGAC
CGCTACATTGCCATTTGCAAACCTCTTTGGTACACCATGATCCTCACCAGCAAAATCATCA
GCCTCATTGCAGGCATTGCTGTCTGAGGAGCTTGACATGGTCATTCCACTGGTGTTCCT
CCTCTTAAGGTTGCCCTTCTGTGGACATCGTATCATCCCTCATACTTACTGTGAGCACATGG
5 GCATTGCCCCGTCTGGCCTGTGCCAGCATCAAAGTCAACATTATGTTTGGTCTTGGCAGTAT
TTCTCTCTTGTATTATTGGATGTGCTCCTTATTATTCTCTCCCATATCAGGATCCTCTATGCTGT
CTTCTGCCTGCCCTCCTGGGAAGCTCGACTCAAAGCTCTCAACACCTGTGGCTCTCACATT
GGTGTATCTTAGCCTTTTCTACACCAGCATTTTCTCTTTCTTTACACACTGCTTTGGCCAT
GATATCCCCCAATATATCCACATTTTCTTGGCTAATCTATATGTGGTTGTTCCTCCCAACCCT
10 CAATCCTGTAATCTATGGGGTCAGAACCAACATATTAGGGAGACAGTGCTGAGGATTTTC
TTCAAGACAGATCACTAA (SEQ ID NO: 510)

AOLFR328 sequences:

MALGNHSTITEFLLGLSADPNIRALLFVFLGIYLLTIMENLMLLLVRADSCLHKPMYFFLSH
15 LSFVDLCFSSVIVPKMLENLLSQRKTIISVEGCLAQVFFVFTAGTEACLLSGMAYDRHAAIRRP
LLYGQIMGKQLYMHLLVWGSWGLGFLDALINVLLAVNMVFCEAKIIHHYSYEMPSLLPLSCSDI
SRSLIVLLCSTLLHGLGNFLLVFLSYTRIISTILSISSTSGRSKAFSTCSAHLTAVTLYYGSGLLRHL
MPNSGSPIELIFSVQYTVVTPMLNSLIYSLKNKEVKVALKRTLEKYLQYTRR (SEQ ID NO: 511)

20 ATGGCCTTGGGGAATCACAGCACCATCACCGAGTTCCTCCTCCTTGGGCTGTCTGCCGACC
CCAACATCCGGGCTCTGCTCTTTGTGCTGTTCTTGGGGATTTACCTCCTGACCATAATGGA
AAACCTGATGCTGCTGCTCGTGATCAGGGCTGATTCTTGTCTCCATAAGCCCATGTATTTCT
TCCTGAGTCACCTCTCTTTTGTGATCTCTGCTTCTCTTCAGTCATTGTGCCCAAGATGCTG
GAGAACCTCCTGTACAGAGGAAAAACATTTAGTAGAGGGCTGCCTGGCTCAGGTCTTCT
25 TTGTGTTTGTCACTGCAGGGACTGAAGCCTGCCTTCTCTCAGGGATGGCCTATGACCGCCA
TGCTGCCATCCGCCGCCCACTACTTTATGGACAGATCATGGGTAAACAGCTGTATATGCAC
CTTGTGTGGGGCTCATGGGGACTGGGCTTTCTGGACGCACTCATCAATGTCTCCTAGCTG
TAAACATGGTCTTTTGTGAAGCCAAAATCATTACCACTACAGCTATGAGATGCCATCCCT
CCTCCCTCTGTCTGCTCTGATATCTCCAGAAGCCTCATCGTTTTGCTCTGCTCCACTCTCC
30 TACATGGGCTGGGAAACTTCCTTTTGGTCTTCTTATCCTACACCCGTATAATCTCTACCATC
CTAAGCATCAGCTCTACCTCGGGCAGAAGCAAGGCCTTCTCCACCTGCTCTGCCACCTCA
CTGCAGTGACACTTTACTATGGCTCAGGTTTGTCTCCGCCATCTCATGCCAACTCAGGTTC
CCCCATAGAGTTGATCTTCTCTGTGCAGTATACTGTAGTCACTCCCATGCTGAATTCCCTCA
TCTATAGCCTGAAAAATAAGGAAGTGAAGGTAGCTCTGAAAAGAACTTTGGAAAAATATT
35 TGCAATATAACCAGACGTTGA (SEQ ID NO: 512)

CLAIMS

What is Claimed:

1. An isolated nucleic acid sequence selected from the group consisting of:
 - 5 (i) an isolated nucleotide sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID

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 SEQ ID NO: 508, SEQ ID NO: 510; and SEQ ID NO: 512, or a fragment thereof

which comprises at least 75 nucleotides;

- 30 (ii) an isolated cDNA or an insoluble RNA transcribed therefrom that encodes a
 polypeptide having an amino acid sequence selected from the group consisting of:
 SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ
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which encodes at least 25 contiguous amino acids of said polypeptide;

(iii) a nucleic acid sequence that comprises at least 30% sequence identity with an isolated nucleic acid sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92,

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SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512, or to a fragment thereof

15 which comprises at least 100 contiguous nucleotides thereof;

(iv) a nucleic acid sequence that encodes a polypeptide having at least 40%
sequence identity at the amino acid level with a polypeptide having an amino acid
sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ
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15 SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID
NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293,
SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID
NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311,
SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID
20 NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329,
SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID
NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347,
SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID
NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365,
25 SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID
NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383,
SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID
NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401,
SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID
30 NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419,
SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID
NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437,
SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID

- NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455,
SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID
NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473,
SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID
5 NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491,
SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID
NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509
and SEQ ID NO: 511 or a nucleic acid sequence encoding at least 50 contiguous
amino acid residues thereof;
- 10 (v) an isolated nucleic acid sequence which encodes an olfactory receptor or a
fragment thereof that specifically hybridizes and exhibits at least 30% sequence
identity under stringent conditions to a nucleic acid sequence selected from the group
consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID
NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID
15 NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID
NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID
NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID
NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID
NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID
20 NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID
NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID
NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID
NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108,
SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID
25 NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126,
SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID
NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144,
SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID
NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162,
30 SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID
NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180,
SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID
NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198,

SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID
NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216,
SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID
NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234,
5 SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID
NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252,
SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID
NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270,
SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID
10 NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288,
SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID
NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306,
SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID
NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324,
15 SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID
NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342,
SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID
NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360,
SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID
20 NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378,
SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID
NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396,
SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID
NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414,
25 SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID
NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432,
SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID
NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450,
SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID
30 NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468,
SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID
NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486,
SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID

NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504,
SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512;

(vi) an isolated nucleic acid sequence that specifically hybridizes to (i) or a portion thereof under stringent hybridization conditions that is at least 20-30 nucleotides in

5 length; and

(vii) a naturally occurring allelic or synthetic variant of a nucleic acid sequence according to (i) or (ii), containing at least one substitution, deletion or addition mutation in the coding region.

10 2. The isolated nucleic acid sequence of Claim 1 which is selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214,

SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, 5 SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID 10 NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, 15 SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID 20 NO: 386, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, 25 SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID 30 NO: 476, SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID

NO: 512 or a fragment thereof which comprises at least 75 contiguous nucleotides thereof.

3. The isolated nucleic acid sequence of Claim 1 which encodes a
5 polypeptide having an amino acid sequence selected from the group consisting of:
SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ
ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ
ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ
ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ
10 ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ
ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ
ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ
ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ
ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ
15 ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ
ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109,
SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID
NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127,
SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID
20 NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145,
SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID
NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163,
SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID
NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181,
25 SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID
NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199,
SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID
NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217,
SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID
30 NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235,
SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID
NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253,
SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID

NO.: 263, SEQ ID NO.: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271,
 SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID
 NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289,
 SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID
 5 NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307,
 SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID
 NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325,
 SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID
 NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343,
 10 SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID
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 NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379,
 SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID
 15 NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397,
 SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID
 NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415,
 SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID
 NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433,
 20 SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID
 NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451,
 SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID
 NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469,
 SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID
 25 NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487,
 SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID
 NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505,
 SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof
 encoding at least 25 contiguous amino acid residues of said polypeptide.

30

4. An isolated nucleic acid sequence having at least 30-60% sequence
 identity with a nucleic acid sequence selected from the group consisting of: SEQ ID
 NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID

NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID
NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID
NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID
NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID
5 NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID
NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID
NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID
NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID
NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ
10 ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,
SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID
NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,
SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID
NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,
15 SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID
NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,
SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID
NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,
SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID
20 NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,
SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID
NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,
25 SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,
SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID
30 NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,
SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID

NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,
 SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID
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 SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID
 5 NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,
 SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID
 NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,
 SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID
 NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,
 10 SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID
 NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,
 SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID
 NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,
 SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID
 15 NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,
 SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID
 NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,
 SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID
 NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,
 20 SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID
 NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,
 SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512; or a fragment thereof
 comprising at least 100 contiguous nucleotides of any of said sequences.

25 5. An isolated nucleic acid sequence having at least 60-80% sequence
 identity with a nucleic acid sequence selected from the group consisting of: SEQ ID
 NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID
 NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID
 NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID
 30 NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID
 NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID
 NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID
 NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID

NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID
NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID
NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ
ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,
5 SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID
NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,
SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID
NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,
SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID
10 NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,
SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID
NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,
SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID
NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,
15 SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID
NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,
SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID
20 NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,
SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,
25 SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,
SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID
NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,
SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID
30 NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,
SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID
NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,
SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID

NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID
NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,
SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID
5 NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,
SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID
NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,
SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID
NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,
10 SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID
NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,
SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID
NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,
SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID
15 NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,
SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a fragment thereof
comprising at least 100 contiguous nucleotides of any of said sequences.

6. An isolated nucleic acid sequence having at least 80-90% sequence
20 identity with a nucleic acid sequence selected from the group consisting of: SEQ ID
NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID
NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID
NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID
NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID
25 NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID
NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID
NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID
NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID
NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID
30 NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ
ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,
SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID
NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,

SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID
NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,
SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID
NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,
5 SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID
NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,
SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID
NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,
SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID
10 NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID
NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,
SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,
15 SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,
SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID
20 NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,
SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID
NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,
SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID
NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,
25 SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID
NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,
SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID
NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID
30 NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,
SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID
NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,
SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID

NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,
SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID
NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,
SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID
5 NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,
SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID
NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,
SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID
NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,
10 SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a fragment thereof
comprising at least 100 contiguous nucleotides of any of said sequences.

7. An isolated nucleic acid sequence having at least 85% sequence
identity with a nucleic acid sequence selected from the group consisting of: SEQ ID
15 NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID
NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID
NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID
NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID
NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID
20 NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID
NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID
NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID
NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID
NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ
25 ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,
SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID
NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,
SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID
NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,
30 SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID
NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,
SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID
NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,

SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID
NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,
SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,
5 SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID
NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,
SEQ ID NO: 238, SEQ. ID NO. 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID
10 NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,
SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,
15 SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID
NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,
SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID
NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,
SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID
20 NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,
SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID
NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID
NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,
25 SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID
NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,
SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID
NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,
SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID
30 NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,
SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID
NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,
SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID

NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,
SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID
NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,
SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512, or a fragment thereof
5 comprising at least 100 contiguous nucleotides of any of said sequences.

8. An isolated nucleic acid sequence having at least 90% sequence
identity with a nucleic acid sequence selected from the group consisting of: SEQ ID
NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID
10 NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID
NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID
NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID
NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID
NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID
15 NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID
NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID
NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID
NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ
ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,
20 SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID
NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,
SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID
NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,
SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID
25 NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,
SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID
NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,
SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID
NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,
30 SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID
NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,

SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, 5 SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, 10 SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, 15 SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, 20 SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, 25 SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, 30 SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a fragment thereof comprising at least 100 contiguous nucleotides of any of said sequences.

9. An isolated nucleic acid sequence according to Claim 1 which encodes a polypeptide having at least 40-60% sequence identity with a polypeptide having an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID

NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291,
 SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID
 NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309,
 SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID
 5 NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327,
 SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID
 NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345,
 SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID
 NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363,
 10 SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID
 NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381,
 SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID
 NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399,
 SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID
 15 NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417,
 SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID
 NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435,
 SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID
 NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453,
 20 SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID
 NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471,
 SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID
 NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489,
 SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID
 25 NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507,
 SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof that comprises at least
 40 contiguous amino acids thereof.

10. An isolated nucleic acid sequence according to Claim 1 which encodes
 30 a polypeptide having at least 60-70% sequence identity with a polypeptide having an
 amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID
 NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID
 NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID

NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID
NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID
NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID
NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID
5 NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID
NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID
NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID
NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ
ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111,
10 SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID
NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129,
SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID
NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147,
SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID
15 NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165,
SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID
NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183,
SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID
NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201,
20 SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID
NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219,
SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID
NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237,
SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID
25 NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255,
SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID
NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273,
SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID
NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291,
30 SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID
NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309,
SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID
NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327,

SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, 5 SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, 10 SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, 15 SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, 20 SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof that comprises at least 40 contiguous amino acids thereof.

11. An isolated nucleic acid sequence according to Claim 1 which encodes 25 a polypeptide having at least 70-80% sequence identity with a polypeptide having an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID

NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID
NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID
NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ
ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111,
5 SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID
NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129,
SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID
NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147,
SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID
10 NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165,
SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID
NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183,
SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID
NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201,
15 SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID
NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219,
SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID
NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237,
SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID
20 NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255,
SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID
NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273,
SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID
NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291,
25 SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID
NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309,
SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID
NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327,
SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID
30 NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345,
SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID
NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363,
SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID

NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381,
SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID
NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399,
SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID
5 NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417,
SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID
NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435,
SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID
NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453,
10 SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID
NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471,
SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID
NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489,
SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID
15 NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507,
SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof that comprises at least
40 contiguous amino acids thereof.

12. An isolated nucleic acid sequence according to Claim 1 which encodes
20 a polypeptide having at least 80-90% sequence identity with a polypeptide having an
amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID
NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID
NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID
NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID
25 NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID
NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID
NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID
NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID
NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID
30 NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID
NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ
ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111,
SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID

NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129,
SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID
NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147,
SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID
5 NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165,
SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID
NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183,
SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID
NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201,
10 SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID
NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219,
SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID
NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237,
SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID
15 NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255,
SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID
NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273,
SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID
NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291,
20 SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID
NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309,
SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID
NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327,
SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID
25 NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345,
SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID
NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363,
SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID
NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381,
30 SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID
NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399,
SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID
NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417,

SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID
NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435,
SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID
NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453,
5 SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID
NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471,
SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID
NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489,
SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID
10 NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507,
SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof that comprises at least
40 contiguous amino acids thereof.

13. An isolated nucleic acid sequence according to Claim 1 which encodes
15 a polypeptide having about 90-99% sequence identity with a polypeptide having an
amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID
NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID
NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID
NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID
20 NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID
NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID
NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID
NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID
NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID
25 NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID
NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ
ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111,
SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID
NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129,
30 SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID
NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147,
SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID
NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165,

SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID
NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183,
SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID
NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201,
5 SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID
NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219,
SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID
NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237,
SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID
10 NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255,
SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID
NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273,
SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID
NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291,
15 SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID
NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309,
SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID
NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327,
SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID
20 NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345,
SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID
NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363,
SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID
NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381,
25 SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID
NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399,
SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID
NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417,
SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID
30 NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435,
SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID
NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453,
SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID

NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471,
SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID
NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489,
SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID
5 NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507,
SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof that comprises at least
40 contiguous amino acids thereof.

14. An isolated nucleic acid sequence which exhibits at least 50%
10 sequence identity with a nucleic acid sequence selected from the group consisting of:
SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ
ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ
ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ
ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ
15 ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ
ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ
ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ
ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ
ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ
20 ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100,
SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID
NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118,
SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID
NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136,
25 SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID
NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154,
SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID
NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172,
SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID
30 NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190,
SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID
NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208,
SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID

NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226,
SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID
NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244,
SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID
5 NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262,
SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID
NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280,
SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID
NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298,
10 SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID
NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316,
SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID
NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334,
SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID
15 NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352,
SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID
NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370,
SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID
NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388,
20 SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID
NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406,
SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID
NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424,
SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID
25 NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442,
SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID
NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460,
SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID
NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478,
30 SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID
NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496,
SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID
NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid

sequence which exhibits at least 50% sequence identity to a fragment comprising at least 100 contiguous nucleotides of said nucleic acid sequence.

15. An isolated nucleic acid sequence which exhibits at least 60% sequence identity with a nucleic acid sequence selected from the group consisting of:
- 5 SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262,

SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, 5 SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, 10 SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, 15 SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, 20 SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, 25 SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence which exhibits at least 60% sequence identity to a fragment comprising at 30 least 100 contiguous nucleotides of said nucleic acid sequence.

16. An isolated nucleic acid sequence that exhibits at least 70% sequence identity with a nucleic acid sequence selected from the group consisting of: SEQ ID

NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID
NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID
NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID
NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID
5 NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID
NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID
NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID
NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID
NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID
10 NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ
ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,
SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID
NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,
SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID
15 NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,
SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID
NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,
SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID
NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,
20 SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID
NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,
SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID
25 NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,
SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,
30 SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,

SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, 5 SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID 10 NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, 15 SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID 20 NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence having at least 70% sequence identity with a fragment thereof comprising at least 100 25 contiguous nucleotides thereof.

17. An isolated nucleic acid sequence that exhibits at least 80% sequence identity with a nucleic acid sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID 30 NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID

NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID
NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID
NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID
NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID
5 NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ
ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,
SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID
NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,
SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID
10 NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,
SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID
NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,
SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID
NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,
15 SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID
NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,
SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID
20 NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,
SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,
25 SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,
SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID
30 NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,
SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID
NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,
SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID

NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,
 SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID
 NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,
 SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID
 5 NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,
 SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID
 NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,
 SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID
 NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,
 10 SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID
 NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,
 SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID
 NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,
 SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID
 15 NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,
 SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID
 NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,
 SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence
 having at least 80% sequence identity with a fragment thereof comprising at least 100
 20 contiguous nucleotides thereof.

18. An isolated nucleic acid sequence that exhibits at least 85% sequence
 identity with a nucleic acid sequence selected from the group consisting of: SEQ ID
 NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID
 25 NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID
 NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID
 NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID
 NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID
 NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID
 30 NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID
 NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID
 NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID
 NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ

ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,
SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID
NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,
SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID
5 NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,
SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID
NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,
SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID
NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,
10 SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID
NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,
SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID
15 NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,
SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,
20 SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,
SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID
25 NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,
SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID
NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,
SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID
NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,
30 SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID
NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID
NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,

SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID
 NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,
 SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID
 NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,
 5 SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID
 NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,
 SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID
 NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,
 SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID
 10 NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,
 SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID
 NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,
 SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence
 having at least 85% sequence identity with a fragment thereof comprising at least 100
 15 contiguous nucleotides thereof.

19. An isolated nucleic acid sequence that exhibits at least 90% sequence
 identity with a nucleic acid sequence selected from the group consisting of: SEQ ID
 NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID
 20 NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID
 NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID
 NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID
 NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID
 NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID
 25 NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID
 NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID
 NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID
 NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ
 ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,
 30 SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID
 NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,
 SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID
 NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,

SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID
NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,
SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID
NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,
5 SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID
NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,
SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID
10 NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,
SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,
15 SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,
SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID
20 NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,
SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID
NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,
SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID
NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,
25 SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID
NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID
NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,
SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID
30 NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,
SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID
NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,
SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID

NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,
 SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID
 NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,
 SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID
 5 NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,
 SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID
 NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,
 SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence
 having at least 90% sequence identity with a fragment thereof comprising at least 100
 10 contiguous nucleotides thereof.

20. An isolated nucleic acid sequence that exhibits at least 95% sequence
 identity with a nucleic acid sequence selected from the group consisting of: SEQ ID
 NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID
 15 NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID
 NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID
 NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID
 NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID
 NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID
 20 NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID
 NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID
 NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID
 NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ
 ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,
 25 SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID
 NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,
 SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID
 NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,
 SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID
 30 NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,
 SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID
 NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,
 SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID

NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,
SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID
5 NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,
SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,
10 SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,
SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID
15 NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,
SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID
NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,
SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID
NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,
20 SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID
NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID
NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,
SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID
25 NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,
SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID
NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,
SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID
NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,
30 SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID
NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,
SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID
NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,

SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID
NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,
SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence
having at least 95% sequence identity with a fragment thereof comprising at least 100
5 contiguous nucleotides thereof.

21. An isolated nucleic acid sequence that exhibits about 96-99% sequence
identity with a nucleic acid sequence encoding an olfactory receptor selected from the
group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8,
10 SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18,
SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28,
SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38,
SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48,
SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58,
15 SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68,
SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78,
SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88,
SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98,
SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID
20 NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116,
SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID
NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134,
SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID
NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152,
25 SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID
NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170,
SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID
NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188,
SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID
30 NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206,
SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID
NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224,
SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID

NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ. ID NO. 240, SEQ ID NO: 242,
SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID
NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260,
SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID
5 NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278,
SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID
NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296,
SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID
NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314,
10 SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID
NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332,
SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID
NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350,
SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID
15 NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368,
SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID
NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386,
SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID
NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404,
20 SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID
NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422,
SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID
NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440,
SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID
25 NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458,
SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID
NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476,
SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID
NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494,
30 SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID
NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512
or a fragment having at least 96-99% sequence identity with a fragment thereof
comprising at least 100 contiguous nucleotides thereof.

22. A nucleic acid sequence which encodes for a functional olfactory receptor polypeptide, wherein said nucleic acid sequence comprises a portion which is at least 100 nucleotides in length and exhibits at least 40% sequence identity with at least 100 contiguous nucleotides of a portion of an olfactory receptor encoding a nucleic acid sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256,

SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID
NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274,
SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID
NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292,
5 SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID
NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310,
SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID
NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328,
SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID
10 NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346,
SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID
NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364,
SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID
NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382,
15 SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID
NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400,
SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID
NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418,
SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID
20 NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436,
SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID
NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454,
SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID
NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472,
25 SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID
NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490,
SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID
NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508,
SEQ ID NO: 510 and SEQ ID NO: 512.

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23. The nucleic acid sequence of Claim 22 which is a chimeric nucleic acid sequence, wherein said nucleic acid sequence is produced by combining portions of at least two different G protein-coupled receptors.

24. The chimeric nucleic acid sequence of Claim 23 wherein said two different G protein-coupled receptors are olfactory receptors.

5 25. The chimeric nucleic acid sequence of Claim 23 wherein said chimeric sequence contains at least 200 contiguous nucleotides that are at least 40% identical to a portion of one of said olfactory receptor encoding nucleic acid sequences.

10 26. An isolated nucleic acid sequence according to Claim 1, wherein said isolated nucleic acid sequence is directly or indirectly attached to a nucleic acid sequence that encodes a detectable polypeptide.

27. The nucleic acid sequence of Claim 26, wherein said detectable polypeptide is green fluorescent protein, or a fragment or variant thereof.

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28. An isolated nucleic acid sequence which encodes a polypeptide that exhibits at least 40% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID

20

25

30

NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161,
SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID
NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179,
SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID
5 NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197,
SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID
NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215,
SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID
NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233,
10 SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID
NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251,
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NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269,
SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID
15 NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,
SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID
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NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,
20 SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID
NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341,
SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID
NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359,
SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID
25 NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377,
SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID
NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395,
SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID
NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413,
30 SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID
NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431,
SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID
NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449,

SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, 5 SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof comprising at least 40 contiguous amino acids thereof that optionally is directly or indirectly attached to a sequence that facilitates the expression and/or 10 translocation of said polypeptide on the surface of a cell.

29. An isolated nucleic acid sequence which encodes a polypeptide that exhibits at least 50% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, 25 SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, 30 SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID

NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197,
SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID
NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215,
SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID
5 NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233,
SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID
NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251,
SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID
NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269,
10 SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID
NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,
SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID
NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305,
SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID
15 NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,
SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID
NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341,
SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID
NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359,
20 SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID
NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377,
SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID
NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395,
SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID
25 NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413,
SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID
NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431,
SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID
NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449,
30 SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID
NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467,
SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID
NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485,

SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof comprising at least 40 contiguous amino acids thereof that optionally is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of said polypeptide on the surface of a cell.

30. An isolated nucleic acid sequence which encodes a polypeptide that exhibits at least 60% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID

NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof comprising at least 40 contiguous amino acids thereof that optionally

is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of said polypeptide on the surface of a cell.

31. An isolated nucleic acid sequence which encodes a polypeptide that exhibits at least 70% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID

NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269,
SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID
NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,
SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID
5 NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305,
SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID
NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,
SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID
NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341,
10 SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID
NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359,
SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID
NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377,
SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID
15 NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395,
SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID
NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413,
SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID
NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431,
20 SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID
NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449,
SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID
NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467,
SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID
25 NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485,
SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID
NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503,
SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a
fragment thereof comprising at least 40 contiguous amino acids thereof that optionally
30 is directly or indirectly attached to a sequence that facilitates the expression and/or
translocation of said polypeptide on the surface of a cell.

32. An isolated nucleic acid sequence which encodes a polypeptide that exhibits at least 80% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,

SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, 5 SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, 10 SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, 15 SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, 20 SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, 25 SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof comprising at least 40 contiguous amino acids thereof that optionally is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of said polypeptide on the surface of a cell.

30 33. An isolated nucleic acid sequence which encodes a polypeptide that exhibits at least 85% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID

NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID
NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID
NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID
NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID
5 NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID
NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID
NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID
NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID
NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107,
10 SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID
NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125,
SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID
NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143,
SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID
15 NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161,
SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID
NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179,
SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID
NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197,
20 SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID
NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215,
SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID
NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233,
SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID
25 NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251,
SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID
NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269,
SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID
NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,
30 SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID
NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305,
SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID
NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,

SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof comprising at least 40 contiguous amino acids thereof that optionally is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of said polypeptide on the surface of a cell.

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34. An isolated nucleic acid sequence which encodes a polypeptide that exhibits at least 90% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID

30

NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID
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5 NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107,
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35. An isolated nucleic acid sequence which encodes a polypeptide that exhibits about 90-99% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID 25 NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID 30 NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID

NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107,
SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID
NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125,
SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID
5 NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143,
SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID
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10 SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID
NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197,
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SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID
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20 SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID
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25 NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,
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36. The isolated nucleic acid sequence according to Claim 26, wherein said isolated nucleic acid sequence is operably linked to a constitutive promoter.

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37. The isolated nucleic acid sequence according to Claim 1, wherein said isolated nucleic acid sequence is operably linked to a regulatable promoter.

38. The isolated nucleic acid sequence of Claim 1, wherein said isolated 25 nucleic acid sequence is directly or indirectly attached to a nucleic acid sequence encoding a mammalian rhodopsin polypeptide or a fragment thereof.

39. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes a fragment of at least 60 contiguous amino acids of a polypeptide having 30 an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID

NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID
NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID
NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID
NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID
5 NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID
NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID
NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ
ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111,
SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID
10 NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129,
SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID
NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147,
SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID
NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165,
15 SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID
NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183,
SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID
NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201,
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20 NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219,
SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID
NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237,
SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID
NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255,
25 SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID
NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273,
SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID
NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291,
SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID
30 NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309,
SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID
NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327,
SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID

NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345,
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5 NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381,
SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID
NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399,
SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID
NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417,
10 SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID
NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435,
SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID
NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453,
SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID
15 NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471,
SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID
NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489,
SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID
NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507,
20 SEQ ID NO: 509, and SEQ ID NO: 511.

40. The isolated nucleic acid molecule of Claim 39, wherein the nucleotide
sequence encodes at least 100 amino acids.

25 41. The isolated nucleic acid molecule of Claim 39, wherein the nucleotide
sequence encodes at least 150 amino acids.

42. The isolated nucleic acid molecule of Claim 39, wherein the nucleotide
sequence encodes at least 200 amino acids.

30 43. The isolated nucleic acid molecule of Claim 39, wherein the nucleotide
sequence encodes at least 250 amino acids.

44. The isolated nucleic acid molecule of Claim 39, wherein the polypeptide is an olfactory G protein-coupled receptor.

45. The isolated nucleic acid molecule of Claim 39, wherein the expression
5 product binds an odorant.

46. The isolated nucleic acid molecule of Claim 1 comprising a nucleotide sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240,

SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID
NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258,
SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID
NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276,
5 SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID
NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294,
SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID
NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312,
SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID
10 NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330,
SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID
NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348,
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15 SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID
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SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID
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20 NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420,
SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID
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25 SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID
NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474,
SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID
NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492,
SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID
30 NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510
and SEQ ID NO: 512.

47. An expression vector that comprises a nucleic acid sequence according to Claim 1.

48. The expression vector of Claim 47, wherein said vector is a
5 mammalian, yeast, bacterial or insect expression vector.

49. A cell which is transfected or transformed with at least one nucleic acid sequence according to Claim 1.

10 50. A mammalian cell according to Claim 49.

51. A human cell according to Claim 50.

52. A yeast or insect cell according to Claim 49.

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53. The mammalian cell according to Claim 49 which is selected from the group consisting of: an olfactory cell, Chinese hamster ovary cell, baby hamster kidney cell, and a myeloma cell.

20 54. A solid phase comprising at least one isolated nucleic acid sequence according to Claim 1.

55. A solid phase comprising at least one isolated nucleic acid sequence according to Claim 1, wherein the solid phase is attached to an array comprising at
25 least one additional nucleic acid sequence.

56. The solid phase according to Claim 55 which comprises an array of at least 4 different nucleic acid sequences that encode olfactory receptors or fragments or variants thereof.

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57. The solid phase according to Claim 55 which comprises at least 10 different nucleic acid sequences that encode olfactory receptors or fragments or variants thereof.

58. The solid phase according to Claim 55 which comprises at least 50 different nucleic acid sequences that encode olfactory receptors or fragments or variants thereof.

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59. The solid phase according to Claim 55 which comprises at least 100 different sequences that encode olfactory receptors or fragments or variants thereof.

60. An isolated polypeptide that is selected from the group consisting of:

- 10 (i) a polypeptide comprising an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215,

SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID
NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233,
SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID
NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251,
5 SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID
NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269,
SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID
NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,
SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID
10 NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305,
SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID
NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,
SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID
NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341,
15 SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID
NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359,
SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID
NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377,
SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID
20 NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395,
SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID
NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413,
SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID
NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431,
25 SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID
NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449,
SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID
NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467,
SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID
30 NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485,
SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID
NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503,
SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511;

- (ii) a polypeptide comprising an amino acid sequence that exhibits at least 40% sequence identity with an amino acid sequence selected from the group consisting of:
- SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289,

- SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511;
- (iii) a polypeptide comprising an amino acid sequence that exhibits at least 60% sequence identity with a fragment of a polypeptide according to (i) which fragment is at least 40 amino acids in length;
- (iv) a chimeric polypeptide that comprises a portion of a polypeptide according to (i) or (ii) that is at least 40 amino acids in length and a portion of at least one other G protein-coupled receptor; and
- (v) a variant of a polypeptide according to (i) which differs by said polypeptide by at least one substitution, addition or deletion modification.

61. An isolated polypeptide according to Claim 60 wherein such polypeptide exhibits at least 70% sequence identity with a polypeptide having a sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275,

SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, 5 SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, 10 SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, 15 SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, 20 SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, 25 SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

62. An isolated polypeptide according to Claim 60 wherein said 30 polypeptide exhibits at least 80% sequence identity with a polypeptide having a sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID

NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID
NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID
NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID
NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID
5 NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID
NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID
NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID
NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ
ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113,
10 SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID
NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131,
SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID
NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149,
SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID
15 NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167,
SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID
NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185,
SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID
NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203,
20 SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID
NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221,
SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID
NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239,
SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID
25 NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257,
SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID
NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275,
SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID
NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293,
30 SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID
NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311,
SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID
NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329,

SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID
NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347,
SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID
NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365,
5 SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID
NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383,
SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID
NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401,
SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID
10 NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419,
SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID
NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437,
SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID
NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455,
15 SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID
NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473,
SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID
NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491,
SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID
20 NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509
and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

63. An isolated polypeptide according to Claim 60 wherein said
polypeptide exhibits at least 90% sequence identity with a polypeptide having a
25 sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ
ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID
NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID
NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID
NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID
30 NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID
NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID
NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID
NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID

NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID
NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ
ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113,
SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID
5 NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131,
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SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID
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NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239,
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NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257,
20 SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID
NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275,
SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID
NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293,
SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID
25 NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311,
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NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329,
SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID
NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347,
30 SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID
NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365,
SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID
NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383,

SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID
NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401,
SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID
NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419,
5 SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID
NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437,
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NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455,
SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID
10 NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473,
SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID
NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491,
SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID
NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509
15 and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

64. An isolated polypeptide according to Claim 60 wherein said
polypeptide exhibits about 80-90% sequence identity with a polypeptide having a
sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ
20 ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID
NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID
NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID
NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID
NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID
25 NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID
NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID
NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID
NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID
NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ
30 ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113,
SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID
NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131,
SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID

NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149,
SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID
NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167,
SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID
5 NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185,
SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID
NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203,
SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID
NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221,
10 SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID
NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239,
SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID
NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257,
SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID
15 NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275,
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NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293,
SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID
NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311,
20 SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID
NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329,
SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID
NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347,
SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID
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SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID
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SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID
NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401,
30 SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID
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SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID
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SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID
NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473,
5 SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID
NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491,
SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID
NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509
and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

10

65. An isolated polypeptide according to Claim 60 wherein said
polypeptide exhibits at least 90-95% sequence identity with a polypeptide having a
sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ
ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID
15 NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID
NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID
NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID
NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID
NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID
20 NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID
NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID
NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID
NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ
ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113,
25 SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID
NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131,
SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID
NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149,
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30 NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167,
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NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185,
SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID

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SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID
NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221,
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5 NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239,
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10 SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID
NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293,
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20 SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID
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SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID
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30 SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID
NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473,
SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID
NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491,

SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

5 66. An isolated polypeptide according to Claim 60 wherein said polypeptide exhibits about 95-99% sequence identity with a polypeptide having a sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID

NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257,
 SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID
 NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275,
 SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID
 5 NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293,
 SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID
 NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311,
 SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID
 NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329,
 10 SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID
 NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347,
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 NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365,
 SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID
 15 NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383,
 SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID
 NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401,
 SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID
 NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419,
 20 SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID
 NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437,
 SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID
 NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455,
 SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID
 25 NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473,
 SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID
 NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491,
 SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID
 NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509
 30 and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

67. A variant according to Claim 60(v) which comprises at least 5 conservative amino acid substitutions.

68. A variant according to Claim 60(v) which comprises at most 5 conservative amino acid substitutions.

5 69. A variant according to Claim 60(v) which comprises 5 to 7 conservative substitution modifications.

70. A variant according to Claim 60(v) which comprises 3 to 4 conservative substitution modifications.

10

71. A variant according to Claim 60(v) which comprises 1 or 2 conservative substitution modifications.

72. A solid phase comprising at least one directly or indirectly
15 immobilized isolated polypeptide according to Claim 60, or a cell which expresses said polypeptide on the surface thereof.

73. The solid phase of Claim 72 comprising at least 4 different immobilized polypeptides according to Claim 60, or a cell which expresses said
20 polypeptide on the surface thereof.

74. The solid phase of Claim 72 comprising at least 16 different immobilized polypeptides according to Claim 60, or a cell which expresses said polypeptide on the surface thereof.

25

75. The solid phase of Claim 72 comprising at least 25 different immobilized polypeptides according to Claim 60 or a cell which expresses said polypeptide on the surface thereof.

30 76. A method of detecting expression of an olfactory receptor gene comprising (a) hybridizing at least one sample with a nucleic acid according to Claim 1 and (b) detecting expression of the olfactory receptor gene by a positive hybridization signal.

77. A method of screening a library comprising (a) hybridizing the library with a nucleic acid according to Claim 1 and (b) detecting one or more olfactory receptor clones in the library by a positive hybridization signal.

5

78. A recombinant polynucleotide comprising a nucleic acid according to Claim 1 attached directly or indirectly to a heterologous nucleic acid.

79. An expression vector comprising the nucleic acid of Claim 1 and an operably linked heterologous nucleic acid that drives expression thereof.

10

80. A transfected or transformed cell comprising the recombinant polynucleotide of Claim 78 introduced into a host cell, or a progeny thereof.

15

81. A transgenic non-human organism comprising the recombinant polynucleotide of Claim 78 introduced into a cell of a host non-human organism, or a progeny thereof.

20

82. A method of making a recombinant polynucleotide comprising ligating the nucleic acid of Claim 1 to a heterologous nucleic acid.

83. The method of Claim 82 wherein the heterologous nucleic acid comprises a translational and/or transcriptional regulatory region.

25

84. A method of making a transfected cell comprising introducing the recombinant polynucleotide of Claim 79 into a host cell, and propagating the host cell in which the recombinant polynucleotide has been introduced.

30

85. A method of detecting specific binding of a putative ligand to an olfactory receptor comprising (a) contacting the putative ligand with a cell in which the expression vector of Claim 79 has been introduced, wherein the olfactory receptor is expressed by the cell thereby, and (b) directly or indirectly detecting specific binding between the putative ligand and the olfactory receptor.

86. A method of making transgenic non-human organism comprising introducing the recombinant polynucleotide of Claim 78 into a cell of a host non-human organism, or propagating the host non-human organism in which the
5 recombinant polynucleotide has been introduced.

87. An isolated protein molecule comprising a fragment of at least 60 contiguous amino acids of a polypeptide having an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID
10 NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID
15 NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ
20 ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151,
25 SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID
30 NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID

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5 NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277,
SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID
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10 SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID
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20 SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID
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SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID
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SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID
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30 SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID
NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO:
511.

88. The isolated protein molecule of Claim 87, wherein the fragment contains at least 100 amino acids.

89. The isolated protein molecule of Claim 87, wherein the fragment
5 contains at least 150 amino acids.

90. The isolated protein molecule of Claim 87, wherein the fragment contains at least 200 amino acids.

10 91. The isolated protein molecule of Claim 87, wherein the fragment contains at least 250 amino acids.

92. The isolated protein molecule of Claim 87, which is a functional olfactory receptor polypeptide.

15

93. The isolated protein molecule of Claim 87, wherein the fragment specifically binds an odorant molecule.

94. A recombinant polypeptide comprising the protein molecule of Claim
20 87 and a heterologous peptide domain.

95. The recombinant polypeptide of Claim 94, wherein the heterologous peptide domain comprises a G protein-coupled receptor transmembrane domain.

25 96. The recombinant polypeptide of Claim 94 comprising a seven-transmembrane receptor with an olfactory receptor ligand-binding domain, wherein the olfactory receptor ligand-binding domain is a chimera of at least two different olfactory receptors.

30 97. A method of detecting specific binding of a ligand to an olfactory receptor comprising (a) contacting the ligand with the protein of Claim 86, and (b) directly or indirectly detecting specific binding between the ligand and the olfactory receptor.

98. An antibody or antibody fragment that specifically binds a polypeptide having an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281,

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5 SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID
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SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID
NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353,
SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID
10 NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371,
SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID
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SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID
NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407,
15 SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID
NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425,
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20 NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461,
SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID
NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479,
SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID
NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497,
25 SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID
NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

99. A method of detecting specific binding of the antibody of Claim 98 to
an olfactory receptor comprising (a) contacting the antibody with a sample comprising
30 the olfactory receptor and (b) detecting specific binding therebetween.

100. The method of Claim 99, wherein specific binding of the antibody to a
cell in the sample identifies the cell as an olfactory cell.

101. A method of screening a library of chemical compounds for compounds that are involved in olfactory sensation comprising contacting compounds in said library with at least one polypeptide according to Claim 87 and identifying
5 compounds that specifically bind to at least one of said polypeptides.

102. The method of Claim 101 wherein said library is a combinatorial chemical library.

10 103. The method of Claim 101 wherein said library is a peptide library.

104. The method of Claim 101 wherein said library is a peptide, encoded peptide, benzodiazepine, diversomer, vinylogous polypeptide, nonpeptidal peptidominetic, or small molecule organic compound library.

15 105. The method of Claim 101 wherein said library is a random combination of compounds.

106. The method of Claim 101 wherein said compounds are screened by
20 high turning point screening.

107. The method of Claim 101 wherein said screening is effected using animal cells or tissues that express at least one of said polypeptides.

25 108. A cell-based assay for identifying molecules that interact with an olfactory receptor comprising:

obtaining a cell that expresses at least one polypeptide according to Claim 60 or a chimeric protein comprising a portion of said protein and that of another G protein-coupled receptor, and which optionally expresses at least one functional G protein;

30 contacting said cell with a molecule to be screened for its ability to modulate an olfactory receptor; and
detecting whether modulation occurs.

109. The method of Claim 108 wherein modulation is detected based on changes in intracellular calcium.

110. The method of Claim 108 wherein modulation is detected by
5 measuring the transfer of ^{32}P from gamma-labeled GTP to the olfactory receptor polypeptide.

111. The method of Claim 108 wherein modulation is determined based on a comparison to a control compound known to modulate the particular olfactory
10 receptor protein.

112. The method of Claim 108 wherein the G protein is $\text{G}\alpha 15$ or $\text{G}\alpha 16$ or another promiscuous G protein.

113. The method of Claim 108 wherein modulation is determined by
15 detecting whether a change in the level of intracellular cyclic nucleotides occurs.

114. The method of Claim 108 wherein modulation is determined based on the level of transcription of said olfactory polypeptide after contacting the cell with the
20 screened compound.

115. The method of Claim 108 when said screened compounds are synthesized by computer assisted drug devices based on the predicted or actual three-dimensional structure of the amino acid sequence of the olfactory protein or a
25 fragment thereof.

116. The method of Claim 108 wherein compounds that modulate olfactory receptor are identified based on whether they specifically bind to a olfactory receptor polypeptide.
30

117. The method of Claim 108 wherein modulation refers to the inhibition of olfactory receptor function.

118. The method of Claim 108 wherein modulation refers to the enhancement of olfactory receptor function.

119. A method for representing the olfactory perception of one or more
5 odors in one or more mammals, comprising:
providing values X_1 to X_n representative of the quantitative stimulation of each of n
odor receptors of said mammals; and
generating from said values a quantitative representation of odor perception, wherein
at least one of said odor receptors is an odor receptor polypeptide having a sequence
10 that is at least about 40% identical to a sequence selected from the group consisting
of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9,
SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19,
SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29,
SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39,
15 SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49,
SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59,
SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69,
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SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89,
20 SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99,
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NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135,
25 SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID
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SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID
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SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID
5 NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261,
SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID
NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279,
SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID
NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297,
10 SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID
NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315,
SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID
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25 NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441,
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SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID
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30 SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID
NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495,
SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID
NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

120. The method of claim 119, wherein said representation constitutes a point or a volume in n-dimensional space.

5 121. The method of claim 119, wherein said representation constitutes a graph or a spectrum.

122. The method of claim 119, wherein said representation constitutes a matrix of quantitative representations.

10

123. The method of claim 119, wherein said providing step comprises contacting a plurality of recombinantly produced olfactory receptors with a test composition, and quantitatively measuring the interaction of said composition with said receptors.

15

124. A method for predicting the odor perception in a mammal generated by one or more molecules or combinations of molecules comprising:

providing values X_1 to X_n representative of the quantitative stimulation of each of n odor receptors of said mammal, for one or more molecules or combinations of molecules yielding known odor perception in a mammal,

20

generating from said values a quantitative representation of odor perception in a mammal for the one or more molecules or combinations of molecules yielding known odor perception in a mammal;

providing values X_1 to X_n representative of the quantitative stimulation of each of n odor receptors of said mammal, for one or more molecules or combinations of molecules yielding unknown odor perception in a mammal;

25

generating from said values a quantitative representation of odor perception in a mammal for the one or more molecules or combinations of molecules yielding unknown odor perception in a mammal; and

30 predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown odor perception in a mammal by comparing the quantitative representation of odor perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown odor

perception in a mammal to the quantitative representation of odor perception in a mammal for the one or more molecules or combinations of molecules yielding known odor perception in a mammal, wherein at least one of said odor receptors is a odor receptor polypeptide having a sequence that is at least about 40% identical to a

5 sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID

10 NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID

15 NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID

20 NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185,

25 SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID

30 NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO:

267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ
ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285,
SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID
NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303,
5 SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID
NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321,
SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID
NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339,
SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID
10 NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357,
SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID
NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375,
SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID
NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393,
15 SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID
NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411,
SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID
NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429,
SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID
20 NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447,
SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID
NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465,
SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID
NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483,
25 SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID
NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501,
SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID
NO: 511.

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AOLFR27 . pr .	M	PS	20	*	40	*	60	*	80	*	100	34
AOLFR28 . pr .	M								QNYSIITSEFNEGFSAPQHLPLELILL			34
AOLFR29 . pr .	M	MSFAPNA							P--NFTDVTETLILCLTCRQE-LQVLEFFVFLA			31
AOLFR30 . pr .	M								SHSPVLELLIGFS-RANISYTLLEFFELA			35
AOLFR31 . pr .	M	GT							GFLSPMHPORPPQRRMAAGHSTVTEIKCLTRAD-LQLPLELFLG			50
AOLFR32 . pr .	M	NSLK							GNDTVVETLIGLSEDTT-VCAILFLVFLG			33
AOLFR33 . pr .	M								DGNHTALTGFIILGLTDDPI-LRVILEMILS			36
AOLFR34 . pr .	M	LE							GV--EH-L-----LLLLLTDVNSKELQSGNOTSVSHFVGLHHPPO-LGAPLEFLAV			54
AOLFR35 . pr .	M	EP							LNRT-----E-VSEFFKCGSGPA-LEHLLFPLCSA			33
AOLFR36 . pr .	M											1
AOLFR37 . pr .	M	EK							ANET-----SPVNCFMILRLSAPE-LEKTFVILL			34
AOLFR38 . pr .	M											1
AOLFR39 . pr .	M								GVKNHSTVTEILSCLTEQAEI-LQLPLELFLG			33
AOLFR40 . pr .	M								SNATLLTATILGLPHAPG-LDAPLFGIFLV			31
AOLFR41 . pr .	M								NPENWTQVTSFVILGEPSSHLLI--QFLVFLGLMW			33
AOLFR42 . pr .	M								NPAHSHQ---VAGEVLGLSOWWEL-REVEFTVESA			33
AOLFR43 . pr .	M	KPQLL							IATSNGLVH-AAVELLIVGIPGLGPTIHFWLAFPLCF			46
AOLFR44 . pr .	M								SSCNFTH-A-TEVLIGIPGLEKA-HFWVGFPLLS			32
AOLFR45 . pr .	M	PSNIT							ST---H-PAVELLIVGIPGLEH-LHAWISIPPCF			35
AOLFR46 . pr .	M								LNKHCGWMIHTWLNITREDDSDFKNFIOIGLSCGNPHSTTSMYELCFCSTSLIGFKVHWSRLIXKLYMASPNNDSTAPVSELLICFPNFQSMOH-WLSLPLSL			107
AOLFR47 . pr .	M	ASNIT							LT---H-PTAFELIVGIPGLEH-LHINISIPFCL			35
AOLFR48 . pr .	M								VDPNNGNESSA-T-VETILIGLPLEEA-QFWLAFPLCS			36
AOLFR49 . pr .	M	LTFHN							PSSEMIIGIPGLES-LHVNLSIPFGS			35
AOLFR50 . pr .	M	LDSFTSFLJ							ALSNSSWRLP-QPSSEIVGIPGLEE-SQHWIALPLGI			51
AOLFR51 . pr .	M								QOILRDCILLIHLICINRKKVSLVM			63
AOLFR52 . pr .	M								ICPAYNHTMETPASLLVIGIPGLQSS-HLWLAISLSA			37

FIG. 1 (CONT-2)

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AOALFR01	pr	QVWVWVGNGLIVALS	FYLH	PMY	FIANF	FAD	SSIS	SV	PKMI	VNIQT	SQS	ISY	ESIT	QV	YESI	VFV	VIDN	LIG	WYAL	FEVA	CHP	PI	YTI	IN	RPR	:	152		
AOALFR02	pr	QVWVWVGNGLIVALS	CH	IK	PKFH	PMY	FISH	FVFC	SS	PKLE	NLM	WADKS	ISY	ESIT	QV	YESI	VFV	VIDN	LIG	WYAL	FEVA	CHP	PI	YTI	IN	RPR	:	141	
AOALFR03	pr	QVWVWVGNGLIVALS	CH	IK	PKFH	PMY	FISH	FVFC	SS	PKMI	VNL	VKDRT	ISY	ELC	VW	GEFF	CTFV	VTESE	FI	LAW	DR	VA	ICN	PI	LYT	VA	SQR	:	140
AOALFR04	pr	QVWVWVGNGLIVALS	CH	IK	PKFH	PMY	FISH	FVFC	SS	PKMI	VNL	VKDRT	ISY	ELC	VW	GEFF	CTFV	VTESE	FI	LAW	DR	VA	ICN	PI	LYT	VA	SQR	:	137
AOALFR05	pr	QVWVWVGNGLIVALS	CH	IK	PKFH	PMY	FISH	FVFC	SS	PKMI	VNL	VKDRT	ISY	ELC	VW	GEFF	CTFV	VTESE	FI	LAW	DR	VA	ICN	PI	LYT	VA	SQR	:	139
AOALFR06	pr	QVWVWVGNGLIVALS	CH	IK	PKFH	PMY	FISH	FVFC	SS	PKMI	VNL	VKDRT	ISY	ELC	VW	GEFF	CTFV	VTESE	FI	LAW	DR	VA	ICN	PI	LYT	VA	SQR	:	141
AOALFR07	pr	QVWVWVGNGLIVALS	CH	IK	PKFH	PMY	FISH	FVFC	SS	PKMI	VNL	VKDRT	ISY	ELC	VW	GEFF	CTFV	VTESE	FI	LAW	DR	VA	ICN	PI	LYT	VA	SQR	:	176
AOALFR08	pr	QVWVWVGNGLIVALS	CH	IK	PKFH	PMY	FISH	FVFC	SS	PKMI	VNL	VKDRT	ISY	ELC	VW	GEFF	CTFV	VTESE	FI	LAW	DR	VA	ICN	PI	LYT	VA	SQR	:	139
AOALFR09	pr	QVWVWVGNGLIVALS	CH	IK	PKFH	PMY	FISH	FVFC	SS	PKMI	VNL	VKDRT	ISY	ELC	VW	GEFF	CTFV	VTESE	FI	LAW	DR	VA	ICN	PI	LYT	VA	SQR	:	139
AOALFR10	pr	QVWVWVGNGLIVALS	CH	IK	PKFH	PMY	FISH	FVFC	SS	PKMI	VNL	VKDRT	ISY	ELC	VW	GEFF	CTFV	VTESE	FI	LAW	DR	VA	ICN	PI	LYT	VA	SQR	:	139
AOALFR11	pr	QVWVWVGNGLIVALS	CH	IK	PKFH	PMY	FISH	FVFC	SS	PKMI	VNL	VKDRT	ISY	ELC	VW	GEFF	CTFV	VTESE	FI	LAW	DR	VA	ICN	PI	LYT	VA	SQR	:	138
AOALFR12	pr	QVWVWVGNGLIVALS	CH	IK	PKFH	PMY	FISH	FVFC	SS	PKMI	VNL	VKDRT	ISY	ELC	VW	GEFF	CTFV	VTESE	FI	LAW	DR	VA	ICN	PI	LYT	VA	SQR	:	189
AOALFR13	pr	QVWVWVGNGLIVALS	CH	IK	PKFH	PMY	FISH	FVFC	SS	PKMI	VNL	VKDRT	ISY	ELC	VW	GEFF	CTFV	VTESE	FI	LAW	DR	VA	ICN	PI	LYT	VA	SQR	:	139
AOALFR14	pr	QVWVWVGNGLIVALS	CH	IK	PKFH	PMY	FISH	FVFC	SS	PKMI	VNL	VKDRT	ISY	ELC	VW	GEFF	CTFV	VTESE	FI	LAW	DR	VA	ICN	PI	LYT	VA	SQR	:	164
AOALFR15	pr	QVWVWVGNGLIVALS	CH	IK	PKFH	PMY	FISH	FVFC	SS	PKMI	VNL	VKDRT	ISY	ELC	VW	GEFF	CTFV	VTESE	FI	LAW	DR	VA	ICN	PI	LYT	VA	SQR	:	139
AOALFR16	pr	QVWVWVGNGLIVALS	CH	IK	PKFH	PMY	FISH	FVFC	SS	PKMI	VNL	VKDRT	ISY	ELC	VW	GEFF	CTFV	VTESE	FI	LAW	DR	VA	ICN	PI	LYT	VA	SQR	:	138
AOALFR17	pr	QVWVWVGNGLIVALS	CH	IK	PKFH	PMY	FISH	FVFC	SS	PKMI	VNL	VKDRT	ISY	ELC	VW	GEFF	CTFV	VTESE	FI	LAW	DR	VA	ICN	PI	LYT	VA	SQR	:	137
AOALFR18	pr	QVWVWVGNGLIVALS	CH	IK	PKFH	PMY	FISH	FVFC	SS	PKMI	VNL	VKDRT	ISY	ELC	VW	GEFF	CTFV	VTESE	FI	LAW	DR	VA	ICN	PI	LYT	VA	SQR	:	138
AOALFR19	pr	QVWVWVGNGLIVALS	CH	IK	PKFH	PMY	FISH	FVFC	SS	PKMI	VNL	VKDRT	ISY	ELC	VW	GEFF	CTFV	VTESE	FI	LAW	DR	VA	ICN	PI	LYT	VA	SQR	:	140
AOALFR20	pr	QVWVWVGNGLIVALS	CH	IK	PKFH	PMY	FISH	FVFC	SS	PKMI	VNL	VKDRT	ISY	ELC	VW	GEFF	CTFV	VTESE	FI	LAW	DR	VA	ICN	PI	LYT	VA	SQR	:	139
AOALFR21	pr	QVWVWVGNGLIVALS	CH	IK	PKFH	PMY	FISH	FVFC	SS	PKMI	VNL	VKDRT	ISY	ELC	VW	GEFF	CTFV	VTESE	FI	LAW	DR	VA	ICN	PI	LYT	VA	SQR	:	137
AOALFR22	pr	QVWVWVGNGLIVALS	CH	IK	PKFH	PMY	FISH	FVFC	SS	PKMI	VNL	VKDRT	ISY	ELC	VW	GEFF	CTFV	VTESE	FI	LAW	DR	VA	ICN	PI	LYT	VA	SQR	:	137
AOALFR23	pr	QVWVWVGNGLIVALS	CH	IK	PKFH	PMY	FISH	FVFC	SS	PKMI	VNL	VKDRT	ISY	ELC	VW	GEFF	CTFV	VTESE	FI	LAW	DR	VA	ICN	PI	LYT	VA	SQR	:	139
AOALFR25	pr	QVWVWVGNGLIVALS	CH	IK	PKFH	PMY	FISH	FVFC	SS	PKMI	VNL	VKDRT	ISY	ELC	VW	GEFF	CTFV	VTESE	FI	LAW	DR	VA	ICN	PI	LYT	VA	SQR	:	139
AOALFR26	pr	QVWVWVGNGLIVALS	CH	IK	PKFH	PMY	FISH	FVFC	SS	PKMI	VNL	VKDRT	ISY	ELC	VW	GEFF	CTFV	VTESE	FI	LAW	DR	VA	ICN	PI	LYT	VA	SQR	:	138

FIG. 1 (CONT-3)

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AOLFR27 . pr	120	140	160	180	200	140
AOLFR28 . pr	120	140	160	180	200	137
AOLFR29 . pr	120	140	160	180	200	141
AOLFR30 . pr	120	140	160	180	200	156
AOLFR31 . pr	120	140	160	180	200	139
AOLFR32 . pr	120	140	160	180	200	135
AOLFR34 . pr	120	140	160	180	200	160
AOLFR35 . pr	120	140	160	180	200	139
AOLFR36 . pr	120	140	160	180	200	106
AOLFR37 . pr	120	140	160	180	200	140
AOLFR38 . pr	120	140	160	180	200	106
AOLFR39 . pr	120	140	160	180	200	139
AOLFR40 . pr	120	140	160	180	200	138
AOLFR41 . pr	120	140	160	180	200	139
AOLFR42 . pr	120	140	160	180	200	139
AOLFR43 . pr	120	140	160	180	200	152
AOLFR44 . pr	120	140	160	180	200	138
AOLFR45 . pr	120	140	160	180	200	141
AOLFR46 . pr	120	140	160	180	200	213
AOLFR47 . pr	120	140	160	180	200	141
AOLFR48 . pr	120	140	160	180	200	142
AOLFR49 . pr	120	140	160	180	200	141
AOLFR50 . pr	120	140	160	180	200	157
AOLFR51 . pr	120	140	160	180	200	169
AOLFR52 . pr	120	140	160	180	200	1432

FIG. 1 (CONT-4)

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AOLFR01 . pr :	220	FGILTVIS	ELSNIA	THLLLIQIFC	NHN-TTHC	260	DIAPLIK	SCSD-TLINE	MF-IVGLSVIIFPTLSFF	300	SVVOTIRAVIRSS	243
AOLFR02 . pr :	220	ALLAGS	LMGFGP	LLCYALRINS	GPN-VINHIC	260	EYALLIS	SGSD-LLPHLI	IF-SPATFNMCTLLIILT	300	SVVLEVTWIKRS	232
AOLFR03 . pr :	220	VILVGS	AMVSCS	LTCSALKICPH	GFN-TTHC	260	EFFSILIS	SCSD-TYINWLI	IF-FLATFNEISILLIILT	300	SVAFIVTTHKRS	231
AOLFR04 . pr :	220	CLMGGA	VGFFHA	QLLEFWQIFPC	GPN-IDHIC	260	DLFQMLI	ACTD-THIGLAV	T-INSGMCAVAILLIA	300	SVTVIICS-IKSYG	227
AOLFR05 . pr :	220	VEIASC	FOITCS	HICLAURIPY	RSN-VINHIC	260	DLPPVIS	ACSD-ITWNET	IF-LVATINESVTIMILT	300	SVLIHTTHKGS	230
AOLFR06 . pr :	220	ALLAGS	TWGI	CS-LTYFELDISC	EST-FINN IC	260	DHSVINGA	SYSD-PYISQRLC	F-ITAFNEVSSILLILT	300	SVMIFFTHKRS	232
AOLFR07 . pr :	220	LLMLG	SCSISH	HS-FRVLMSRLSC	ASH-IKHC	260	DTQPVIKI	SCSD-TSSQWVM	-TETLAVITVPELOIF	300	SVLRNVTVIRPS	267
AOLFR08 . pr :	220	SIMAVV	SLF	WAT-HTTRMSVISC	RSN-TSHIC	260	DILPHIL	SCSS-THINEI	IF-IIGCVNTLATLAILI	300	SVAFHSILICHS	230
AOLFR09 . pr :	220	SMITFAA	MLAGAT	AHTGCMRLITFC	SAN-IINHIC	260	DILPHIL	QSCS-TYNEVWL	-IVWGTNITVPSCTULL	300	SVVFIHTSHKRS	230
AOLFR10 . pr :	220	SMITFAA	MLAGAT	AHTGCMRLITFC	SAN-IINHIC	260	DILPHIL	QSCS-TYNEVWL	-IVWGTNITVPSCTULL	300	SVVFIHTSHKRS	230
AOLFR11 . pr :	220	FLIFGCS	VEFAGAN	AHTGCMRLITFC	DES-VIDIC	260	DVLEPHIL	QSCS-THVSEIVFF	-IVWGTNITVPSCTULL	300	SVVFIHTSHKRS	229
AOLFR12 . pr :	220	CVLIVLS	CIPFHS	HILLTQILFC	ASN-VHIC	260	DDQPVIKI	SCSS-HFVKETIWM	-TEGLAVITVPSCTULL	300	SVLRNVTVIRPS	280
AOLFR13 . pr :	220	VIMASTS	VIGFANS	QIV-ILLITFC	G-RNKIC	260	EVPLIKI	ACVD-TTNESEI	IF-FVSIVILLVPAIIF	300	SVSQIVRAVIRKS	230
AOLFR14 . pr :	220	LALLGAS	GLGAVSAF	HTTFRILSC	RSR-KINS IC	260	DIPPLIAI	SCSD-TSINELL	IF-AICGFIQTATVIAITY	300	SVGFIAGAVIHTRS	255
AOLFR15 . pr :	220	SIMAGS	INANA	PHTL-TASLSC	GNQ-EVAN IC	260	DITPLIKI	SCSD-IHF-HVNM	-YLGVGIFSVPILLOIV	300	SVIRFESTFQVPS	229
AOLFR16 . pr :	220	SEITVP	YALTC	HEMTWYNLAF	GPN-EINHIC	260	ADPPLIKI	ACSD-TYNKELSF	-IVAGWNLFSFLIC	300	SVLYFPATIKRS	229
AOLFR17 . pr :	220	VIRUTFP	YFLTS	AATLWYGLYFC	GKI-EINHIC	260	ADPPLIKI	ACAG-TFVKETIWM	-ILAGINFTYSILVIL	300	SVLFIHTHMRPS	228
AOLFR18 . pr :	220	ICLATFP	YEFSDG	FQAI-TFRILTC	RSN-VINHIC	260	ADPPLIKI	SCSD-TYVKEHAF	-ISAGFNLSSSILVIL	300	SVAFIHTHMRPS	229
AOLFR19 . pr :	220	HLLMLG	SCSISHSL	FRVLMSRLSC	ASH-IKHC	260	DTQPVIKI	SCSD-TSSQWVM	-TETLAVITVTPCLTIF	300	SVLQIVTVIRPS	231
AOLFR20 . pr :	220	IQUTTGA	AGNLHSM	HVG-VFRLVFC	GLN-HINHIC	260	DTPLPLIKI	SCVD-PFINEI	MF-IFSGSVQVFTIGSMIL	300	SVLYHILLTFRMKS	230
AOLFR21 . pr :	220	VILVWS	GGFLOS	FQLS-IVGLPFC	GPN-VIDHIC	260	DMVPLIKI	ACTD-THVIGL	IV-ANGGLSCTIAFLIILI	300	SVGVILHS-IKKIS	227
AOLFR22 . pr :	220	FLVXX	GGFVHSA	FQI-IVSLPFC	GPX-VIHIC	260	DMHPLIE	ACTD-TYFICGL	IV-VNSGALCWVINIILI	300	SVGVILSS-IKTYS	226
AOLFR23 . pr :	220	MSVGA	CGVSGA	RTTCTFTLSFC	KDN-QINF IC	260	DLPLIKI	ACSD-TANIEI	IVII-FFGNFVILANASVILI	300	SVLLIKTILKRS	230
AOLFR25 . pr :	220	VGVVAT	GGFVHSA	QIALMLPLPFC	GPN-IIDHIC	260	DVPCVIRI	ACTD-TSLEFLKI	-SNSGLLDVWFFILM	300	SVLFIHTHMRPS	229
AOLFR26 . pr :	220	VLLILGA	MGFAGAN	AHTGCMRLITFC	ADN-IINHIC	260	DILPLIEI	SCNS-SYNNEL	MF-IVVANDVGMPIVTVFI	300	SVAILISSLIHNS	229

FIG. 1 (CONT-5)

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AOLFR27	. pr	D	AH	ACT	AG	S	MG	-	AV	VE	TEC	-----	GSN	-	VH	HC	-----	HVLS	IK	AC	EN	KTS	SV	IM	QW	-	LVC	T	AL	IG	CL	F	I	L	-----	SV	F	VA	A	T	R	I	P	S	-----	232																																																									
AOLFR28	. pr	V	RL	SV	X	Y	FS	V	-	CT	TY	G	YEC	-----	GNF	-	E	IN	HC	-----	AD	PP	HI	Q	AC	GR	-	VH	KE	I	WI	-	VI	AG	IN	TY	S	I	S	W	L	I	-----	SV	T	L	V	V	A	I	R	S	-----	228																																																	
AOLFR29	. pr	R	AC	L	S	V	S	I	HT	-	RV	G	V	-	EP	IC	WT	G	D	AG	N	V	N	I	P	HC	-----	D	HR	P	I	R	A	S	C	S	D	-	I	H	S	N	E	L	A	F	-	F	E	G	G	F	M	G	P	C	A	I	V	L	-----	SV	V	R	J	CA	A	T	R	I	P	S	-----	236																													
AOLFR30	. pr	T	L	L	AV	W	A	L	G	S	T	-	ET	G	M	L	P	Y	C	-----	EH	-	L	I	S	HC	-----	D	IL	P	M	K	I	C	S	S	-	T	Y	D	EM	W	I	F	-	F	S	A	G	N	I	V	T	S	I	V	L	-----	SV	T	F	L	S	S	I	C	I	S	-----	246																																	
AOLFR31	. pr	I	L	L	G	N	S	-	G	C	N	A	M	-	T	F	I	C	L	L	R	S	E	C	-----	GP	N	-	K	N	H	HC	-----	D	Y	S	P	I	K	I	C	A	S	H	-	D	F	E	I	I	P	A	-	I	S	S	G	S	I	V	A	T	V	C	M	A	I	-----	SV	I	H	I	T	H	A	S	-----	230																									
AOLFR32	. pr	S	V	Q	L	L	W	A	F	I	A	-	S	T	T	S	F	E	L	E	C	-----	GP	N	-	Q	N	H	HC	-----	D	F	A	P	L	E	L	S	C	S	D	-	I	S	V	T	V	M	S	-	F	S	S	G	I	I	V	T	V	C	M	A	I	-----	SV	I	H	I	T	H	A	S	-----	226																													
AOLFR33	. pr	N	S	L	A	L	T	G	T	H	S	-	F	O	T	S	F	R	E	P	E	C	-----	GP	N	-	R	D	Y	HC	-----	D	I	P	A	M	I	R	A	C	A	D	-	T	A	I	N	E	L	V	T	-	A	D	I	G	E	L	A	T	C	E	M	I	T	-----	SV	I	H	I	T	H	A	S	-----	251																											
AOLFR34	. pr	V	L	L	G	A	A	V	L	C	L	K	S	-	T	E	M	V	S	M	R	L	P	E	C	-----	G	-	H	V	V	S	H	HC	-----	K	I	L	A	V	I	K	I	A	C	G	N	-	T	S	V	E	D	E	L	-	A	G	S	I	L	L	P	V	L	A	F	I	C	L	-----	SV	L	I	I	A	T	H	A	S	-----	230																					
AOLFR35	. pr	V	F	F	L	V	S	-	E	L	S	I	-	D	E	O	-	L	H	S	M	V	L	O	T	F	-----	K	N	V	E	I	S	N	V	HC	-----	E	P	S	Q	L	I	K	I	A	C	D	S	V	-	I	N	S	I	F	I	-	F	O	N	T	M	F	G	L	P	I	S	G	I	L	-----	SV	K	W	P	S	H	R	I	S	-----	197																			
AOLFR36	. pr	A	Y	M	P	A	S	S	-	A	I	G	G	A	S	-	V	H	T	S	-	A	I	Q	P	E	C	-----	G	-	D	N	V	I	N	HC	-----	E	L	A	V	I	K	I	A	C	A	D	-	I	S	I	N	V	I	S	E	-	V	T	N	V	I	F	L	G	V	P	L	F	I	S	-----	SV	F	L	I	T	H	A	S	-----	231																				
AOLFR37	. pr	G	V	H	L	V	S	-	E	L	S	I	-	D	E	O	-	L	H	S	M	V	L	O	T	F	-----	K	N	V	E	I	S	N	V	HC	-----	D	P	S	Q	L	I	K	I	A	C	D	S	V	-	I	N	S	I	F	I	-	L	D	S	I	M	F	G	L	P	I	S	G	I	L	-----	SV	A	N	N	P	S	H	R	I	S	-----	197																		
AOLFR38	. pr	S	I	L	L	R	A	V	-	S	V	G	T	D	A	V	-	I	H	G	G	L	L	R	S	E	C	-----	G	S	N	-	I	K	N	HC	-----	D	I	V	A	P	L	E	K	I	C	S	S	-	T	Y	I	D	E	L	I	H	E	-	V	I	G	E	N	N	A	T	S	I	I	-----	SV	A	F	I	T	S	H	R	I	S	-----	230																			
AOLFR39	. pr	S	A	L	I	A	T	G	L	S	-	H	S	A	-	V	O	T	I	-	T	F	H	P	Y	C	-----	G	P	N	-	I	Q	H	HC	-----	D	A	P	P	I	K	I	A	C	A	D	-	T	S	A	N	E	W	I	F	-	W	N	I	G	L	V	A	S	G	F	I	V	L	-----	SV	S	V	I	C	S	H	R	I	-----	229																					
AOLFR40	. pr	S	O	L	V	L	A	S	-	I	A	F	-	W	L	-	C	T	V	A	M	A	S	E	P	E	C	-----	G	P	N	-	G	I	D	HC	-----	D	S	W	P	L	I	R	S	R	G	D	-	T	H	L	K	L	V	A	F	-	M	L	S	T	V	L	L	G	S	A	L	T	S	V	-----	SV	A	C	H	A	T	V	R	A	P	I	-----	230																	
AOLFR41	. pr	A	L	L	A	A	S	-	V	G	-	F	H	S	I	-	V	O	I	A	-	T	I	Q	P	E	C	-----	G	P	N	-	G	I	D	HC	-----	D	V	P	Q	L	I	K	I	A	C	T	D	-	T	F	V	E	L	L	I	V	-	S	N	N	G	L	V	I	M	C	F	I	L	G	-----	SV	T	A	L	I	V	M	-	H	R	S	-----	229																	
AOLFR42	. pr	T	V	A	K	I	G	S	A	L	T	-	F	F	F	P	L	P	I	-	K	-	M	E	S	Y	C	-----	Q	T	H	N	T	H	S	HC	-----	L	H	O	D	I	M	K	I	C	S	T	D	R	N	V	V	Y	G	I	F	-----	I	L	S	V	M	G	V	D	S	I	F	I	G	S	I	I	I	W	A	V	E	-----	SV	I	I	I	W	A	V	E	-----	SS	-----	243											
AOLFR43	. pr	T	A	Q	I	G	I	V	A	V	R	-	S	-	F	F	F	P	L	L	-	K	-	R	L	A	E	C	-----	H	S	N	V	L	S	H	S	HC	-----	V	H	O	D	I	M	K	I	A	C	A	D	T	I	P	N	V	V	Y	G	I	F	A	-----	I	L	L	V	M	G	V	D	M	F	I	S	I	S	F	I	I	I	T	V	L	Q	P	S	-----	SV	F	I	I	I	T	V	L	Q	P	S	-----	229		
AOLFR44	. pr	I	T	K	I	G	M	A	V	A	R	A	V	T	M	T	P	L	P	E	L	-	R	-	R	F	H	Y	C	-----	R	G	P	V	I	A	H	HC	-----	E	H	M	A	V	R	I	A	C	D	T	S	F	N	N	I	Y	G	I	A	-----	V	A	M	S	W	L	D	I	F	V	I	L	S	V	F	I	I	O	A	V	I	C	A	S	-----	SV	F	I	I	O	A	V	I	C	A	S	-----	232					
AOLFR45	. pr	F	V	A	R	A	V	F	I	A	R	A	F	S	I	P	V	M	L	S	A	-	R	I	P	Y	C	-----	A	G	N	I	K	N	HC	-----	S	N	L	A	S	K	I	S	-	D	D	I	T	F	N	Q	L	Y	Q	F	V	A	G	N	T	-----	I	L	G	S	D	I	L	I	V	I	S	I	S	F	I	I	K	W	I	R	K	A	-----	SV	F	I	I	K	W	I	R	K	A	-----	304						
AOLFR46	. pr	I	T	K	I	G	M	A	V	A	R	A	V	T	M	T	P	-	P	E	L	-	R	-	C	F	H	Y	C	-----	R	G	P	V	I	A	H	HC	-----	E	H	M	A	V	R	I	A	C	D	T	S	F	N	N	I	Y	G	I	A	-----	V	A	M	F	I	V	L	D	I	L	V	I	L	S	I	F	I	I	O	A	V	I	C	A	S	-----	SV	F	I	I	O	A	V	I	C	A	S	-----	232				
AOLFR47	. pr	R	V	T	I	G	V	A	V	R	C	A	L	M	A	P	-	P	V	F	-	K	-	Q	I	P	E	C	-----	R	S	N	I	L	S	H	S	HC	-----	L	H	O	D	I	M	K	I	A	C	D	D	I	R	N	V	V	Y	G	I	V	-----	I	I	S	A	I	G	L	D	S	I	L	I	S	F	S	V	L	I	I	K	T	V	I	C	I	-----	SV	F	I	I	K	T	V	I	C	I	-----	232				
AOLFR48	. pr	V	G	R	I	G	L	V	S	I	-	R	G	V	-	I	T	G	P	-	P	I	M	-	R	L	P	Y	C	-----	K	T	H	V	L	S	H	S	HC	-----	E	H	M	A	V	R	I	A	C	D	S	R	N	V	N	Y	G	I	S	-----	I	G	F	I	V	L	D	S	V	A	I	A	S	W	-	I	F	R	A	V	N	G	I	A	-----	SV	F	I	I	R	A	V	N	G	I	A	-----	233					
AOLFR49	. pr	I	G	H	I	G	M	V	I	-	R	G	L	-	L	I	-	P	F	L	I	-	R	-	K	L	I	F	C	-----	Q	A	T	I	G	H	A	Y	C	-----	E	H	M	A	V	R	I	A	C	S	E	T	T	W	N	R	A	Y	G	I	F	-----	V	A	L	L	V	V	G	L	D	V	I	A	T	G	S	V	A	H	I	I	O	A	V	I	K	P	G	-----	SV	F	I	I	O	A	V	I	K	P	G	-----	248
AOLFR50	. pr	M	L	G	S	M	A	I	T	-	R	A	I	-	A	L	T	P	-	S	M	-	S	-	H	L	P	E	C	-----	G	S	N	V	V	H	S	HC	-----	E	H	I	A	R	I	A	C	A	D	P	V	P	S	L	Y	S	I	G	S	-----	S	L	M	V	G	S	D	V	A	F	A	A	S	V	I	I	I	K	A	V	F	I	C	S	-----	SV	F	I	I	K	A	V	F	I	C	S	-----	260					
AOLFR51	. pr	M	L	G	S	M	A	I	T	-	R	A	I	-	A	L	T	P	-	S	M	-	S	-	H	L	P	E	C	-----	G	S	N	V	V	H	S	HC	-----	E	H	I	A	R	I	A	C	A	D	P	V	P	S	L	Y	S	I	G	S	-----	S	L	M	V	G	S	D	V	A	F	A	A	S	V	I	I	I	K	A	V	F	I	C	S	-----	SV	F	I	I	K	A	V	F	I	C	S	-----	260					
AOLFR52	. pr	M	L	G	S	M	A	I	T	-	R	A	I	-	A	L	T	P	-	S	M	-	S	-	H	L	P	E	C	-----	G	S	N	V	V	H	S	HC	-----	E	H	I	A	R	I	A	C	A	D	P	V	P	S	L	Y	S	I	G	S	-----	S	L	M	V	G	S	D	V	A	F	A	A	S	V	I	I	I	K	A	V	F	I	C	S	-----	SV	F	I	I	K	A	V	F	I	C	S	-----	234					

FIG. 1 (CONT-6)

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	340	360	380	400	420	*
AOLFR01 . p	TOA-KA-ISTCASHLITW--	ILFY--I--VGV--EF	HPEDTKIGALIF--	WTPMNEFIYSIRNDKGA	IRKILNRKISSL--	325
AOLFR02 . p	VS-HKA-ISTASHLITAI--	TIFH--IL--IL--CV	NSKNSR---Q-TVKASVFI	WPNLNEFIYSIRNDKDK	FWKLHTQVFFH--	314
AOLFR03 . p	VS-RKA-ISTCASHLITA--	TIFH--IL--IL--CV	NSKNSR---H-TVKASVFI	WPNLNEFIYSIRNDKDK	TEILDTKVFYS--	313
AOLFR04 . p	SK-HKA-ISTCASHLITV--	VLFVFP--CIIL--M	WTHPI-----DKAMVSDS	ILWPNLNEFIYSIRNDK	SKLWKEALACK--	309
AOLFR05 . p	AE-HKA-ISTCASHLITA--	TVFH--VL--SH--C	SSGNSG---D-ADKATVFI	WPNLNSVIYSIRNDCKE	IRKVGSKLHS--	311
AOLFR06 . p	AS-QKT-ISTCASHLITA--	TIFH--IL--IL--CV	NPKTSS---L-IVTVASVFI	APMNEFIYSIRNDINN	EFEKLVTKLIYH--	314
AOLFR07 . p	AA-HKA-ISTCASHLITA--	ALFY--SI--IYV--F	LSM-----YSVVRDRTAT	WTPMNEFIYSIRNDKRC	KKLQDRIYR--	347
AOLFR08 . p	TE-QSKA-ISTCASHLITA--	GIFV--SIT--M--F	PSSTW---E-KEKSSVFI	ILWPNLNEFIYSIRNDK	KNAIKKTRGRQS--S	311
AOLFR09 . p	TO-QSKA-ISTCASHLITA--	SLFF--SAA--M--I	-YSSGSM---E-QGKFSVFI	WPNLNEFIYSIRNDKVA	IRKALIKIQRRNIF--	313
AOLFR10 . p	TO-QSKA-ISTCASHLITA--	SLFF--SAA--M--I	-YSSGSM---E-QGKFSVFI	WPNLNEFIYSIRNDKVA	IRKALIKIQRRNIF--	313
AOLFR11 . p	AE-QSKA-ISTCASHLITA--	ALFF--SGT--T--L	TTSPPGSM---N-HGRFASVFI	WPNLNEFIYSIRNDKLA	GKTLKRVLF--	309
AOLFR12 . p	AA-RKA-ISTCASHLITV--	TLEF--SI--SYV--FQ	LSN-----YTV-KDQATII	WTPMNEFIYSIRNDKOC	AKLMHRMKCQ--	360
AOLFR13 . p	AT-QRV-ISTCASHLITW--	SLFY--A--IYA--LQ	-----GNVSDQGXLSIF	ILWPNLNEFIYSIRNDK	GAUKVWKNVDSR--	312
AOLFR14 . p	VE-SRA-ASTCASHLITA--	AMM--LI--M--I	SSSYAL---DTD-KBASVFI	ILWTPSLNEFIYSIRND	KEARQTSRHFPCGQSQ--	341
AOLFR15 . p	TK-VKA-ISTCASHLITV--	SLYV--V--MGT--F	LTN-----YS-LKQAMTVFI	WTPMNEFIYSIRNDKKA	IRKLFNKRIS--	309
AOLFR16 . p	TE-QKA-ISTCASHLITA--	TIEVA--LF--M--I	PSKESV---E-QGKWAFFFI	WPNLNEFIYSIRNDKKA	IRKLSMKIYFS--	311
AOLFR17 . p	AE-QKA-ISTCASHLITA--	IIFY--LI--M--I	RPTESV---E-QGKWAFFFI	WPNLNEFIYSIRNDKKA	MMKVISRSC--	307
AOLFR18 . p	AE-HKA-ISTCASHLITW--	TLEF--LF--OM--I	PDKTV---E-ESKILAVFI	EVSPLNEFIYSIRNDKQ	AKNVLR--	305
AOLFR19 . p	AA-HKA-ISTCASHLITW--	VLFV--SV--IYV--F	LSM-----YSWVKGRMAT	WTPMNEFIYSIRNDKRC	KKLHRHYS--	311
AOLFR20 . p	KE-HKA-ISTCASHLITV--	SLFY--SIF--M--I	NLLEE---GGNDIPAAHFI	ILWPNLNEFIYSIRND	SVLRKILKIKSQGSVWK--	316
AOLFR21 . p	OK-QKA-ISTCASHLITW--	VFFVFP--CIIL--M	ARTFSI---DKSVSVFI	WTPMNEFIYSIRNSPT	SAKKL--	299
AOLFR22 . p	QEK-GKA-ISTCASHLITW--	VLFVFP--CIIL--M	VSNFPI---DKFVTVFI	ILWTPMNEFIYSIRNS	ERNALEKLGKLTIFIGGVSLM--	315
AOLFR23 . p	SG-KAT-ISTCASHLITV--	ALFF--ALI--M--I	LOSQSKLS---EED-KVVS	WPNLNEFIYSIRNDKDK	AFKRVARRLOVLSM--	314
AOLFR25 . p	GEAR-KA-ASTCASHLITW--	SMIFVFP--SIYLA--F	FPFPM---DKLVSIG	WTPMNEFIYSIRNDQ	QAARRLGRHLV--	307
AOLFR26 . p	TE-QKA-ISTCASHLITW--	SLFF--SGA--M--I	LSILPL---E-QGKVSIFFI	ILWPNLNEFIYSIRND	DKVIRRTILGRKIFS--	310

FIG. 1 (CONT-7)

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AOLFR27 . pr :	AEHT--STCGSHLTW--VTHS--FAS--I--KGLHSM-----YSDALMATYTVTFTEF--ISF--FSLRKEKNA--KKNFYRKFCCPSS-----	340	360	380	400	420	*	316
AOLFR28 . pr :	ADRA--STCGSHLTW--SFEY--PI--W--L--PTEESV-----E-QGVAVEYTVTPMNEFYSLRNDKEA--KNAITKTYRQ-----							310
AOLFR29 . pr :	AAARA--STCGSHLTW--GFLV--IIC--V--FQ--PF-----QNSQYQDMASQWYATATPLANEFYSLRNDKGA--CRILLEWVKVP-----							318
AOLFR30 . pr :	TEASA--STCGSHLAAM--GFEY--TA--W--L--STSSSL-----T-QENVASVEYTVTPMNEFYSLRNDKGA--OKTLRCKLF-----							326
AOLFR31 . pr :	TKARA--STCTSHLTW--TFY--IT--L--V--KSSYST-----D-QNKVSVFYTVTPMNEFYSLRNDKGA--KRELRKIFS-----							311
AOLFR32 . pr :	TEARA--STCTSHLTW--TFY--IT--L--V--NFSYST-----D-QNKVSVLYTVTPMNEFYSLRNDKGA--KRELRKILSHDACVFSRTSNNDIT-----							322
AOLFR34 . pr :	ADARA--STCAAHLTW--IVYVP--CT--L--CSDPEL-----DGVANFYTVTPMNEFYSLRNDKGA--ORLGGHKEVQPH-----							332
AOLFR35 . pr :	AARCKA--STCOLAHIAW--LIFY--I--L--KSKA-----HISDEFVLYAVYTVTPMNEFYSLRNDKGA--ARVWGRSASR-----							312
AOLFR36 . pr :	SDARA--STCGCHIAW--OLEY--GIGVY--TSVAPP--RNG-----WASQYAVYTPMNEFYSLRNDKGA--ARVWCVKTVESHDLFHPFSCVWKGOP-----							394
AOLFR37 . pr :	AEARA--STCSAHLTW--IVFY--L--H--G--KSKDSMGADKEDLSK--L--P--FYGVWTPMNEFYSLRNDKGA--ARVWLLRPGFTQ-----							319
AOLFR38 . pr :	SDARA--STCGSHIAW--OLEY--GIGVY--TSVAPP--RNG-----WASQYAVYTPMNEFYSLRNDKGA--ARVWLLRPGFTQ-----							294
AOLFR39 . pr :	KKARA--STCGSHLTW--IVFY--LM--S--L--ASSSSL-----T-QEKSSFYTVTPMNEFYSLRNDKGA--ARVWLLRPGFTQ-----							314
AOLFR40 . pr :	SDARA--STCASHCTW--LQFY--GLF--L--PGSRDAL-----HGVANFYTVTPMNEFYSLRNDKGA--ARVWLLRPGFTQ-----							311
AOLFR41 . pr :	ADARA--STCASHLTW--VITY--SI--F--L--MSEAGSK-----LLNGCASLSCTPLMNEFYSLRNDKGA--ARVWLLRPGFTQ-----							323
AOLFR42 . pr :	REARA--LSTCASHIAW--TLFVP--CIYV--T--PFRTPPM-----DRAVSILYTVTPMNEFYSLRNDKGA--ARVWLLRPGFTQ-----							318
AOLFR43 . pr :	RRAARA--NTCISHICAM--IVFYVPLIGLSVH--LGGP-----TSLHVMANTYLLPVPVNEFYVCAAT--EICSRVLCMFESOGGK-----							324
AOLFR44 . pr :	KSEARA--CTCVSHIGW--LAFVVPPLIGLSVH--FGNS--L-----HPVVRVWMDIVLLPVPVNEFYVCAAT--EICSRVLCMFESOGGK-----							320
AOLFR45 . pr :	QARA--CTCVSHICAM--LSTVTPVWISSVH--VARHAA-----PR-VHILAFILFLLFPVWNEFYVCAAT--EICSRVLCMFESOGGK-----							314
AOLFR46 . pr :	EGAVARA--LSTCGSHFII--LFFS--VILLV--ITNLARKRI-----PDPVPI--LNLHHL--P--FALNEFYVCAAT--EICSRVLCMFESOGGK-----							384
AOLFR47 . pr :	QARA--CTCVSHICAM--LAFVTV--VWISSVH--VARHAA-----PH--VHILAFILFLLFPVWNEFYVCAAT--EICSRVLCMFESOGGK-----							314
AOLFR48 . pr :	REAOARA--CTCVSHVCAW--FIYVVPFGLSVH--FSKR--R-----DSPLPVLANILYLLPVPVNEFYVCAAT--EICSRVLCMFESOGGK-----							318
AOLFR49 . pr :	PEARA--LSTCASHICAM--LIFVVPVAVSSVH--FGQC--V-----PPVHTILANILYLLPVPVNEFYVCAAT--EICSRVLCMFESOGGK-----							317
AOLFR50 . pr :	NEARA--LSTCGSHVCI--LIFYVPGMFSVTH--FGHH--V-----PHVHVILANILYLLPVPVNEFYVCAAT--EICSRVLCMFESOGGK-----							319
AOLFR51 . pr :	KTAQARA--LSTCGSHVGM--ALYVLP--PGWASIIYAANL--GQDV-----PLHTOV--LADIV--PATINEFYVCAAT--EICSRVLCMFESOGGK-----							350
AOLFR52 . pr :	KTAQARA--LSTCGSHVGM--ALYVLP--PGWASIIYAANL--GQDIV-----PLHTOV--LADIV--PATINEFYVCAAT--EICSRVLCMFESOGGK-----							324

FIG. 1 (CONT-8)

440

AOLFR01 . pr	---	---	---
AOLFR02 . pr	---	---	---
AOLFR03 . pr	---	---	---
AOLFR04 . pr	---	---	---
AOLFR05 . pr	---	---	---
AOLFR06 . pr	---	---	---
AOLFR07 . pr	---	---	---
AOLFR08 . pr	---	---	---
AOLFR09 . pr	---	---	---
AOLFR10 . pr	---	---	---
AOLFR11 . pr	---	---	---
AOLFR12 . pr	---	---	---
AOLFR13 . pr	---	---	---
AOLFR14 . pr	---	---	---
AOLFR15 . pr	---	---	---
AOLFR16 . pr	---	---	---
AOLFR17 . pr	---	---	---
AOLFR18 . pr	---	---	---
AOLFR19 . pr	---	---	---
AOLFR20 . pr	---	---	---
AOLFR21 . pr	---	---	---
AOLFR22 . pr	---	---	---
AOLFR23 . pr	---	---	---
AOLFR25 . pr	---	---	---
AOLFR26 . pr	---	---	---

FIG. 1 (CONT-9)

AOLFR27	.	pr	:	:	440	:	:	-
AOLFR28	.	pr	:	:	---	:	:	-
AOLFR29	.	pr	:	:	---	:	:	-
AOLFR30	.	pr	:	:	---	:	:	-
AOLFR31	.	pr	:	:	---	:	:	-
AOLFR32	.	pr	:	:	---	:	:	-
AOLFR34	.	pr	:	:	---	:	:	-
AOLFR35	.	pr	:	:	---	:	:	-
AOLFR36	.	pr	:	:	HSIPTSANPAP	:	:	305
AOLFR37	.	pr	:	:	---	:	:	-
AOLFR38	.	pr	:	:	EKGQPH---	:	:	300
AOLFR39	.	pr	:	:	---	:	:	-
AOLFR40	.	pr	:	:	---	:	:	-
AOLFR41	.	pr	:	:	---	:	:	-
AOLFR42	.	pr	:	:	---	:	:	-
AOLFR43	.	pr	:	:	---	:	:	-
AOLFR44	.	pr	:	:	---	:	:	-
AOLFR45	.	pr	:	:	---	:	:	-
AOLFR46	.	pr	:	:	---	:	:	-
AOLFR47	.	pr	:	:	---	:	:	-
AOLFR48	.	pr	:	:	---	:	:	-
AOLFR49	.	pr	:	:	---	:	:	-
AOLFR50	.	pr	:	:	---	:	:	-
AOLFR51	.	pr	:	:	---	:	:	-
AOLFR52	.	pr	:	:	---	:	:	-

FIG. 1 (CONT-10)

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AOLFR54 . pr :	KT	---	SUSNLSDNHL	---	PDYFHTCIPGL	---	AAHFWIA	P	CANY	---	ALUGNAAILL	50
AOLFR57 . pr :	---	---	SFOVT	---	YMFYLHWTM	---	EKSNS	---	ILFELIGSONKN	---	E LO	59
AOLFR58 . pr :	---	---	MTMIPQIDLKQIFLCPNCRLLYMPVG	---	A	---	FIFSLG	---	NM	---	QOLV	99
AOLFR59 . pr :	---	---	---	---	---	---	GDMN	---	---	---	Y HSNIS	49
AOLFR60 . pr :	---	---	---	---	---	---	FLPNDTQFHT	---	SEHILIGPGL	---	T H WIGFF	49
AOLFR61 . pr :	---	---	---	---	---	---	SIIN	---	---	---	TSYVE	49
AOLFR62 . pr :	---	---	---	---	---	---	---	---	---	---	PDYHKSIFHPVT	49
AOLFR63 . pr :	---	---	---	---	---	---	---	---	---	---	TSYVE	49
AOLFR64 . pr :	---	---	---	---	---	---	---	---	---	---	NSSLQORAT	49
AOLFR65 . pr :	---	---	---	---	---	---	---	---	---	---	AGRMSTSNHTQFHT	53
AOLFR66 . pr :	---	---	---	---	---	---	---	---	---	---	FLNGTSLTPAS	49
AOLFR67 . pr :	---	---	---	---	---	---	---	---	---	---	CDNSSLTPGFT	49
AOLFR68 . pr :	---	---	---	---	---	---	---	---	---	---	NDTILS	51
AOLFR69 . pr :	---	---	---	---	---	---	---	---	---	---	SHGVVHSF	86
AOLFR70 . pr :	---	---	---	---	---	---	---	---	---	---	DKLSSG	77
AOLFR71 . pr :	---	---	---	---	---	---	---	---	---	---	GR	47
AOLFR72 . pr :	---	---	---	---	---	---	---	---	---	---	AP	47
AOLFR74 . pr :	---	---	---	---	---	---	---	---	---	---	EQ	47
AOLFR75 . pr :	---	---	---	---	---	---	---	---	---	---	E	47
AOLFR76 . pr :	---	---	---	---	---	---	---	---	---	---	E	45
AOLFR77 . pr :	---	---	---	---	---	---	---	---	---	---	GD	47
AOLFR78 . pr :	---	---	---	---	---	---	---	---	---	---	TPG	49
AOLFR79 . pr :	---	---	---	---	---	---	---	---	---	---	EG	54
AOLFR80 . pr :	---	---	---	---	---	---	---	---	---	---	K	47
AOLFR81 . pr :	---	---	---	---	---	---	---	---	---	---	---	65

FIG. 2 (CONT-1)

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AOLFR82 . pr :	QANN	EFHILGLTQDPF-WKKIV	RLM	GHGALILII	:	45
AOLFR83 . pr :	GNWTA	EFHILGLTQDPF-WKKIV	RLM	GHGALILII	:	46
AOLFR85 . pr :	CAKNN	EFHILGLTQDPF-WKKIV	RLM	GHGALILII	:	45
AOLFR86 . pr :	QNLV	EFHILGLTQDPF-WKKIV	RLM	GHGALILII	:	72
AOLFR87 . pr :	QNLV	EFHILGLTQDPF-WKKIV	RLM	GHGALILII	:	101
AOLFR88 . pr :	LD	EFHILGLTQDPF-WKKIV	RLM	GHGALILII	:	47
AOLFR89 . pr :	LD	EFHILGLTQDPF-WKKIV	RLM	GHGALILII	:	72
AOLFR90 . pr :	LD	EFHILGLTQDPF-WKKIV	RLM	GHGALILII	:	99
AOLFR91 . pr :	LD	EFHILGLTQDPF-WKKIV	RLM	GHGALILII	:	45
AOLFR92 . pr :	LD	EFHILGLTQDPF-WKKIV	RLM	GHGALILII	:	45
AOLFR93 . pr :	LD	EFHILGLTQDPF-WKKIV	RLM	GHGALILII	:	46
AOLFR94 . pr :	LD	EFHILGLTQDPF-WKKIV	RLM	GHGALILII	:	48
AOLFR95 . pr :	LD	EFHILGLTQDPF-WKKIV	RLM	GHGALILII	:	72
AOLFR96 . pr :	LD	EFHILGLTQDPF-WKKIV	RLM	GHGALILII	:	47
AOLFR97 . pr :	LD	EFHILGLTQDPF-WKKIV	RLM	GHGALILII	:	98
AOLFR98 . pr :	LD	EFHILGLTQDPF-WKKIV	RLM	GHGALILII	:	48
AOLFR99 . pr :	LD	EFHILGLTQDPF-WKKIV	RLM	GHGALILII	:	47
AOLFR101 . p :	LD	EFHILGLTQDPF-WKKIV	RLM	GHGALILII	:	47
AOLFR102 . p :	LD	EFHILGLTQDPF-WKKIV	RLM	GHGALILII	:	51
AOLFR103 . p :	LD	EFHILGLTQDPF-WKKIV	RLM	GHGALILII	:	47
AOLFR105 . p :	LD	EFHILGLTQDPF-WKKIV	RLM	GHGALILII	:	47
AOLFR106 . p :	LD	EFHILGLTQDPF-WKKIV	RLM	GHGALILII	:	47
AOLFR107 . p :	LD	EFHILGLTQDPF-WKKIV	RLM	GHGALILII	:	47
AOLFR108 . p :	LD	EFHILGLTQDPF-WKKIV	RLM	GHGALILII	:	63
AOLFR109 . p :	LD	EFHILGLTQDPF-WKKIV	RLM	GHGALILII	:	47

FIG. 2 (CONT-2)

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AOLFR54 . pr	ATAMONA-LAPMYFLICLL	LTAL	--STTPMIAI	LNHAG-EISGCLAQMF	-CVHSTYVAI	ESSILAM	FDRYVAICN	PIRTIINHA	IGRIGFVGLF	153
AOLFR57 . pr	STCTO-LLOPNYFLINVL	LSJCY	T--PBLVNDI	ABR--TISYNNC	IOLETT-THFRGGIE	IFHTGMA	VDRYVAICN	PIHTIIM	ROKNTIIVCCT	162
AOLFR58 . pr	TLSSPALLVSPWFFIGFI	TPACF	V--T--PBMIVDS	YVT--TISFGCM	QOLFA-EHFPAGME	VIVITAM	VDRYVAICN	PIHSSINRR	GLIMGVA-T	203
AOLFR59 . pr	TIWESS-LQPNYFISILAVNDIGM	--	--STTPMIAVLWLDAP	-EIOASAC	YAOLEF-IHTTFT	ESSVLAM	FDRFVAICN	PIHTIINS	IGKIGLACI	152
AOLFR60 . pr	TKTDSS-LQPMYFLIAMATTANGI	--	--TATPDMIGFWNL	-GIIIEAC	LIQMF-IHNFTIL	ESAVIVAM	VDSYVAICN	PIQISAIL	NKVSIGLGV	152
AOLFR61 . pr	HTKTEPS-LQPMYFLSMIAWS	IGLC	--SSPTVISIF	FNAP-ETSSAC	FAEEF-IHGESV	IESSVLIN	SDFRFLA	HNPIRTSIL	TVRVAQIGIVFSE	152
AOLFR62 . pr	ATKVEOT-LKEPMYFLIAL	ITLAL	--ATSPTMIGLFWEDAY	-EINIGAC	VQMF-LIGAPT	GAEVILAM	FDRYVAICN	PIHATIL	SLLVGISWCIV	152
AOLFR63 . pr	IKTEPS-LQPMYFLSMIAWS	IGLC	--SSPTVISIF	FNAP-EISSNAC	FAEEF-IHGESV	IESSVLIN	SDFRFLA	HNPIRTSIL	TVRVAQIGIVFSE	152
AOLFR64 . pr	VICTDAT-LQPNYFLIGIAVIT	IGLC	--STTPMIGLFWED	-EIGIPAC	ETOLF-IHTLSS	IESSVLIN	SDFRFLA	HNPIRTSIL	PACIVKGLSSV	152
AOLFR65 . pr	VTQTEQS-LQPMYFLIAMS	IGLC	--TATPDMIGLFWENT	-EISFGCL	SIWF-IHFTTAM	ESIVIVAM	FDRYVAICN	PIRTWIL	SKISLIAGIAT	156
AOLFR66 . pr	ZYCDRA-LQPMYFLIAL	ITVLMC	--TSTNTL	FTLWNL-EIDFKAC	LAQMF-VHFTTG	ESGVIMIL	LEHCA	VALCPIRTATIL	NSLAKAGFLT	152
AOLFR67 . pr	TSHEBA-LQPMYFLIAL	ITVNL	--TTPMIM	CLFWNL-EIDNAC	LAQMF-VHMTTG	ESGVIMIL	LEHCA	VALCPIRTATIL	NPITAKAGLAT	152
AOLFR68 . pr	TLWLEAS-LQPLYLISIL	LTNLVLC	--TVPDAVIT	FWEDL-PESFPAC	FIQMF-IHNCFL	AMSCTEFW	VDRYVAICN	PIRPSIL	DHFVVKAMFILT	154
AOLFR69 . pr	WIRDSQ-LQPMYFLIS	LSACV	V--T--TANILVDET	TNNV-ISFGC	VQVFLAC-SFGTE	CEFLAAM	VDRYVAICN	PIILSVSM	PRYMPIINAS	189
AOLFR70 . pr	WIEDSW-LQPMYFLIS	LSACV	V--TPKMINV	FLAKNS-ISFGC	ATQVLLAV-TEGTE	CEFLAAM	VDRYVAICN	PIILSVSM	PRYVPLITAS	180
AOLFR71 . pr	FRLDQ-LQPMYFLIT	LSISV	V--TPITLANI	TS-NY-ISFMCC	FAQMFV-FLGAAC	CEFLISS	VDRYVAICN	PIRPMIM	DRCAIVTGP	149
AOLFR72 . pr	TSVDSR-LQPMYFLIQHIAL	NLGN	V--APKMINF	VKK-T-TSHYEC	ATQIGEL-FFIVSE	VIMILAMQ	QDRYVAICN	PIILMMVVR	RLIIVSLT	150
AOLFR74 . pr	TKLDSR-LQPMYFLIRHIAL	NLGY	T--CPKMINV	VDXNI-ISYFEC	ATQIAEL-L-VFIGS	ELIISAN	SIDYVAICN	PIITVINRR	QVIVAIIP	150
AOLFR75 . pr	ATGSDHC-LQPMYFLIANI	LSICLP	AT--TPKMIN-	QTOQI	ISYFEC	LAQMFYFCM-MEAMND	FLITVMA	VDRYVAICN	PIHSTIALR	150
AOLFR76 . pr	ELLDSH-LQPMYFLIS	LSAGIFY	AL--TPKVI	TGLIEDA-ISISAC	AAQMFCA-VFATV	ENYINISSMA	VDRYVAICN	PIHTTITR	AOAIGC	148
AOLFR77 . pr	TRVDSR-LQPMYFLISQI	LEP1	--GCPVTP	PMASDFRCEG-ATSYG	GGAOI-ITLTM	GVAVGVLIVIM	SIDRYVAICN	PIQIPVIMRRQ	LIIMGSSP	150
AOLFR78 . pr	VRADTR-LQPMYFLIGNI	CEILL	V--TPMISN	ELSGRHTIS	FACTICEYF-FLGAS	ELIIMAVE	SIDRYVAICN	PIRPIIMGA	FRVALAOF	152
AOLFR79 . pr	PTTDSH-LQPMYFLINVL	LSICY	V--TPKMINV	VSD-SISFEC	VQIAELV-VHVTA	BSFILASMA	VDRYVAICN	PIHGSIMRGT	LQIVAVSA	157
AOLFR80 . pr	WQINHS-LQPMYFLIANI	LEIYS	S--TTPALANI	SMGTPT	ISICGQMFV-FLGGAC	OVIMWVMA	VDRYVAICN	PIRIRILIMS	VELLVGSL	151
AOLFR81 . pr	ATTFNPG-LQPMYFLINL	LTAL	IC--TPKALAS-	VSEESS	ISYGCMQI	FLTMAASSELILITVMA	VDRYVAICN	PIHSSMKVFE	SGIATAVFE	168

FIG. 2 (CONT-3)

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AOLFR82 . pr :	SVKASQA-LKPNMFFELFVLS-TCL-SIA--PRMIVDA-LKKT-TISFSDM-OVFS-SHVFCLEIFILITLWDRYVDCKPIHYMTLH-QW-GVIMAVAV	120	140	160	180	200	148
AOLFR83 . pr :	TWLSCSR-LTPMYFFLQNL-ILILFV--SPAVL-AN-GRDKHISFACITCYEF-F-FLGTVEFILLITWSDRYATCCPIRYTTINRPS-IGTVVFSV						149
AOLFR85 . pr :	TL-NARKTIDSPMYFFLSQ-LFALICVP-TTI--PMIADTFVEH--ILSFNGMTOLFS-AHFFGSTEFLITAMADRYVAICRPIHYTAINDCRK-GLIAGASL						148
AOLFR86 . pr :	TTSSPTL-ASPVFFELANL-FTEYSIA--PLIADS-YEGR-TISEECMAOLFG-AHFLGGVEILLITWADRYVAICPKPHNTITINRH-ANINGVAL						175
AOLFR87 . pr :	TTTSPA-LDSPVFFLSFF-FVGCST-A--PMIIFDL-TEK-TISESCMTQLHV-EHFFGGVEILLITWADRYVAICPKPIYLLITNRQ-GLIVAMAV						204
AOLFR88 . pr :	TCIDQ-LTPMYFFLSQ-LIMIMHV--TILWATNY-SGK-SISFVCATCHEIL-LCL-GGAECHELIANSDRYVAICHPPIRYAVENKK-GLMAYVNSL						150
AOLFR89 . pr :	TCIDQ-LTPMYFFLSQ-LIMIMHV--TILWATNY-SGK-SISFVCATCHEIL-LCL-GGAECHELIANSDRYVAICHPPIRYAVENKK-GLMAYVNSL						175
AOLFR90 . pr :	TLSSPALLVSPNFFELGIL-FVACHV-T--PMIIVDS-YVTF-TISEEGMWOIFA-EGFFAGVEVITITAMADRYVAICPKPIHYSSINRR-GLIMGVA-T						203
AOLFR91 . pr :	FWIDGR-LQTPMYFFLSQ-LFALILV--V--TPKLL-AC-LGEKHTISFACMITCYEF-F-FLGTVEFILLITWSDRYVAICDPPIHYTAINRRA-LIIVLGC-V						148
AOLFR92 . pr :	TWAEPR-LQTPMYFFLQNL-FEIMWT--TPKLL-GTFVWARTVCMSCCLLCAFFHF-FVGTTEFILLITWSDRYVAICDPPIHYTAINRRA-LIIVLGC-V						148
AOLFR93 . pr :	FWCVDKR-LOSEMYFFELGIL-AEILV--I--TPWIMGL-LPCQNTYLSACVQLEIL-L-AVGTTEFALIGANSDRYVAICDPPIHYTAINRRA-LIIVLGC-V						150
AOLFR94 . pr :	FLYMDPH-LTPMYFFLSQ-LIMIMHV--TTPVQVAAHF-SGR-SISFVCGIOLGLVCLVG-SEGILIGIMADRYVAICHPPIRYAVENKK-LQITGSSA						151
AOLFR95 . pr :	FWTDR-LTPMYFFLQNL-FEILFV--V--EPALINWSEN-S-ISFAGVAQLEIL-A-LLIVTEGELIANSDRYVAICDPPIHYTAINRRA-LIIVLGC-V						175
AOLFR96 . pr :	TSVDLA-LQTPMYFFLQNL-FEILFV--V--TPKLLVDSVPR-I-ISEFVCGTQMYEF-F-FFGSSECHISWADRYVAICDPPIHYTAINRRA-LIIVLGC-V						150
AOLFR97 . pr :	FWVSAT-LTPMYFFLSQ-LFALICVP-TTI--PMIIVDS-YVTF-TISEEGMWOIFA-EGFFAGVEVITITAMADRYVAICPKPIHYSSINRR-GLIMGVA-T						201
AOLFR98 . pr :	FWRESWT-LTPMYFFLQNL-FEILFV--V--EPALINWSEN-S-ISFAGVAQLEIL-A-LLIVTEGELIANSDRYVAICDPPIHYTAINRRA-LIIVLGC-V						151
AOLFR99 . pr :	FWTDR-LTPMYFFLQNL-FEILFV--V--EPALINWSEN-S-ISFAGVAQLEIL-A-LLIVTEGELIANSDRYVAICDPPIHYTAINRRA-LIIVLGC-V						150
AOLFR101 . p :	FWCDSR-LTPMYFFLSQ-LFALICVP-TTI--PMIIVDS-YVTF-TISEEGMWOIFA-EGFFAGVEVITITAMADRYVAICPKPIHYSSINRR-GLIMGVA-T						150
AOLFR102 . p :	FWTDR-LTPMYFFLQNL-FEILFV--V--EPALINWSEN-S-ISFAGVAQLEIL-A-LLIVTEGELIANSDRYVAICDPPIHYTAINRRA-LIIVLGC-V						154
AOLFR103 . p :	FWTDR-LTPMYFFLQNL-FEILFV--V--EPALINWSEN-S-ISFAGVAQLEIL-A-LLIVTEGELIANSDRYVAICDPPIHYTAINRRA-LIIVLGC-V						150
AOLFR105 . p :	FWTDR-LTPMYFFLQNL-FEILFV--V--EPALINWSEN-S-ISFAGVAQLEIL-A-LLIVTEGELIANSDRYVAICDPPIHYTAINRRA-LIIVLGC-V						150
AOLFR106 . p :	FWTDR-LTPMYFFLQNL-FEILFV--V--EPALINWSEN-S-ISFAGVAQLEIL-A-LLIVTEGELIANSDRYVAICDPPIHYTAINRRA-LIIVLGC-V						150
AOLFR107 . p :	FWTDR-LTPMYFFLQNL-FEILFV--V--EPALINWSEN-S-ISFAGVAQLEIL-A-LLIVTEGELIANSDRYVAICDPPIHYTAINRRA-LIIVLGC-V						150
AOLFR108 . p :	FWTDR-LTPMYFFLQNL-FEILFV--V--EPALINWSEN-S-ISFAGVAQLEIL-A-LLIVTEGELIANSDRYVAICDPPIHYTAINRRA-LIIVLGC-V						166
AOLFR109 . p :	FWTDR-LTPMYFFLQNL-FEILFV--V--EPALINWSEN-S-ISFAGVAQLEIL-A-LLIVTEGELIANSDRYVAICDPPIHYTAINRRA-LIIVLGC-V						151

FIG. 2 (CONT-4)

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AOLFR54 . pr : RSVAVSPFFI RRLVYCGHRV-MTHYCEHMGIAIACANITNI-YGLTVALIAI GLDS IIA SVGFIHAMGHP-SHDAQKAI TCGSHIGI IHCYIPA : 258
AOLFR57 . pr : GFI HSASQFI TIFVFCGP-E-IDHFCO VYPLHLAGSNH -IG-I IANSGLIA VTF IIA SVIVFIHYTYR--AYSARISKALATCGSHIV MIFAPA : 266
AOLFR58 . pr : GFI HS QILTFQIFCGP-V-INHFCO LYPLEIACD H -FGM VINSGE C INFESI IIA SVAVILSR--THSECAKAI TCGSHIAV IIFVPC : 307
AOLFR59 . pr : RSLGFIPTPI RHYHYCHG-A-LSHAFCHQDVLISBARTNS-YGLCWATIAGVDS FII SVVIHINTV DIA-SREQIKALANTOVSHICV IIFVPV : 257
AOLFR60 . pr : RALIFVPSII LRLIFCGNV-IPTHYCEHMGIAHISASIKNI-YGLCAICNI -EDIT IIA SVVHICAMERIP-THEP IASITCGSHVCV IIAVTPA : 256
AOLFR61 . pr : KSM IIVPFPFTRSRVCKK-Q-LSHYSYCHQDVMHLAGSNR DV-YGFFGALC -VDF IIA SVTIHKTVPICIA-SKKEIKALANTOVSHICA IIFVLP : 256
AOLFR62 . pr : RPV LIPMWI TYRLIFCOAHI-IAHYSYCEHMGIAHISCGNIR NG-YGLFWVSFF -LNL IIG SVVYTHRAVERIP-SHDAQKAI TCGAHGV QVYIPS : 256
AOLFR63 . pr : KSM IIVPFPFT RSLRVCKK-Q-LSHYSYCHQDVMHLAGSNR DV-YGFFGALC -VDF IIA SVTIHKTVPICIA-SKKEIKALANTOVSHICA IIFVLP : 256
AOLFR64 . pr : RSA LIPLPF KRFQYCHSRV-IAHAYCHLEHLAGSSII NH-YGLFWVACT GVDS FII SVVALIHTV SIA-SHOE IRLANTOVSHICA IIFVYIPM : 257
AOLFR65 . pr : RSLYV PLVI LRLIFCGHRI-IPTHYCEHMGIAIACASIKNI-REGCNISL -LDV IIA SVVRHYANECIP-SWEAIKALANTOVSHIGV IIA FTPA : 260
AOLFR66 . pr : RVLV PSTF TKRLVYCKGV-IPTHYCHMSVAKISGNVR NA-YGLIVALL GCFDI QIT SYMTIIOAVSIS-SADA QKAFETCAHVA MITYPA : 257
AOLFR67 . pr : RNV LIPFTI TKRLVYCRGP-IPTHYCHMSVAKISGNFKNA-YGLMVALI GVEDICOIS SYMTIIOAVSIS-SADA HKAFETOTSHCS MITYVAA : 257
AOLFR68 . pr : RNVMT PIPI SAQIRVCGRAV-IENCJCANMSISLSDVTNH-YQFAGGTI GSDI FII SVTHIRAMRIK-AEGAVAKAI TCGSHF-M IIFESTI : 258
AOLFR69 . pr : AETI HATHTVATESLSTGABE-IRRVFC IPPMIAISTD HTN-Q IIFVFGS E VTI IIA SVGLILAHKNY-SAEGRRVH TCGAHITG SYMTI : 294
AOLFR70 . pr : AETI HATHTVATESLSCGS E-IRRVFC MPPLAISSD HTN-Q IIFVFGS E VTI IIA SVGLILAHKNY-SAEGRRVH TCGAHITG SYMTI : 285
AOLFR71 . pr : ISF NSF NVWV SKLHFCDSV-VRHFC TSPILALSCD YDI-E M HLAGSTH VSL IISASVSHISTH KIN-STSC QKAI TCGASHIGV IIFVYM : 254
AOLFR72 . pr : YFSTA VSSY FSVSICSS I-INHYC NVPLAISSD YP-ETV FISAATN GSI IUL SFNVLSTH KIC-SSECAKAF TCGASHMA IIFVTL : 255
AOLFR74 . pr : YCTGIS VTIK FTLSFCGYV-LSHYC SLPLPLICSN HEI-E IIFLFAID SSL IIA SVGLILAHKNY-SAEGRRVH TCGAHITG IIFVYT : 254
AOLFR75 . pr : IALNP HTI AHLHFCSDV-IHHFC INSLPLSCD SN-Q S LATVGLI F YPS Q IIA SVIIVSAMKWP-SAOG IKAFTCGSHIAL IIFVAN : 255
AOLFR76 . pr : IEFNAS QIGDTFRLSTOMS V-IHHFC KPAVITINGSEDH S-E IIFLISFN FPAI T IISVLIHTH KRH-TCKGYQKPI TCGSHI IIA IIFVITV : 253
AOLFR77 . pr : VAVNAS QTS TLHFFVQASRI-VHFECEVPALIKISQAD CA-YEAA STSGVIL LPLS IATSIGHVIOAV SNR-SEEA HKAVITCGSHITV GFIYAA : 255
AOLFR78 . pr : GFI PVGPVIA ALIPCKQCAVMOHFECSGPLHIACTN KK-LEETDFVLSI SSL IIA SVGLIVLAW SIP-SASGCKAF TCGSHI IIV IIFVSA : 258
AOLFR79 . pr : FEGANSA QTCN FALFCGP-Q-ITHYCI IPPHLAGANATA-RIV VVSFAL T LPAAL IIA TSICIVLALGNR-SVAG EXDITCGASHFLA IIFVTV : 262
AOLFR80 . pr : IET LSLPLTI FHLFC-H-DEIHYC KPAVITINGSEDH R-H-YTA YIISFI STPLS IIS SVVFIIVAI RIR-SAEGCKAF TCGSHI IIV IIFVCT : 256
AOLFR81 . pr : LCA NTA HTG LRLIFCGP V-IHHFECEVPPLILICSS Y N-CAM VLADAFYGVNF T IASIGHVSS IIA IIFVITV QVYITAV : 273

FIG. 2 (CONT-5)

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AOLFR82 . pr : GSC HS QILF ALSL FCGP V-INFCFC LQPL QACSE Y-VN L VNSGA CAVS VLF FSVIFHSR--NFAEVINKELTCVSHIINITE PC : 252
AOLFR83 . pr : GCF SV EPTI SOLFEC GSWIINHFC SGPMALQAD TA-IE MORLSSW CCI VAVSYTYLTIRIP-SASG KKFATVQASHIINIPPS IT : 254
AOLFR85 . pr : ACF HS QILF TVQJ FCGP E-IDNFC VHPLEIACAD Y-VCI VANSGL SASFEL ISVHILNMR--SOSSEDKAVTCGSHIIVILMPP : 252
AOLFR86 . pr : GCF HS QILF LML FCGP V-INFC LYPLEIACAD Y-ICIL VANSGL CINF HAASVIVILYSR--SISADGCKELTCGAHFIIVALEFVPC : 279
AOLFR87 . pr : GCF HA QML VML FCGP V-IDNFC LEPLEIACAD Y-FQIF AANSGL C LIFSIL TSVHILCSOR-----KALTOAHITVWVLEFVPC : 300
AOLFR88 . pr : GASANS HMA MHF FCGP RK-VHFCYCEPAWVIVCGELT YETTYISSIL LPPI ISTSVFIIQSWQMR-SSGSRNFAVATCGSHITVSHIFAC : 254
AOLFR89 . pr : GASANS HMA MHF FCGP RK-VHFCYCEPAWVIVCGELT YETTYISSIL LPPI ISTSVFIIQSWQMR-SSGSRNFAVATCGSHITVSHIFAC : 279
AOLFR90 . pr : CAL HS QILF FQJ FCGP V-INFC LYPLEIACAD Y-FQIM VINSGL CINFSELS SVAVILSR--TISSECKKALTCGSHIIVALEFVPC : 307
AOLFR91 . pr : GAF SV EPTI FRLVYC--RKEINHFQ IAPILQACIN H-IEKINELLSAL SSLAFTGCSVYIISTIRIP-STQCKAFATVQASHITVSHIFAC SN : 252
AOLFR92 . pr : VFTIVFCQW LQLFC GNVISUYCH VGPSIACID S-LE LGVIATIL PGSL FNMISVYIISALIRIP-SATGCHITVTOASHITVSHIFAC AV : 253
AOLFR93 . pr : FCF FQ WPVY FQJLYCKS-NWNNFQ RGQILKSONN LF-TEFI FLMAVH FCSL PTSSNAYLISTIKIP-SSGSRKSHATVQASHITVSHIFAC SC : 255
AOLFR94 . pr : FFI DC QWV ANF VCGLRK-VHFCYCEMLSILQADV S-LEKVFACCVH FPFESILASVHIGTVMCH-SANAWKALATCGSHITVSHIFAC AA : 256
AOLFR95 . pr : CAC SS QTS FTLISQASRA-VHFCYCSRPICLSLSELFH-RUISFSLC LPTI LMSVYINVTAKIH-STEGCHKAFATCGSHICVSHIFAC AV : 280
AOLFR96 . pr : SAVPS QOTAWAL FCGP A-VHFCYCGPPVIVVVD-TMYE QALASTIL FPFQILVSVTRIIITIRUS-SATGCKAFATCGSHIIVSHIFAC TA : 255
AOLFR97 . pr : ACF HS HTGC FSLKFCGAHV-VHFCYCGPPILISQVD S-C-E LIFACGN SCTI LMSVFIINTHIKWS-SAQCKAFATVQASHITVSHIFAC TT : 306
AOLFR98 . pr : TFFIA ATN CDMR FCGP R-VHFCYCGPPVIVVVD-TMYE QALASTIL FPFQILVSVTRIIITIRUS-SATGCKAFATVQASHITVSHIFAC CA : 255
AOLFR99 . pr : CFTVAQ ITS FHLFVSS Q-LEHFC IAPVILASHHNHS-Q-V FMCCTI ATPIL LMSVHILSALIQFP-STLGCKAFATVQASHITVSHIFAC CA : 255
AOLFR101 . p : GLAGP EIS SRJFC GPNRICHVFC FPPVILACTD S-NV VDFVINSCK ATPIL CSVQICTVIRIP-SAAG RKALTCVSHITVSHIFAC SI : 255
AOLFR102 . p : LALPS OLTA FTLFCGHQHEINFC ICPVPMILACALIRH-QAV YVVSIL TTPFICISVVFICALIRIP-SAECRRATTCVSHITVSHIFAC CC : 260
AOLFR103 . p : ABL SA RTVSAFTLSFGTSE-IDFEC LPLILKLGESTYQ-EL IMFAIF PASMILMSVLFILVAINCGL--PAGSOAKTTCVSHITVSHIFAC TL : 254
AOLFR105 . p : GLANG VTSAL FGLAFGCHK-IEHFCYCHVPPILKACEDV VVAKG GLVCITA GCFILMSVAFIVAAIKIP-SAECNKALTCVSHITVSHIFAC EA : 256
AOLFR106 . p : GCF HS QVLA VMLFCGP E-IDNFC ITOVVRACAN PP-EE V ICSSGL SVCL PLUMSVAFILALFKILSCGENTVWATVSHITVSHIFAC PS : 256
AOLFR107 . p : LAS SA YTYVTHYVFORAOE-IRILICEPILHACAD SR-YEM YMGVTF FSLANIASYTOILLTVMIRIP-SNEG KVALTCVSHITVSHIFAC AA : 255
AOLFR108 . p : SFA VSDTSFTHLRYMGQ I-INFCYCEPAMILASID-YSTEA FSGVVRAPVSLICSVWNIISTV QVQ-SCEG IKAFTTCVSHITVSHIFAC SG : 271
AOLFR109 . p : FHLNG FLEV SREFF-RRDNHIESFCEAPVIVICSGLPQFSL-WA FADAIV SPMCT TTSVHILATILS-KGSSGCKTTCVSHITVSHIFAC TSA : 256

FIG. 2 (CONT-6)

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[illegible]

FIG. 2 (CONT-7)

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AOLFR110 . p	:	LEIGN-LAFDASYSFIVAPMVD-FL-SEK--VISRCC	:	TOFELHFLGCGEGLLWMAEDRVAICRPIHCSTWNPRA	:	YAMLAALG	:	FVHS IQVVL	:	164
AOLFR111 . p	:	EEIKN-LFDCLIJSVTAPESIAN-SLIHNS--ISLGG	:	ISOLSSASBELLLITWSEDRTALICHPHNDVINDRST	:	VORATVSLY	:	Q IAHMTACTF	:	191
AOLFR113 . p	:	LCITL-SVFFPSWCGIQFELSRLCLIPSVRP	:	PFLLDASFRPSSPTWGCACCYLLTAMAYDRVAICRPIHPPIIM	:	TIKAAACQ	:	F CFSVILAS	:	189
AOLFR114 . p	:	FFLSF-LTDCFTSWPESIMN-FLSEK--FTIS	:	AGCTQFELVALGNSLSOJAMAFDRVAVGCFEHTVTTH	:	HHH VILVAFSCSPHHS	:	LHTIN	:	165
AOLFR115 . p	:	FFIAN-LTDCFTSWPESIMN-ITQOS--QIIS	:	SCCAAFELMFGGLDNCILAMAYDRVAICRPIHSTST	:	POIALGLVC	:	VLNCPAMHTIT	:	181
AOLFR116 . p	:	FFLAN-LIINVFCSTAPMVD-LF-RKH--FTIS	:	GGGVCFEIHAVGCTEMWILAMAFDRVAICRPIHVLTMNQR	:	ILFLVISII	:	LIHS IQLAIV	:	164
AOLFR117 . p	:	FELOH-LAFDCYSALTPEMLOS-FTEEK--NLIL	:	OGGICFLVATFATSDCYLJAMAFDRVAICRPIHVTINRT	:	IRIVAGS	:	IM SINASVQTGTC	:	212
AOLFR118 . p	:	IFLG-ILCWDGLAITIPKALFWF---DAVIS	:	LPQFAQVAIHFFVGNESGILLOAFDRVAICRPIRPSIV	:	SS ILKATLFWLRNG	:	FVTPVPVAA	:	173
AOLFR119 . p	:	EFFGHALIDLTCTTIPKALFWF---SLSEIN	:	NACJAEFVHGTGVSQVIMLIDRVAICRPIRATTINP	:	IAKAEALR	:	VLM PFPEK	:	173
AOLFR120 . p	:	FEITH-LEC E WYFSYTPALAG-FIGVDCGNIS	:	ACCSCFFITLIGATECHILAMAYDRVAICRPIHGAFA	:	NGT IRIAAAC	:	LM F TPLPIYS	:	168
AOLFR121 . p	:	FEISM-PASSEVYLVIPEWILS-LIFHN--OPT	:	S LAGATOCFFVILATWNCHEITACGDRVAICRPIRTVTIM	:	KG AQIVCGS	:	GI LTMA LHVTAIF	:	164
AOLFR122 . p	:	FEELN-LFDCYPTSSTIVS-FLSER--FTIS	:	SCCAVACGLANGTTECVILGMAEDRVAICRPIRPIIM	:	KNAYVPVAGSFA	:	IVNSAVQTTFV	:	164
AOLFR123 . p	:	FEELN-LFDCYPTSSTIVS-FLSER--FTIS	:	SCCAVACGLANGTTECVILGMAEDRVAICRPIRPIIM	:	KNAYVPVAGSFA	:	IVNSAVQTTFV	:	196
AOLFR124 . p	:	VELT-LAVDICTSIPEMCT-MTSE--NTIS	:	ACCSHFLTWSLGAEMVFTTHAYDRVAICRPIHSTWNNH	:	VALLSMVAIAVTSWVHTAM	:		:	161
AOLFR125 . p	:	FEERH-LFDCCLISATPESILN-SVASTDS--	:	ISLGGICQFLVLLAGEIGITATSDRVAICRPIHCEAV	:	RG VQIMALS	:	INRGALCGLYTACTF	:	162
AOLFR126 . p	:	LELGS-LAFDASLSIVTPMILN-FLAKS--	:	MSLSECVCHSLVTVTTECFILATMAYDRVAICRPIHPTINE	:	IQILVLS	:	IG LHA THEAFSE	:	180
AOLFR127 . p	:	FEELGS-LAFDASLSIVTPMILN-FLAKN--	:	RMSLSECVCHSLVTVTTECFILATMAYDRVAICRPIHPTINE	:	IRILAES	:	IG LHA THEAFSE	:	169
AOLFR128 . p	:	FEELN-LAFDASYFIVPMDVD-FL-SEK--VIS	:	RSCITOFELHFLGCGEGLLWMAEDRVAICRPIHSTTHNPRA	:	YALSLVL	:	LG FIHSVQVDEL	:	164
AOLFR129 . p	:	FEELN-LFDCYPTSSTIVS-FLSER--FTIS	:	SCCAVACGLANGTTECVILGMAEDRVAICRPIHPTINE	:	KNAYVPVAGSFA	:	IVNSAVQTTFV	:	195
AOLFR130 . p	:	IFLG-ILCWDGLAITIPKALFWF---DAVIS	:	LPQFAQVAIHFFVGNESGILLOAFDRVAICRPIRPSIV	:	SS ILKATLFWLRNG	:	FVTPVPVAA	:	173
AOLFR131 . p	:	FEELSC-LLESYSTIAPFID-LI-AKI--FTIS	:	LEGGTQFELHFLGCGEGLLWMAEDRVAICRPIHPTINE	:	ROHILVAGS	:	LG FCHS IQIL	:	162
AOLFR132 . p	:	FEELSY-LFDCYCSWAPMVD-FS-IKR--EVIS	:	KLGGTQFELHFLGCGEGLLWMAEDRVAICRPIHPTINE	:	ROHILVAGS	:	LG FCHS IQIL	:	162
AOLFR133 . p	:	FEELSY-LFDCYCSWAPMVD-FS-IKR--EVIS	:	KLGGTQFELHFLGCGEGLLWMAEDRVAICRPIHPTINE	:	ROHILVAGS	:	LG FCHS IQIL	:	156
AOLFR134 . p	:	FEELSH-LFDCYCSWAPMVD-FS-IKR--EVIS	:	KLGGTQFELHFLGCGEGLLWMAEDRVAICRPIHPTINE	:	ROHILVAGS	:	LG FCHS IQIL	:	169
AOLFR135 . p	:	FEELN-LFDCYCSWAPMVD-FS-IKR--EVIS	:	KLGGTQFELHFLGCGEGLLWMAEDRVAICRPIHPTINE	:	ROHILVAGS	:	LG FCHS IQIL	:	179

FIG. 3 (CONT-3)

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AOLFR136	. p	YELSS-ILFEDCLV	VITER	ILVN-FLGKK--NTIL	SECV	VOE	FFVVFVVAZ	GVLIT	MAYDRVAICSP	ILNATH	SW	SLIVLAA	ELF	SA	THTSAM	: 164
AOLFR137	. p	FEISH-IALTD	SFS	VTPLMWN-MOTQH--LAF	KCC	STY	FFFFFADLDS	ILITS	MAYDRVAICHPHYATIK	QSC	VM	VAGS	IACACA	LHT	IA	: 164
AOLFR138	. p	FEISH-ILFDMW	SVN	VTPLMWN-LFSDK--ITS	ADCI	AC	FFFTALVHE	IFILAA	FAEDRVVIGNPILYGS	KRC	IR	ITTE	VEF	TS	TATLWY	: 162
AOLFR139	. p	YELG-ILAMG	GLATTIP	ILAILWF--NA	TSLL	CFACQ	YAHCFVANESS	FVQMA	DRVAICPRIPSP	IL	ES	VFRANGFA	RNS	CL	SVPLAA	: 150
AOLFR140	. p	YELA-MLFDD	VMCSSTP	ALCIFWF--HIL	DIC	DCQ	VOE	FFHTFTG	ESGMILMA	DRVAICPYRSTII	NP	IAKVGTA	R	V	LI	: 166
AOLFR141	. p	LEIC-MLTED	AAVSTPH	ALIFWC--GAGH	SASCI	ACQ	FFHAF	FCWSE	STVLLA	WEDRVVAICHPRIATII	DE	IAH	GVAAR	R	S	: 174
AOLFR143	. p	YELIS-MLAND	GVFEST	PTLSTFCF--NYNH	VA	NAC	VOE	FFHTFS	WESGILLAS	DRVAICPYRIVVIL	HN	ILAN	GLGILTK	STTLE	PPFP	: 166
AOLFR144	. p	YELIS-MLFSD	ALMAY	PTLSTFCF--NAN	T	DI	IOEL	IFFSW	WESGILLAS	EDRVVAICDPIRVATVI	TE	IAN	GLGAA	RSF	TLFPLP	: 164
AOLFR145	. p	YELIS-ILALTD	GLCVST	PTTGIFWF--NSOS	Y	GACIO	Q	FIHS	FSESSVILMA	SEDRVAICHPYRISVIL	GO	VRAGL	IVIFR	P	AT	: 176
AOLFR146	. p	LEIS-MLALTD	GL	LTTP	COLLWF--NV	RISSE	ACQ	FFHLG	FSESSVILLAS	Q	VAICOPHYASTII	NE	IGRTGLA	ICCCV	AV	: 166
AOLFR147	. p	FEIS-MLAMTD	IL	ACQ	ALISIFWL--GAE	ET	RCQ	T	FEELH	NEVLD	SALIMAF	FEHVAICSPRITII	PKYI	K	SAMG	: 172
AOLFR148	. p	LEIC-MLAGAD	VL	CTPQ	ALIFWF--RAGD	ISLDR	TO	FFHST	FISEGILLMA	FEHVAICPYRVTII	NA	IKK	CVTVS	RSYGT	PIPIIF	: 166
AOLFR149	. p	YELTN-ILFDD	WV	PTPLMWT-LVFP	SG	ALIS	HSQ	ACQ	FFHFLG	TECHYRMS	QDRILASYP	RTSN	G	S	HS	: 163
AOLFR150	. p	FLURN-ILAI	CD	CTTAP	ALD-LI-SKK--TIS	TSC	TO	FFHL	LGADIFES	WALC	MAISKPIH	VILM	RCQ	TAL	ISAS	: 164
AOLFR151	. p	FEIGH-ILFDD	CT	NVTEN	LHN-FLSEQ--ITS	ACQ	CLL	FIAL	VITEFYI	ILAS	VAIDRVVAICSPHSSR	KN	VO	VTIP	Y	: 164
AOLFR152	. p	FLURN-K	VED	VE	ITP	FLVD-LI-DSR--TIS	NDQ	ACQ	FFHFFAG	ADIFES	WALYDRVLAIAKPIH	VIMRKE	WVA	IWAS	S	: 164
AOLFR153	. p	YELTN-ILFDD	WV	PTPLMWT-LVSP	SG	ALIS	HSQ	ACQ	FFHFLG	TECHYRMS	QDRILASYP	RTSN	G	S	HS	: 163
AOLFR156	. p	NEISI-F	FE	WYATP	ALISN-LISEK--ALIS	MTCC	IO	YFFH	SLENS	EGIMTT	MAIDRVVAICNPRVQIM	PP	AL	SAGAC	FE	: 180
AOLFR157	. p	FEISN-ILFDD	CYC	ASQ	ALVH-CFSTH--PULS	PRO	ACQ	TSVSLA	LAFAECILMA	WALYDRVAICSNPR	SVWNGP	VO	IATS	GTS	LTAML-I	: 163
AOLFR158	. p	ELISI-ILFDD	CT	TPPLMWN-IOAQA--QSN	TCC	TO	CFVL	VFG	ENCIIM	WALYDRVAICHPRIANINPK	GL	LLLS	VS	DA	LHTIM	: 164
AOLFR159	. p	ELLEN-ILFDD	CL	TPPLMWN-IOAQN--QSN	TCC	TO	CLVL	VFAG	LESCIFAN	WALYDRVAICHPRIVIMNVHFGIL	ILL	SMF	MTMDA	VQSL	IL	: 164
AOLFR160	. p	FEISN-ILFDD	CT	TPPLMWN-IOAQN--SIT	SCQ	TO	CFVL	FFAG	ENCIIM	WALYDRVAICHPRIVIMNPR	GL	LLLS	TS	V	NAL	: 185
AOLFR161	. p	FFIAN-ILFDD	CL	TPPLMWN-IOAQN--PQ	IO	YFFH	FGIV	DSVIM	ILAM	WALYDRVAICHPHAKIM	LR	RUL	VGA	IAF	SCFIS	: 164
AOLFR162	. p	FEISS-ILFDD	AS	SVT	PLMWN-LMAEN--ALIS	HQ	ACQ	FFTS	GLTECHILMA	WALYDRVAICNPRILPVL	GR	ET	IATS	AL	CGNA	: 171
AOLFR163	. p	EFFCN-ILFDD	WY	VTPLMWT-CISED--SIS	ACQ	CO	FFS	AGL	AYSECYILIA	WALYDRVAICSPHIAQOM	IK	AL	IVAVS	CG	F	: 163

FIG. 3 (CONT-4)

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220	*	240	*	260	*	280	*	300	*	320
: 267	: 267	: 265	: 253	: 269	: 277	: 269	: 267	: 279	: 269	: 275
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: 267	: 267	: 265	: 253	: 269	: 277	: 269	: 267	: 279	: 269	: 275
: 267	: 267	: 265	: 253	: 269	: 277	: 269	: 267	: 279	: 269	: 275
: 267	: 267	: 265	: 25							

FIG. 3 (CONT-6)

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AOLFR110 . p	: A	-----DKA	SFHT	IFPP	NNP	Y	LR	Q	TS	MR	SRHVVCQVDFIIRN	316
AOLFR111 . p	: :	-----SILDA	S	FY	TP	PP	TP	NP	Y	LR	Q	318
AOLFR113 . p	: L	-----TLDR	A	V	S	TP	NP	Y	LR	Q	342	
AOLFR114 . p	: V	KDH	-----	JAT	V	WT	SS	LN	PP	Y	LR	309
AOLFR115 . p	: TERES	-----	RAA	L	M	TP	NP	Y	LR	Q	330	
AOLFR116 . p	: L	-----DKF	A	F	D	A	TP	NP	Y	LR	312	
AOLFR117 . p	: QENW	-----	KA	F	E	G	V	TP	NP	Y	LR	357
AOLFR118 . p	: A	TLIPV	-----	N	L	H	N	TP	NP	Y	LR	324
AOLFR119 . p	: T	PPSLHI	-----	N	A	N	L	TP	NP	Y	LR	324
AOLFR120 . p	: IN	-----FNR	S	F	E	S	TP	NP	Y	LR	317	
AOLFR121 . p	: IE	-----KDL	S	V	T	TP	NP	Y	LR	Q	309	
AOLFR122 . p	: L	NSDDLDTK	-----	S	F	E	G	TP	NP	Y	LR	318
AOLFR123 . p	: :	-----NTSD	E	S	G	V	TP	NP	Y	LR	346	
AOLFR124 . p	: FER	-----	DK	A	A	L	TP	NP	Y	LR	307	
AOLFR125 . p	: :	-----SILDI	S	F	E	S	TP	NP	Y	LR	315	
AOLFR126 . p	: :	DDQD	-----	N	E	S	TP	NP	Y	LR	325	
AOLFR127 . p	: :	DDQD	-----	M	D	S	TP	NP	Y	LR	314	
AOLFR128 . p	: A	-----	DK	S	F	H	TP	NP	Y	LR	308	
AOLFR129 . p	: V	-----	DKF	A	F	TP	NP	Y	LR	343		
AOLFR130 . p	: A	TLIPV	-----	N	L	H	N	TP	NP	Y	LR	324
AOLFR131 . p	: E	-----	DK	A	F	TP	NP	Y	LR	309		
AOLFR132 . p	: A	-----	DK	A	F	TP	NP	Y	LR	305		
AOLFR133 . p	: I	-----	DK	A	F	TP	NP	Y	LR	303		
AOLFR134 . p	: YN	-----	SNK	S	L	TP	NP	Y	LR	325		
AOLFR135 . p	: LERD	-----	KA	F	E	G	TP	NP	Y	LR	327	

FIG. 3 (CONT-7)

	*	20	*	40	*	60	*	80	*	100
AOLFR188 . p :	MK	----	----	----	----	----	----	----	KNNVTEFIIGC	QNPGE
AOLFR189 . p :	MQ	----	----	----	----	----	----	----	QNNSVPEFIIGC	QOPLR
AOLFR218 . p :	META	----	----	----	----	----	----	----	ATKITEFVIIGC	QTREW
AOLFR191 . p :	MT	----	----	----	----	GGG	----	----	ATEFTVEFIIGC	DPRPI
AOLFR192 . p :	M	----	----	----	----	E	----	----	NNEFEFIIGC	DDPEL
AOLFR193 . p :	M	----	----	----	----	E	----	----	KKEFTQEFIIGC	DNSEI
AOLFR194 . p :	M	----	----	----	----	ERQ	----	----	OCVEFEFIIGC	NYPEL
AOLFR195 . p :	M	IVOLICTV	----	CFLAVNTF	----	HVRSSFDLKADMEI	----	----	CLSEFIIGC	GVPKI
AOLFR196 . p :	ML	----	----	----	----	ES	----	----	VMPTEFIIGC	DYLPRI
AOLFR197 . p :	M	----	----	CYLSQLCL	----	SLGEHTLMGMVRHT	----	----	ENNACTEFIIGC	DYPOLI
AOLFR198 . p :	M	----	----	----	----	E	----	----	CEFTFKTEFIIGC	SVPEL
AOLFR199 . p :	MD	----	----	----	----	TGNKTL	----	----	POCFELIGCFPSQHL	----
AOLFR200 . p :	MT	----	----	----	----	RK	----	----	VTSLETFEVIIGC	ADTLEI
AOLFR201 . p :	M	----	----	----	----	EWE	----	----	HTILVEFEFIIGC	GEPRI
AOLFR202 . p :	M	----	----	----	----	EWE	----	----	HTILVEFEFIIGC	GHPRI
AOLFR203 . p :	M	----	----	----	----	KRO	----	----	OSCVVEFEFIIGC	NFPPEL
AOLFR204 . p :	ME	----	----	----	----	----	----	----	KKKNVTEFIIGC	ONPIM
AOLFR205 . p :	MESE	----	----	----	----	----	----	----	RTTVIREFEFIIGC	POSQDI
AOLFR206 . p :	MA	----	----	----	----	----	----	----	RNNVTEFIIGC	ENPKAI
AOLFR190 . p :	M	----	----	----	----	QR	----	----	SNHTVTEFIIGC	TDPCKM
AOLFR207 . p :	M	----	----	----	----	ERT	----	----	DSTSTEFEFIIGC	AGPKUI
AOLFR208 . p :	M	FPA	----	----	----	----	----	----	VTSSVKVEFEFIIGC	FHYPKUI

FIG. 4 (CONT-2)

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AOLFR165 . p :	FFPMLIGLYLALAMNLSLIAHKM	SHLEPNYFELSNL	FLDLC	VSSAKKMLSDI	TEQ-	TISAVGCA	---	TCYFVFCG	LTECLLAAMAYDRYVAIC	: 128
AOLFR166 . p :	VFLFLLVYVPLIGNLLIM	FWTCERLHPNYLHLH	IADIC	SSITFKVLYDL	SER-	TISNHC	---	TCMFLFHL	GVDVFSISVMAIDRYVAIS	: 127
AOLFR167 . p :	ALFVTLGLVLTALAMNLANLEIRG	THIGCPNYFHSN	SAI	FIDIC	SSAVANML	TDFWEQ-	TISAVGCA	---	ACFFFFVCG	: 130
AOLFR168 . p :	KUDFWSEFFVILIGNMLIM	FWCLSNLEKPNYFELSEL	FVDIC	SSVTAPKMLVDL	AKD-	TISVVGOM	---	ICLLGVHFF	CTEFLITVMAYDRYVAIC	: 125
AOLFR169 . p :	HIIEALFFFYLLALMGNTVIL	VCV	KRLQ	PNYFELSHL	TEILV	TIIVEMWINGL	---	ELGQOYLSLHVSINFSC	TMEFALIGVMAYDRYVAVC	: 123
AOLFR170 . p :	ALVCPILAVLAFMGNTVIL	AVIA	THEHPNYFELG	FL	IL	ELVMTAVFRL	SDI	VPH-	VITTCOM	: 211
AOLFR171 . p :	-----	VGNLLIM	TTIGSPSIG	INVEFLAYE	ILMDAL	STAMCKML	IDL	CDK-	IAISLSAOM	: 89
AOLFR172 . p :	TWTIVGPIVILALGNCAIPAWMI	STLHCNMLLAL	IAATD	IGL	ISIAEGH	AVLWLG	PRSMFNAVCL	---	YCMFVFA	: 132
AOLFR172 . p :	WMSPLICIVITAVLGNLSIL	IVMERNLHPMYFRLSM	AVMDIL	ISTTTV	KALAEFLWQ	AHNIA	DACV	---	TCGFVHM	: 129
AOLFR175 . p :	ILFLETLVILALMGNSILICAHW	ORLHPNYLIL	F	FL	IC	VTSVPESMLANF	SDT-	ILISGOF	---	: 165
AOLFR176 . p :	SCFESFILVILALGNCAIVCAKIL	RRLEHPNYLILG	FAFL	EW	ISSTVENMLVNI	SEI-	TISVWCF	---	ICFYFFFS	: 145
AOLFR177 . p :	EFESLILVILALGNCAIIVARC	PLLEHPNYGLIF	FAFL	EW	VSSTLENMLVNI	SKT-	IAISGOF	---	ICFYFFFS	: 137
AOLFR178 . p :	ILLFSSFYKAMGNSILITVTS	PHLEHPNYLILAL	FIDIG	VSSTSKML	VDLFRKH	EVISGCCI	---	ACIFLTHV	GVMWLLTAMAFDRYVAIC	: 127
AOLFR179 . p :	ILLFSLFVEFAMGNSIVETVM	AYLHPNYLILAL	IIDNA	CSITAKML	CDIFKKH	-	IAISRGCI	---	ICIFESHA	: 127
AOLFR180 . p :	WMSPVCCLETLALGNVIL	ITITRRLEHPNYLILSV	IAVDICL	ITTT	ETVLGVLWPH	-	AEISKACF	---	ICMFFVHAFSLIESVIVAMAFDRYVAIC	: 156
AOLFR181 . p :	WFSPLICWYLALGNCLIL	FKTESLHPMYLILAM	AVSDNGI	SLSSIT	MLRVF	FN	AMGISPNAF	---	ACEFFHGHFTVMSVILMSIDRFIAIH	: 127
AOLFR182 . p :	WMSPLCEWYLALGNCLIL	FKTESLHE	WYLILSV	IALD	IGISLCT	ETVLGIFWVG	-	AEISHDACF	---	: 132
AOLFR183 . p :	PMAPPLGLVTLALGNCLIL	AKVESLHE	TYVILSIAL	ALDUSIS	MLTSM	SIYWN	-	APQIMEDACI	---	: 129
AOLFR184 . p :	SWWTPLIAVYLALGNCLIL	IALQALPRLR	HEFL	ETL	VSDIGLYTAL	ETL	GIA	AG	-	: 135
AOLFR185 . p :	WMAFPICATVAVVGNLIL	HLIRI	HTLHPNYLILAM	AITD	IVISSTOKML	IAFWFH	-	AHEIQHACL	---	: 209
AOLFR186 . p :	ALFEGILVYVPLIGNMLIL	ILVIRV	SHLSHPNYLIL	ETL	FIDWES	IVTVKMLMTI	SPSC	IAISPHSCV	---	: 126
AOLFR187 . p :	WMSPLICWYLALGNCLIL	ILSOAILHE	PNYLILSM	ASADVILI	STTTPEKAL	ANLWLG	-	YSHISHDCL	---	: 146

FIG. 4 (CONT-4)

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AOLFR188 . p :	KVFTLILVW	INGNLLIT	TIMASQIC	PMYFRIAS	FLITV	ISTAPKMI	VDL	SEK	ITISQCC	---	ACIFMDHLF	GAEVILLI	VWMA	DRVAIC	: 125
AOLFR189 . p :	KBFTLILVW	IVVGNMLIT	TIKSSRTG	PMYFRIAS	PACSC	ISTAPKMI	VDL	SEK	ITTYNEOM	---	TQVFAHLHF	CWEIFVILLI	MA	DRVAIC	: 125
AOLFR218 . p :	KVFTLILVW	LSMIFLPGN	ILLICTIRL	PHET	PMYFRIAS	FLITV	ISTAPKMI	IDFVER	ITISGCGI	---	ACIFLHF	ASEMFLI	VWMA	DRVAIC	: 127
AOLFR191 . p :	KVFTLILVW	ITVITL	AMNLSL	IRW	SHLH	PMYFRIAS	FLITV	ISTAPKMI	VDL	---	IQVIFSTW	LSESCIT	MA	DRVAIC	: 128
AOLFR192 . p :	KVFTLILVW	LVGNLME	ILLI	SCHE	PMYFRIAS	FLITV	ISTAPKMI	VWGH	TGD	---	TQVFAFITA	ESHLIAS	MA	DRVAIC	: 125
AOLFR193 . p :	KVFTLILVW	LVGNLGI	ILLI	SCHE	PMYFRIAS	FLITV	ISTAPKMI	VWGH	TGD	---	ACQVIFVAFAT	VENYLIAS	MA	DRVAIC	: 125
AOLFR194 . p :	GOFEALILVW	LLIGNAIL	IVST	QSLHVPWIL	ILLI	WDLIS	SAVIMPE	KLIVLSTK	TTISGCGI	---	ACQVILHF	GAECFLIG	MA	DRVAIC	: 127
AOLFR195 . p :	KVFTLILVW	LLIGNVIL	IASIF	SHLH	PMYFRIAS	FLITV	ISTAPKMI	VWGH	TGD	---	ACQVIFVAFAT	VENYLIAS	MA	DRVAIC	: 157
AOLFR196 . p :	KVFTLILVW	LLIGNVIL	IASIF	SHLH	PMYFRIAS	FLITV	ISTAPKMI	VWGH	TGD	---	ACQVIFVAFAT	VENYLIAS	MA	DRVAIC	: 127
AOLFR197 . p :	KVFTLILVW	LLIGNVIL	IASIF	SHLH	PMYFRIAS	FLITV	ISTAPKMI	VWGH	TGD	---	ACQVIFVAFAT	VENYLIAS	MA	DRVAIC	: 147
AOLFR198 . p :	KVFTLILVW	LLIGNVIL	IASIF	SHLH	PMYFRIAS	FLITV	ISTAPKMI	VWGH	TGD	---	ACQVIFVAFAT	VENYLIAS	MA	DRVAIC	: 125
AOLFR199 . p :	KVFTLILVW	LLIGNVIL	IASIF	SHLH	PMYFRIAS	FLITV	ISTAPKMI	VWGH	TGD	---	ACQVIFVAFAT	VENYLIAS	MA	DRVAIC	: 127
AOLFR200 . p :	KVFTLILVW	LLIGNVIL	IASIF	SHLH	PMYFRIAS	FLITV	ISTAPKMI	VWGH	TGD	---	ACQVIFVAFAT	VENYLIAS	MA	DRVAIC	: 127
AOLFR201 . p :	KVFTLILVW	LLIGNVIL	IASIF	SHLH	PMYFRIAS	FLITV	ISTAPKMI	VWGH	TGD	---	ACQVIFVAFAT	VENYLIAS	MA	DRVAIC	: 127
AOLFR202 . p :	KVFTLILVW	LLIGNVIL	IASIF	SHLH	PMYFRIAS	FLITV	ISTAPKMI	VWGH	TGD	---	ACQVIFVAFAT	VENYLIAS	MA	DRVAIC	: 127
AOLFR203 . p :	KVFTLILVW	LLIGNVIL	IASIF	SHLH	PMYFRIAS	FLITV	ISTAPKMI	VWGH	TGD	---	ACQVIFVAFAT	VENYLIAS	MA	DRVAIC	: 127
AOLFR204 . p :	KVFTLILVW	LLIGNVIL	IASIF	SHLH	PMYFRIAS	FLITV	ISTAPKMI	VWGH	TGD	---	ACQVIFVAFAT	VENYLIAS	MA	DRVAIC	: 125
AOLFR205 . p :	KVFTLILVW	LLIGNVIL	IASIF	SHLH	PMYFRIAS	FLITV	ISTAPKMI	VWGH	TGD	---	ACQVIFVAFAT	VENYLIAS	MA	DRVAIC	: 127
AOLFR206 . p :	KVFTLILVW	LLIGNVIL	IASIF	SHLH	PMYFRIAS	FLITV	ISTAPKMI	VWGH	TGD	---	ACQVIFVAFAT	VENYLIAS	MA	DRVAIC	: 125
AOLFR190 . p :	KVFTLILVW	LLIGNVIL	IASIF	SHLH	PMYFRIAS	FLITV	ISTAPKMI	VWGH	TGD	---	ACQVIFVAFAT	VENYLIAS	MA	DRVAIC	: 125
AOLFR207 . p :	KVFTLILVW	LLIGNVIL	IASIF	SHLH	PMYFRIAS	FLITV	ISTAPKMI	VWGH	TGD	---	ACQVIFVAFAT	VENYLIAS	MA	DRVAIC	: 127
AOLFR208 . p :	KVFTLILVW	LLIGNVIL	IASIF	SHLH	PMYFRIAS	FLITV	ISTAPKMI	VWGH	TGD	---	ACQVIFVAFAT	VENYLIAS	MA	DRVAIC	: 127

FIG. 4 (CONT-5)

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AOLFR209 . p :	120	140	160	180	200	*	:	127
AOLFR210 . p :	120	140	160	180	200	*	:	127
AOLFR211 . p :	120	140	160	180	200	*	:	127
AOLFR212 . p :	120	140	160	180	200	*	:	127
AOLFR213 . p :	120	140	160	180	200	*	:	168
AOLFR214 . p :	120	140	160	180	200	*	:	127
AOLFR215 . p :	120	140	160	180	200	*	:	127
AOLFR216 . p :	120	140	160	180	200	*	:	127
AOLFR217 . p :	120	140	160	180	200	*	:	137

FIG. 4 (CONT-6)

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AOLFR165 . p	: NPLVTVLI HT LKOWGAY GELISSE EYYS -YQHFCI PYLWVCHC PVLALSCSD FTS VTFIVSVVG VSWLV SYGYVAAM -K SAT	: 234
AOLFR166 . p	: KPLVATH RH IGTVAAM GEFVHSI QLSL -LPFEC PVL T VCH HRVKKIAHTDFIL LMISNGLLTWEEF SVIHLSPKSOAG--E	: 232
AOLFR167 . p	: SPLVPTIM QG TRWVGAY GELISSE QASS -FRIHFC PVLWVCHC PVLALSCSD FLS VNFLVVTWGGSFIC SYGYVSAM -K PAE	: 236
AOLFR168 . p	: KPLVMTNRET NKVLGTH GEFVHSI QVAL -VQIFEC PELWVCHC HPVKKIACFE YVGVVTANSCTA GSFVIL SYGIVSRKOSA--E	: 230
AOLFR169 . p	: NPLRNIHNSST IHWVIVSM EGEIS-E WPIYATQFIRKS SLWVCHC CPGHKKISQDN LLT FILFLMAVFI GSLIPT SYTIISII -K PAAS	: 229
AOLFR170 . p	: HPLRGTH RAH VQJAGAAAPFLAN- PTVLSRAHLDVCHG INWVCHC NEPLIQSCSD RLL FWDFLMALTV SSFL T SYGYVTVV -R PIASS	: 317
AOLFR171 . p	: KPLEVANIIRL ILLWAM GEFVHSI QVVF -YSIPIC PVLWVCHC SVCHYPHEILCLD IFIC TVWANGGIIQ VIFTH SCGVINFIKYSO--EE	: 194
AOLFR172 . p	: RPLHPVLY KACGVYAALALA KAVAI-V PEPL VAKFEHFOAKTIC TYCAHMAVFI VVGMOATN YGLALSLSAISGMDIIC TGSYGLHAGV -K PREA	: 238
AOLFR173 . p	: APLRVTVL WP GRALAVITRSFCI-IFPVIF LKRIPECLT VPA YCHICVARIACADITVNIWVGFSVPVWV LDVHFA SVSIIIRAV -FR PODA	: 235
AOLFR175 . p	: RPLRVPTM RR TMVNVCH IGEIWF PIVN -SQMSFC SR ILM ICPAPITITCKKGPVI VFSVLSPLPVMLFIEI GSAIVRAV -R PAA	: 271
AOLFR176 . p	: RPLRPSIK GXE ILLVCCH GEFVHSI QVVF -SOLPEC PVLWVCHC LVC PHLFALACISAPST ICYTFSMLIFGPFSI GSYTIIRAV -C PIGA	: 251
AOLFR177 . p	: HPLQVPAH VRF GKIVSFCM IGEI GYP PIFY -SOLPEC PVLWVCHC ICDPFLMAISAPAPIT CIFYQSSIVLFTSVYI PSLIILITAV -FQ PAA	: 243
AOLFR178 . p	: KPLQLTLM PRG MFFLVAAH TGLIHSV QLVF -VNLPFC PVLWVCHC PRHKKIACFE YRL FMVTANSGFIS GSEFFI SYWVIL LVLKHSAA--	: 232
AOLFR179 . p	: KPLRVLTLM PRG LYFLATSS IGLIHSV QLVF -VDLPFC PVLWVCHC PRHRIACFM OEI FMVTVNSGLIS GSEFFI SYVIFL FVWKHSSG--	: 232
AOLFR180 . p	: NPLRVATIL DRNVLVGLVIC RPAVF-L PLLVAINTVSH GHEISL PCYHPEVKKIYTSKPVWISSFWGLFIQLYINGTDVIEI FSVIILIRAV -G VARKK	: 262
AOLFR181 . p	: NPLRVSSIL SURVANGLIILA RSILL-V PEPFTLRRIKYOX ILSL CHQDINKIAGSNKNTV YGFFIALCTM-LDLAII SYVILIKII -S LAE	: 232
AOLFR182 . p	: HPLRVSLTNT IGRIGVLSIGRSVAL-IFPLPMLKREFYV SPVLSL CLHQFWKKIACALMKANS YGMFVIVSTVGTDSLEI FSVALLIRAV -S LAE	: 238
AOLFR183 . p	: NPLRVSLI HDI IRKTGISVLRVCV-VFPVPF IKCLPCHSWILSS CLHONWRIACAS RINS YGLIIVIFLGLDVI T SVLTKV -G VERGE	: 235
AOLFR184 . p	: RPLRVPALNG ISKISLAI SFRCLGL-G PLPFL LAYMPCLPOLVTS CLHPDVARIACPEANGAA-YSLFVLSAMGLDPIEFSSYGLIKVIL -G VERED	: 240
AOLFR185 . p	: FPLRVSSIL PSVIVKIGTIVM RGLIIV-VSPFCFVSMRPFQHOAIPOS CEHMAVKKIACAD SISRCYGLFVAFSVAGFDMVIG SVWIIIRAV -C PIGA	: 315
AOLFR186 . p	: YPLRVTSMA GSR ALIATCTM SSLSHSA QFILT-PLHPVC PVLWVCHC CHAPPLIKIACAD SANVAVIFVDIGIVASGCFV SVSVIICSI -R RPSD	: 232
AOLFR187 . p	: SPLRVTVL SK GKVATATLSRSII-L-MFPSIF LEHIFCOI ILEI TCEHMGIAHLSCEISINWVGLIAAALLSTGLDIMEI SVIHLIOAV -FR PODA	: 252

FIG. 4 (CONT-7)

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AOLFR188 . p	220	KPLHLLTNR	240	260	280	300	320	230
AOLFR189 . p	220	KPLRYPPTM	240	260	280	300	320	230
AOLFR218 . p	220	RPLHYATNRR	240	260	280	300	320	234
AOLFR191 . p	220	NPLLYSSIM	240	260	280	300	320	234
AOLFR192 . p	220	KPLHYTTN	240	260	280	300	320	231
AOLFR193 . p	220	KPLHYTTN	240	260	280	300	320	231
AOLFR194 . p	220	HPINQVIMK	240	260	280	300	320	233
AOLFR195 . p	220	NPLRPIIL	240	260	280	300	320	263
AOLFR196 . p	220	NPLLYTTM	240	260	280	300	320	233
AOLFR197 . p	220	RPLHTVIMH	240	260	280	300	320	253
AOLFR198 . p	220	KPLHYTTM	240	260	280	300	320	231
AOLFR199 . p	220	YPLHGCIM	240	260	280	300	320	233
AOLFR200 . p	220	RPLLYSLM	240	260	280	300	320	233
AOLFR201 . p	220	NPLRPIIM	240	260	280	300	320	233
AOLFR202 . p	220	NPLRPIIM	240	260	280	300	320	233
AOLFR203 . p	220	HPINYPVIM	240	260	280	300	320	233
AOLFR204 . p	220	KPLANTTH	240	260	280	300	320	230
AOLFR205 . p	220	RPLHYPTN	240	260	280	300	320	232
AOLFR206 . p	220	KPLHYTTN	240	260	280	300	320	230
AOLFR190 . p	220	KPLHYAQT	240	260	280	300	320	231
AOLFR207 . p	220	YPLRYPVIM	240	260	280	300	320	233
AOLFR208 . p	220	NPLRYPVIM	240	260	280	300	320	233

FIG. 4 (CONT-8)

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AOLFR209 . p	:	NPLRPIITANKV	YVLT	SVSM	SG	INST	QTS	LA	MR	FC	NR	IN	ICE	LA	WIKI	AC	ST	IS	WN	TL	AV	SN	IA	FL	LP	IL	EF	SM	FI	YH	RT	MA	:	233			
AOLFR210 . p	:	SPLHTVITPRK	LA	IT	GP	IG	DS	NV	VS	SR	HE	CD	IN	CH	TS	PI	AM	CT	DN	AL	FI	AG	ST	VS	LI	IS	AS	VS	II	SH	KN	TS	:	233			
AOLFR211 . p	:	SPLHTVITPRK	LA	IT	GP	IG	DS	NV	VS	SR	HE	YD	IN	CH	TS	PI	AM	CT	DN	AL	FI	AG	ST	VS	LI	IS	AS	VS	II	SH	KN	TS	:	233			
AOLFR212 . p	:	NPLVSVW	OK	SN	IG	VM	PI	IG	TS	SS	LA	FC	DS	NR	IN	ICE	LA	WIKI	AC	ST	IS	WN	TL	AV	SN	IA	FL	LP	IL	EF	SM	FI	YH	RT	MA	:	232
AOLFR213 . p	:	KPLFVWITNPR	QO	AS	IS	SM	SG	LA	SS	HA	FT	LO	IC	NR	IN	ICE	LA	WIKI	AC	ST	IS	WN	TL	AV	SN	IA	FL	LP	IL	EF	SM	FI	YH	RT	MA	:	274
AOLFR214 . p	:	KPLFVWITNPR	RT	TV	WM	IS	MA	VS	IM	HT	LS	FT	VS	NR	IN	ICE	LA	WIKI	AC	ST	IS	WN	TL	AV	SN	IA	FL	LP	IL	EF	SM	FI	YH	RT	MA	:	232
AOLFR215 . p	:	KPLFVWITNPR	VI	FS	IS	MA	VS	IM	HT	LS	FT	VS	NR	IN	ICE	LA	WIKI	AC	ST	IS	WN	TL	AV	SN	IA	FL	LP	IL	EF	SM	FI	YH	RT	MA	:	232	
AOLFR216 . p	:	KPLFVWITNPR	PO	VA	IS	MA	VS	IM	HT	LS	FT	VS	NR	IN	ICE	LA	WIKI	AC	ST	IS	WN	TL	AV	SN	IA	FL	LP	IL	EF	SM	FI	YH	RT	MA	:	232	
AOLFR217 . p	:	KPLFVWITNPR	RR	VG	IS	MA	VS	IM	HT	LS	FT	VS	NR	IN	ICE	LA	WIKI	AC	ST	IS	WN	TL	AV	SN	IA	FL	LP	IL	EF	SM	FI	YH	RT	MA	:	242	

FIG. 4 (CONT-9)

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AOLFR165 . p .	340	360	380	400	420	*	324
	HTATLFTVSGFVYR	SSSVSLNRD	VSSTVALIPVNPVLIYSF	FEIANMA	AME	DPGLSHGQPFIENTLG	
AOLFR166 . p .	RKAISTCTHTATLFTVPC	VARFTALPMD	FAISFTVISPINPLIYTLR	HEMS	REGLVPSDRK		311
AOLFR167 . p .	WKAATCAHMAVWILLAT	YRASSVLLGRD	WVSFVSIPMPINPLIYSLR	ELKALQ	LEKKVFS		315
AOLFR168 . p .	RKALSTCGHMAVWIFTEP	CTVARIDTSES	WVAVEHITPMINPLIYTLR	AEAVN	WGNVFEAKCK		311
AOLFR169 . p .	RKAFTCAHFTCWIGK	SCLEVYKQOGVE	YNSLVWMLTPEHNPETFLR	DKVE	CCQLLK-D		310
AOLFR170 . p .	CKAFSTCGHITVFTIGYST	IVRAGKAHSVQ	VRVALVTWTEFLNPEL	IFEC	OTVTVI	OGOMOLKGLCKAQ	399
AOLFR171 . p .	RKALPTCIHILVALVFP	CLVAVRVSNPFD	WMTVEHITPMINPLIYS	POSEMEN	WCKELSVRKRVSP	TINIFIPSSKATNRR	292
AOLFR172 . p .	HAKFEGTCHICILAF	IPGLFSYLACRFGHT	VPRPVHILSNITILLPE	ANPLINGART	QIDRI	LETTFRKSP-L	320
AOLFR173 . p .	RKALSTCGHICILMEVPSF	FTLTHHFCRNI	PQHVIHLANLVANP	PMNPVYGVAT	QIEGVAHRRFDIK	TWCCTSPLG-S	323
AOLFR175 . p .	RKAFTSGHIAVSVFYSV	VYSGSPSKNE	AGQIVTIEV	VTPLNPVIYSLR	DMKEL	FWGT	345
AOLFR176 . p .	HTKAFTSGHIMVSVFNT	LMVYSTSGNP	AGQITIVYANT	HPINPLIYSLR	DMKD	ALGLTVSQN	330
AOLFR177 . p .	RKAFTSGHIAVSVFNR	WVYVYSTYGP	TLLQITIVVNT	PEINPLIYTLR	DMIL	LELFGWIRQNS	324
AOLFR178 . p .	LSKALSTLSAHSVW	LEFTEPLIYTW	SPSTHLD				291
AOLFR179 . p .	LAKELSTLSAHTW	LEFTEPLIYTW	SPTSULD				312
AOLFR180 . p .	QOKALSTCVCHICAVT	IFYVPLIS	LAGRLFHST				354
AOLFR181 . p .	RKALNTCVHICAMLT	WPIITA	AMHFAKHK				312
AOLFR182 . p .	RKALNTCVHICAMLT	FPPIG	ES-VTHREKQA				314
AOLFR183 . p .	LKTLSTCLHGSTV	LFYVPMGAASMI	HRFWEHL				302
AOLFR184 . p .	WKEGOTCAHLSAM	LEYIPMLA	LINHPELPI				323
AOLFR185 . p .	RKAFTSTRAHICILAL	YIPAL	FSELYRFGHD				394
AOLFR186 . p .	RRRPFOTCAHCTVLC	FFVPCWV	RGSDMAMD				311
AOLFR187 . p .	ASKALSTCGHICIL	IFYWPA	LSFAVR				335

FIG. 4 (CONT-10)

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AOLFR188 . p	PRKAFSTCAHHTVWILEFVPCU	VAR NSTFPID	STVL	ETIPWLNPIIYTLR	EVKAM	LWS	KVSLACKWLYHS	314
AOLFR189 . p	PRKALSTCAHHTVWILEFVPCU	TR PTFPMO	AVAVH	ETIPWLNPIIYTLR	EVKAM	WVT	VILCEK	298
AOLFR218 . p	TRPAMTCVHHTVWILEFVPCU	PSD VAR FDSFSD	AVSV	ETIPWLNPIIYTLR	EVKAM	WVT	VILCEK	313
AOLFR191 . p	SPKAFSTCAHHTVWILEFVPCU	WSSSGSSFD	EVSV	ETIPWLNPIIYTLR	EVKAM	WVT	VILCEK	311
AOLFR192 . p	PRKAFSTCAHHTVWILEFVPCU	R NSSHFMTD	AVSV	ETIPWLNPIIYTLR	EVKAM	WVT	VILCEK	314
AOLFR193 . p	YOKPISTCAHHTVWILEFVPCU	SSSHSMDTD	AVSV	ETIPWLNPIIYTLR	EVKAM	WVT	VILCEK	314
AOLFR194 . p	PRKAFSTCAHHTVWILEFVPCU	Q KSGYSPETK	AVSV	ETIPWLNPIIYTLR	EVKAM	WVT	VILCEK	314
AOLFR195 . p	PRKAFSTCAHHTVWILEFVPCU	Q KSGYSPETK	AVSV	ETIPWLNPIIYTLR	EVKAM	WVT	VILCEK	314
AOLFR196 . p	PRKAFSTCAHHTVWILEFVPCU	Q KSGYSPETK	AVSV	ETIPWLNPIIYTLR	EVKAM	WVT	VILCEK	314
AOLFR197 . p	PRKAFSTCAHHTVWILEFVPCU	Q KSGYSPETK	AVSV	ETIPWLNPIIYTLR	EVKAM	WVT	VILCEK	314
AOLFR198 . p	PRKAFSTCAHHTVWILEFVPCU	Q KSGYSPETK	AVSV	ETIPWLNPIIYTLR	EVKAM	WVT	VILCEK	314
AOLFR199 . p	PRKAFSTCAHHTVWILEFVPCU	Q KSGYSPETK	AVSV	ETIPWLNPIIYTLR	EVKAM	WVT	VILCEK	314
AOLFR200 . p	PRKAFSTCAHHTVWILEFVPCU	Q KSGYSPETK	AVSV	ETIPWLNPIIYTLR	EVKAM	WVT	VILCEK	314
AOLFR201 . p	PRKAFSTCAHHTVWILEFVPCU	Q KSGYSPETK	AVSV	ETIPWLNPIIYTLR	EVKAM	WVT	VILCEK	314
AOLFR202 . p	PRKAFSTCAHHTVWILEFVPCU	Q KSGYSPETK	AVSV	ETIPWLNPIIYTLR	EVKAM	WVT	VILCEK	314
AOLFR203 . p	PRKAFSTCAHHTVWILEFVPCU	Q KSGYSPETK	AVSV	ETIPWLNPIIYTLR	EVKAM	WVT	VILCEK	314
AOLFR204 . p	PRKAFSTCAHHTVWILEFVPCU	Q KSGYSPETK	AVSV	ETIPWLNPIIYTLR	EVKAM	WVT	VILCEK	314
AOLFR205 . p	PRKAFSTCAHHTVWILEFVPCU	Q KSGYSPETK	AVSV	ETIPWLNPIIYTLR	EVKAM	WVT	VILCEK	314
AOLFR206 . p	PRKAFSTCAHHTVWILEFVPCU	Q KSGYSPETK	AVSV	ETIPWLNPIIYTLR	EVKAM	WVT	VILCEK	314
AOLFR190 . p	PRKAFSTCAHHTVWILEFVPCU	Q KSGYSPETK	AVSV	ETIPWLNPIIYTLR	EVKAM	WVT	VILCEK	314
AOLFR207 . p	PRKAFSTCAHHTVWILEFVPCU	Q KSGYSPETK	AVSV	ETIPWLNPIIYTLR	EVKAM	WVT	VILCEK	314
AOLFR208 . p	PRKAFSTCAHHTVWILEFVPCU	Q KSGYSPETK	AVSV	ETIPWLNPIIYTLR	EVKAM	WVT	VILCEK	314

FIG. 4 (CONT-11)

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AOLFR209 . p	340	*	360	*	380	*	400	*	420	*	318
AOLFR210 . p											312
AOLFR211 . p											312
AOLFR212 . p											310
AOLFR213 . p											350
AOLFR214 . p											323
AOLFR215 . p											311
AOLFR216 . p											314
AOLFR217 . p											325

FIG. 4 (CONT-12)

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AOLFR235	. p	ND	SLOCFVLC	SDHPO	MIH	IALES	IL	IAN	ST	IL	SRL	A	:	53
AOLFR236	. p	TSQRD	TAI	YS	IN	SV	FA	K	M	T	SR	V	:	87
AOLFR237	. p	DQNY	R	V	K	E	T	T	C	T	Q	S	R	53
AOLFR238	. p	APEN											53	
AOLFR239	. p												53	
AOLFR240	. p												53	
AOLFR241	. p												73	
AOLFR242	. p												52	
AOLFR243	. p												53	
AOLFR244	. p												103	
AOLFR245	. p												53	
AOLFR246	. p												53	
AOLFR247	. p												53	
AOLFR248	. p												74	
AOLFR249	. p												93	
AOLFR250	. p												51	
AOLFR251	. p												52	
AOLFR252	. p												53	
AOLFR253	. p												71	
AOLFR254	. p												50	
AOLFR255	. p												53	
AOLFR256	. p												52	

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FIG. 5 (CONT-2)

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Aolfr24B . p	SHQ-PWYFLLAMISWGLSTSTPKWGLGFWF----	NIQETS	GCCLIQEFHMFCTG	TMILVWYDRVAICNPICQ	TMITNT	ISILASVWVGRNL	L	: 157
Aolfr33B . p	SHQ-PWYFLLAMISWGLSTSTPKWGLGFWF----	NIQETS	GCCLIQEFHMFCTG	TMILVWYDRVAICNPICQ	TMITNT	ISILASVWVGRNL	L	: 157
Aolfr130B .	HLE-PWYFLLAMISWGLSTSTPKWGLGFWF----	NIQETS	GCCLIQEFHMFCTG	TMILVWYDRVAICNPICQ	TMITNT	ISILASVWVGRNL	L	: 155
Aolfr142B .	SIN-PWYFLLAMISWGLSTSTPKWGLGFWF----	NIQETS	GCCLIQEFHMFCTG	TMILVWYDRVAICNPICQ	TMITNT	ISILASVWVGRNL	L	: 160
Aolfr171C .	RLE-PWYFLLAMISWGLSTSTPKWGLGFWF----	NIQETS	GCCLIQEFHMFCTG	TMILVWYDRVAICNPICQ	TMITNT	ISILASVWVGRNL	L	: 155
Aolfr218 . p	HLE-PWYFLLAMISWGLSTSTPKWGLGFWF----	NIQETS	GCCLIQEFHMFCTG	TMILVWYDRVAICNPICQ	TMITNT	ISILASVWVGRNL	L	: 155
Aolfr219 . p	RLE-PWYFLLAMISWGLSTSTPKWGLGFWF----	NIQETS	GCCLIQEFHMFCTG	TMILVWYDRVAICNPICQ	TMITNT	ISILASVWVGRNL	L	: 179
Aolfr220 . p	ALH-PWYFLLAMISWGLSTSTPKWGLGFWF----	NIQETS	GCCLIQEFHMFCTG	TMILVWYDRVAICNPICQ	TMITNT	ISILASVWVGRNL	L	: 183
Aolfr221 . p	SLR-PWYFLLAMISWGLSTSTPKWGLGFWF----	NIQETS	GCCLIQEFHMFCTG	TMILVWYDRVAICNPICQ	TMITNT	ISILASVWVGRNL	L	: 155
Aolfr222 . p	HLE-PWYFLLAMISWGLSTSTPKWGLGFWF----	NIQETS	GCCLIQEFHMFCTG	TMILVWYDRVAICNPICQ	TMITNT	ISILASVWVGRNL	L	: 155
Aolfr223 . p	ALH-PWYFLLAMISWGLSTSTPKWGLGFWF----	NIQETS	GCCLIQEFHMFCTG	TMILVWYDRVAICNPICQ	TMITNT	ISILASVWVGRNL	L	: 156
Aolfr224 . p	RLE-PWYFLLAMISWGLSTSTPKWGLGFWF----	NIQETS	GCCLIQEFHMFCTG	TMILVWYDRVAICNPICQ	TMITNT	ISILASVWVGRNL	L	: 155
Aolfr225 . p	HLE-PWYFLLAMISWGLSTSTPKWGLGFWF----	NIQETS	GCCLIQEFHMFCTG	TMILVWYDRVAICNPICQ	TMITNT	ISILASVWVGRNL	L	: 153
Aolfr226 . p	TLK-PWYFLLAMISWGLSTSTPKWGLGFWF----	NIQETS	GCCLIQEFHMFCTG	TMILVWYDRVAICNPICQ	TMITNT	ISILASVWVGRNL	L	: 160
Aolfr227 . p	RLE-PWYFLLAMISWGLSTSTPKWGLGFWF----	NIQETS	GCCLIQEFHMFCTG	TMILVWYDRVAICNPICQ	TMITNT	ISILASVWVGRNL	L	: 155
Aolfr228 . p	HLE-PWYFLLAMISWGLSTSTPKWGLGFWF----	NIQETS	GCCLIQEFHMFCTG	TMILVWYDRVAICNPICQ	TMITNT	ISILASVWVGRNL	L	: 155
Aolfr229 . p	RLE-PWYFLLAMISWGLSTSTPKWGLGFWF----	NIQETS	GCCLIQEFHMFCTG	TMILVWYDRVAICNPICQ	TMITNT	ISILASVWVGRNL	L	: 176
Aolfr230 . p	RLE-PWYFLLAMISWGLSTSTPKWGLGFWF----	NIQETS	GCCLIQEFHMFCTG	TMILVWYDRVAICNPICQ	TMITNT	ISILASVWVGRNL	L	: 156
Aolfr231 . p	LLK-PWYFLLAMISWGLSTSTPKWGLGFWF----	NIQETS	GCCLIQEFHMFCTG	TMILVWYDRVAICNPICQ	TMITNT	ISILASVWVGRNL	L	: 155
Aolfr232 . p	HLE-PWYFLLAMISWGLSTSTPKWGLGFWF----	NIQETS	GCCLIQEFHMFCTG	TMILVWYDRVAICNPICQ	TMITNT	ISILASVWVGRNL	L	: 187
Aolfr233 . p	HLE-PWYFLLAMISWGLSTSTPKWGLGFWF----	NIQETS	GCCLIQEFHMFCTG	TMILVWYDRVAICNPICQ	TMITNT	ISILASVWVGRNL	L	: 159
Aolfr234 . p	SLM-PWYFLLAMISWGLSTSTPKWGLGFWF----	NIQETS	GCCLIQEFHMFCTG	TMILVWYDRVAICNPICQ	TMITNT	ISILASVWVGRNL	L	: 153

FIG. 5 (CONT-4)

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	*	120	*	140	*	160	*	180	*	200	*												
Aolfr235 . p :	RLH	-PMVFLSHLAI	SALATSS	PMIL	LWG	PKTIS	GCTIOYV	WLGAT	CI	VM	EDRVA	VGRPR	RYTA	IN	PCML	IAVIA	C	LG	N	: 155			
Aolfr236 . p :	HLH	-PMVFLSHLAI	FACLSVT	PKWAGL	TL	DKWIS	ECAVOIC	HFLAST	CE	YTVA	EDRVA	ICQPH	VPVNR	CAE	AGIT	AI	ATH		: 190				
Aolfr237 . p :	HLH	-PMVFLSHLAI	ICSSITAP	KVII	IS	ETKIS	SCTVOFF	HLGGAD	VES	SV	EDRVA	ISKPI	PMIT	SRGCTG	IV	FLGG	IL	H	: 155				
Aolfr238 . p :	RLQ	-PMVFLSHLAI	VLGNST	VIAPK	IME	V	KKKTIS	YECAT	GG	FFIVS	VM	AM	YDRVA	ICP	ILM	VSRLCLL	IV	ST	Y	FST	: 155		
Aolfr239 . p :	CLH	-PMVFLSHLAI	ANOLASE	ATPK	IR	F	S	DKLIS	GCAO	CH	FELH	FTGGA	MM	VS	YDRVA	ICQPH	PMIT	LSNOT	CIR	IVLAS	VFFH	: 156	
Aolfr240 . p :	ALH	-PMVFLSHLAI	QVLL	TTDI	PP	LA	IGS	PHQ	ALS	QCAO	CH	IV	IVIGIS	CC	TAM	YDRVA	ICQPH	PRVST	ILIS	PCLA	IVGSS	TLIT	: 156
Aolfr241 . p :	SLH	-PMVFLSHLAI	QVLL	TTDI	PP	LA	IGS	PHQ	ALS	QCAO	CH	IV	IVIGIS	CC	TAM	YDRVA	ICQPH	PRVST	ILIS	PCLA	IVGSS	TLIT	: 156
Aolfr242 . p :	SLH	-PMVFLSHLAI	S	PGLSEST	PKWIGTFF	---	TLRESRE	GLTCA	FFHLCTG	SA	VAM	YIC	VAICD	PICT	YITVA	VS	WALAI	RPI	F	: 154			
Aolfr243 . p :	ALH	-PMVFLSHLAI	CSCEIC	TTVI	PKWIV	IS	---	OKKTIS	ILCAIOFS	FFGSSHST	AM	YDRVA	ICQPH	PRVST	ILIS	PCLA	IVGSS	TLIT	: 155				
Aolfr244 . p :	RLH	-PMVFLSHLAI	QVLL	TTDI	PP	LA	IGS	PHQ	ALS	QCAO	CH	IV	IVIGIS	CC	TAM	YDRVA	ICQPH	PRVST	ILIS	PCLA	IVGSS	TLIT	: 155
Aolfr245 . p :	TLH	-PMVFLSHLAI	QVLL	TTDI	PP	LA	IGS	PHQ	ALS	QCAO	CH	IV	IVIGIS	CC	TAM	YDRVA	ICQPH	PRVST	ILIS	PCLA	IVGSS	TLIT	: 155
Aolfr246 . p :	HLH	-PMVFLSHLAI	QVLL	TTDI	PP	LA	IGS	PHQ	ALS	QCAO	CH	IV	IVIGIS	CC	TAM	YDRVA	ICQPH	PRVST	ILIS	PCLA	IVGSS	TLIT	: 155
Aolfr247 . p :	HLH	-PMVFLSHLAI	QVLL	TTDI	PP	LA	IGS	PHQ	ALS	QCAO	CH	IV	IVIGIS	CC	TAM	YDRVA	ICQPH	PRVST	ILIS	PCLA	IVGSS	TLIT	: 155
Aolfr248 . p :	HLH	-PMVFLSHLAI	QVLL	TTDI	PP	LA	IGS	PHQ	ALS	QCAO	CH	IV	IVIGIS	CC	TAM	YDRVA	ICQPH	PRVST	ILIS	PCLA	IVGSS	TLIT	: 155
Aolfr249 . p :	RLQ	-PMVFLSHLAI	QVLL	TTDI	PP	LA	IGS	PHQ	ALS	QCAO	CH	IV	IVIGIS	CC	TAM	YDRVA	ICQPH	PRVST	ILIS	PCLA	IVGSS	TLIT	: 155
Aolfr250 . p :	HLH	-PMVFLSHLAI	QVLL	TTDI	PP	LA	IGS	PHQ	ALS	QCAO	CH	IV	IVIGIS	CC	TAM	YDRVA	ICQPH	PRVST	ILIS	PCLA	IVGSS	TLIT	: 155
Aolfr251 . p :	KLH	-PMVFLSHLAI	QVLL	TTDI	PP	LA	IGS	PHQ	ALS	QCAO	CH	IV	IVIGIS	CC	TAM	YDRVA	ICQPH	PRVST	ILIS	PCLA	IVGSS	TLIT	: 155
Aolfr252 . p :	SLH	-PMVFLSHLAI	QVLL	TTDI	PP	LA	IGS	PHQ	ALS	QCAO	CH	IV	IVIGIS	CC	TAM	YDRVA	ICQPH	PRVST	ILIS	PCLA	IVGSS	TLIT	: 155
Aolfr253 . p :	RLH	-PMVFLSHLAI	QVLL	TTDI	PP	LA	IGS	PHQ	ALS	QCAO	CH	IV	IVIGIS	CC	TAM	YDRVA	ICQPH	PRVST	ILIS	PCLA	IVGSS	TLIT	: 155
Aolfr254 . p :	RLH	-PMVFLSHLAI	QVLL	TTDI	PP	LA	IGS	PHQ	ALS	QCAO	CH	IV	IVIGIS	CC	TAM	YDRVA	ICQPH	PRVST	ILIS	PCLA	IVGSS	TLIT	: 155
Aolfr255 . p :	RLH	-PMVFLSHLAI	QVLL	TTDI	PP	LA	IGS	PHQ	ALS	QCAO	CH	IV	IVIGIS	CC	TAM	YDRVA	ICQPH	PRVST	ILIS	PCLA	IVGSS	TLIT	: 155
Aolfr256 . p :	KLH	-PMVFLSHLAI	QVLL	TTDI	PP	LA	IGS	PHQ	ALS	QCAO	CH	IV	IVIGIS	CC	TAM	YDRVA	ICQPH	PRVST	ILIS	PCLA	IVGSS	TLIT	: 155

FIG. 5 (CONT-5)

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[illegible]

FIG. 5 (CONT-6)

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220	*	240	*	260	*	280	*	300	*	320
p	:	p	:	p	:	p	:	p	:	p
AOOLFR24B	:	AOOLFR24B	:	AOOLFR24B	:	AOOLFR24B	:	AOOLFR24B	:	AOOLFR24B
AOOLFR33B	:	AOOLFR33B	:	AOOLFR33B	:	AOOLFR33B	:	AOOLFR33B	:	AOOLFR33B
AOOLFR130B	:	AOOLFR130B	:	AOOLFR130B	:	AOOLFR130B	:	AOOLFR130B	:	AOOLFR130B
AOOLFR142B	:	AOOLFR142B	:	AOOLFR142B	:	AOOLFR142B	:	AOOLFR142B	:	AOOLFR142B
AOOLFR171C	:	AOOLFR171C	:	AOOLFR171C	:	AOOLFR171C	:	AOOLFR171C	:	AOOLFR171C
AOOLFR218	:	AOOLFR218	:	AOOLFR218	:	AOOLFR218	:	AOOLFR218	:	AOOLFR218
AOLfr219	:	AOLfr219	:	AOLfr219	:	AOLfr219	:	AOLfr219	:	AOLfr219
AOLfr220	:	AOLfr220	:	AOLfr220	:	AOLfr220	:	AOLfr220	:	AOLfr220
AOLfr221	:	AOLfr221	:	AOLfr221	:	AOLfr221	:	AOLfr221	:	AOLfr221
AOLfr222	:	AOLfr222	:	AOLfr222	:	AOLfr222	:	AOLfr222	:	AOLfr222
AOOLfr223	:	AOOLfr223	:	AOOLfr223	:	AOOLfr223	:	AOOLfr223	:	AOOLfr223
AOLfr224	:	AOLfr224	:	AOLfr224	:	AOLfr224	:	AOLfr224	:	AOLfr224
AOOLFR225B	:	AOOLFR225B	:	AOOLFR225B	:	AOOLFR225B	:	AOOLFR225B	:	AOOLFR225B
AOLfr226	:	AOLfr226	:	AOLfr226	:	AOLfr226	:	AOLfr226	:	AOLfr226
AOLfr227	:	AOLfr227	:	AOLfr227	:	AOLfr227	:	AOLfr227	:	AOLfr227
AOLfr228	:	AOLfr228	:	AOLfr228	:	AOLfr228	:	AOLfr228	:	AOLfr228
AOLfr229	:	AOLfr229	:	AOLfr229	:	AOLfr229	:	AOLfr229	:	AOLfr229
AOLfr230	:	AOLfr230	:	AOLfr230	:	AOLfr230	:	AOLfr230	:	AOLfr230
AOLfr231	:	AOLfr231	:	AOLfr231	:	AOLfr231	:	AOLfr231	:	AOLfr231
AOLfr232	:	AOLfr232	:	AOLfr232	:	AOLfr232	:	AOLfr232	:	AOLfr232

FIG. 5 (CONT-7)

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AOLfr233 . p :	220	240	*	260	*	280	*	300	*	320	:	265
AOLfr234 . p :	220	240	*	260	*	280	*	300	*	320	:	259
AOLfr235 . p :	220	240	*	260	*	280	*	300	*	320	:	261
AOLfr236 . p :	220	240	*	260	*	280	*	300	*	320	:	296
AOLfr237 . p :	220	240	*	260	*	280	*	300	*	320	:	260
AOLfr238 . p :	220	240	*	260	*	280	*	300	*	320	:	261
AOLfr239 . p :	220	240	*	260	*	280	*	300	*	320	:	261
AOLfr240 . p :	220	240	*	260	*	280	*	300	*	320	:	262
AOLfr241 . p :	220	240	*	260	*	280	*	300	*	320	:	281
AOLfr242 . p :	220	240	*	260	*	280	*	300	*	320	:	259
AOLfr243 . p :	220	240	*	260	*	280	*	300	*	320	:	261
AOLfr244 . p :	220	240	*	260	*	280	*	300	*	320	:	311
AOLfr245 . p :	220	240	*	260	*	280	*	300	*	320	:	260
AOLfr246 . p :	220	240	*	260	*	280	*	300	*	320	:	261
AOLfr247 . p :	220	240	*	260	*	280	*	300	*	320	:	261
AOLfr248 . p :	220	240	*	260	*	280	*	300	*	320	:	282
AOLfr249 . p :	220	240	*	260	*	280	*	300	*	320	:	301
AOLfr250 . p :	220	240	*	260	*	280	*	300	*	320	:	259
AOLfr251 . p :	220	240	*	260	*	280	*	300	*	320	:	259
AOLfr252 . p :	220	240	*	260	*	280	*	300	*	320	:	261

FIG. 5 (CONT-8)

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AOLFR253 . p : GLLTTP TMSF TQSRKILSFFCTPALLSLS VS YKQ TYLCCIL TPIMTSSSVTILHIL HANSAA RKALATCSSHITIVILF ASE IVVL : 279
AOLFR254 . p : GFLTTP TMMVYCGSRINFECE PAVILACIA SYLTY YICCVI IPISITSTSILILTI HMPSAE KKAATCSSHITWSTHY AAF IVVL : 258
AOLFR255 . p : GFLTTP TMOF TFCASREINFECE PALIKLSST SAYTA YVCCIM IPFSITSGSYTRILITV YWSEAE GKAVATCSSHIVVSTSY AAF IVVL : 261
AOLFR256 . p : ALVHTHILRP TCGPQKINEFFCO MSVFALACGPR NO YAGSAF EGPIOE SNLHILSRHLEDPNGRAADRLTIPA PSHIOWCELE STVMWA : 261
AOLFR257 . p : ALVHTIIRLTTCGPQKINEFFCO MSVFALACIA RNO FAGSAF GPLOVSYLHILVAIL KOSGE RKAATCSSHICWCELE SALVWA : 260
AOLFR259 . p : ALINLL LRLTECGPOETNFECE LSVILACIA WNF FAGGVH GPISMLISYMRILAIL KOSKE KKAATCSSHICWCELE MAIVVIV : 260
AOLFR274B . : SLQVAFISLATCQAQIDEFFCO PPMWVWCAQ H HOS LVAAILA AVPEFTTSTFIVAIL KHSAAH KKAATCSSHITWILCY CCAVILC : 252
AOLFR276B . : VFPLPF LKRLTCKASWLAHSYCHADLIRLPWGDITNS YGLEFIVISAFGVDSH LSVILHSLVIA IASRGE IKTANTCSSHIVAVILYVPMVSVNV : 264
AOLFR311B . : ALIHTAFRICCGSNEINEFFCO PPHILSRS QN FTVFGE STISGVFISYCIILSVL EHSAPFKALTCSSHISAVILC TTYFER : 261
AOLFR314 . p : SSILTS TFTLYCGPNENDFECE PALIPACIA SAR SFTNVL S VCFILTSYTRITISI LSRTTE RRAATCSAHILAILCAY PITVIO : 261
AOLFR324B . : VIPLVF LRLTECGHRIIP TYCEHMGALACASIK NIEGL-GSIS LDVILSHIRILYAVFG IPSWEALKALINTCSSHICVILASTPAF SEFT : 262
AOLFR328 . p : LDALIN LLAANNVCEAKIHHYSVEMPSILPLSQ D SRS VLICST HCLGNELFLSYTRIISTIL--SISSTSGPSKAFSCSAHTATLYYGSGLRH : 259

FIG. 5 (CONT-9)

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	*	340	*	360	*	380	*						
AOLFR24B . p	:	HRFGQNI	PHYTHI	ANIMW	PEALNPVIY	RT	CI	EQIV	EVQKE	----	:	312	
AOLFR33B . p	:	HRFGHNI	PHYTHI	ANIMW	PEALNPVIY	RT	CI	EQIV	NPYSFWHEDPKRIFHNNSVRQ	----	:	327	
AOLFR130B .	:	PLSSYSLEK	----	ITSV	IPWNPVIY	TRN	DI	EAV	A	GRKQPPVFSSDI	----	:	317
AOLFR142B .	:	PSSSHALDT	----	ATV	IPWNPVIY	TRN	DI	EAV	A	INK-N	----	:	314
AOLFR171C .	:	PKSNHSLDT	----	ATV	IPWNPVIY	TRN	DI	EAV	A	DKGCENQILTFKIRKLY	----	:	324
AOLFR218 . p	:	PFD--SFSL	----	ITV	IPWNPVIY	TRN	DI	EAV	A	TKYLCEK	----	:	313
Aolfr219 . p	:	PFS--SYSV	----	ATV	IPWNPVIY	TRN	DI	EAV	A	KSRYLKPSQSVVIR-NWLFLETK	----	:	348
Aolfr220 . p	:	FSATYSVEW	----	ATV	IPWNPVIY	TRN	DI	EAV	A	EHYQKRWAGK	----	:	343
Aolfr221 . p	:	PRAMYTNNH	----	ITV	IPWNPVIY	TRN	DI	EAV	A	MGRCYPRDVQD	----	:	317
Aolfr222 . p	:	PKASYSLER	----	ATV	IPWNPVIY	TRN	DI	EAV	A	NAFRGLLGK	----	:	313
Aolfr223 . p	:	ATSRREAW	----	ATV	IPWNPVIY	TRN	DI	EAV	A	IGRRISADS	----	:	316
Aolfr224 . p	:	SIRNYSRE	----	ATV	IPWNPVIY	TRN	DI	EAV	A	MRGRDSG	----	:	311
AOLFR225B .	:	PSAKEGGAF	----	ITV	IPWNPVIY	TRN	DI	EAV	A	DSKKIVKL	----	:	309
Aolfr226 . p	:	PKALSADT	----	ITV	IPWNPVIY	TRN	DI	EAV	A	HLVQHDPPKASRN	----	:	327
Aolfr227 . p	:	PSPHLLPEI	----	ITV	IPWNPVIY	TRN	DI	EAV	A	RRKCGILWSTSKRKFLY	----	:	322
Aolfr228 . p	:	PPSNTWDX	----	ITV	IPWNPVIY	TRN	DI	EAV	A	SRSQAVAHACNLTG	----	:	322
Aolfr229 . p	:	PHSYHTPEQ	----	ATV	IPWNPVIY	TRN	DI	EAV	A	GRCVSSGKVTF	----	:	338
Aolfr230 . p	:	PHSYHTPEK	----	ATV	IPWNPVIY	TRN	DI	EAV	A	GRCSSQSIRVATVIRKG	----	:	324
Aolfr231 . p	:	PFS--RYSV	----	ITV	IPWNPVIY	TRN	DI	EAV	A	CI	----	:	304
Aolfr232 . p	:	PSSVHTPEK	----	ATV	IPWNPVIY	TRN	DI	EAV	A	TVEPAFQKAME	----	:	348
Aolfr233 . p	:	PSSVHTPEK	----	ATV	IPWNPVIY	TRN	DI	EAV	A	TVRFVL	----	:	315
Aolfr234 . p	:	PPATPAATQ	----	ITV	IPWNPVIY	TRN	DI	EAV	A	KRIFISENV	----	:	312

FIG. 5 (CONT-10)

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Aolfr235 . p	PAKSKQDQ--GAF	YSI	TPWNPLIYTLRMEV	GA	PKGREVG	312	
Aolfr236 . p	PRS--SEAG--ACAPA	YTI	TPMNPFIYTLRN	EAHALC	CSSFRESTAGSPPP	332	
Aolfr237 . p	PET--ALPT--TA	IFTV	SPLNPIIYTLRQEM	IAA	KRRLQSERILIQ	314	
Aolfr238 . p	PQTHSLDT--	YTI	IPMINPLIYSLRNN	VVAU	FENPCYFSGM	315	
Aolfr239 . p	PFS--REFV--	YTI	ETPLNPIIYTLRNEA	IAA	QNRRTFQ	310	
Aolfr240 . p	PQAGSVTI--	YTV	TPMNPFIYTLRN	DAHALH	KRQRPSP	313	
Aolfr241 . p	PTANVSNK--	YTI	IPLNPMVYSLRN	DVQIAL	GKKGSLKLYN	335	
Aolfr242 . p	HRCGRNIPHFHI	ANVW	PPALNSVIYGVH	QIAQVI	QFNNK	308	
Aolfr243 . p	EKTWTSQ--	YTI	TPLENPMIYSLRN	EFSA	IGOTFYPLS	313	
Aolfr244 . p	PHSYHKPAQ--	YTI	TPMNPFIYSLRN	DTGAL	A GREKGPQVSGGVF	369	
Aolfr245 . p	PFS--SLAS--	YTV	TPLNPSIYTLRN	KQFAL	RFQYVSSAQNF	312	
Aolfr246 . p	PTVSSIDK--	V	YTV	TPMNPFIYSLRN	DEALC	FSRATFFSM	313
Aolfr247 . p	PNSTHFFDT--	YTI	IPMINPLIYSLRNEE	NA	Y	EEN	307
Aolfr248 . p	PAKTSHEQ--GAF	YTV	TPANPLIYTLRNTA	SALH	LENCCGSACKLAOI	340	
Aolfr249 . p	PQSNNSQEN--	YGI	IPMINPLIYSLRN	EG		338	
Aolfr250 . p	PPSTASEEK--	YTI	TPMNPFIYSLRN	DA	GA	FSHRISIVSS	311
Aolfr251 . p	PKSRHPEEQ--	Q	YSLFNPMNPFIYSLRNEA	GA	IA	ARKERLT	309
Aolfr252 . p	PSSYOTPEK--	YTI	TPVINPIYSLRN	DVTRAL	SVQKPPY	312	
Aolfr253 . p	RSSYHTAEQ--	YTI	ETPMNPFIYSLRN	DVTRAL	S	QSRMNQEK	331
Aolfr254 . p	PQSEHTPEQ--	YTI	TPMNPFIYSLRN	DVIGAL	EACCSAQKVATSDA	316	
Aolfr255 . p	PHSYHTPEQ--	YTI	TPMNPFIYSLRN	DTGALC	GRCVSSGKVTF	317	
Aolfr256 . p	PKSRHPEEQ--QAVL	YSLFNPMNPFIYSLRNEA	GA	IA	WKQSK	311	

FIG. 5 (CONT-11)

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AOLFR257 . p	PKSSHQER--R	YSLEFNPILNPLIYSIRNAEV	CAI	WKQRSM	310
AOLFR259 . p	PONSQRQKQ--Q	YSLEFNPILNPLIYSIRNAQV	CAIY	QKKRTM	310
AOLFR274B .	PSSSYNPKQ--F	WTLCHPLNPLIYPRNSFM	CANG	TRNCLSQNS	305
AOLFR276B .	HRFGRHAPE--YVHKF	SLCTSNAIPMYIEHOD			295
AOLFR311B .	PSSSYSLDQ--T	YVTLVPLNPLIYSIRNAV	CAI	KNKILF	310
AOLFR314 . p	PTPNPMLGT---	Q LANNI CPMNPLIYTIIRNAEV	TAI	HRTGHVPES	312
AOLFR324B .	HCFGHDIPQYIHIE	ANIVW	PTENPVYCVRT	FI	FFKTDH
AOLFR328 . p	LMNSGSPIEL----	IFSQYTVVTPMNSLIYSI	KEVVVALKRTLEKVLQYTRR		312

FIG. 5 (CONT-12)

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DECLARATION OF NON-ESTABLISHMENT OF INTERNATIONAL SEARCH REPORT

(PCT Article 17(2)(a), Rules 13ter and 39)

Applicant's or agent's file reference 278005PCT	IMPORTANT DECLARATION	Date of mailing (day/month/year) 05 SEP 2001
International application No. PCT/US01/07771	International filing date (day/month/year) 15 MARCH 2001	(Earliest) Priority Date (day/month/year) 15 MARCH 2000
International Patent Classification (IPC) or both national classification and IPC Please See Continuation Sheet.		
Applicant SENOMYX, INC.		

This International Searching Authority hereby declares, according to Article 17(2)(a), that no international search report will be established on the international application for the reasons indicated below.

1. ☒ The subject matter of the international application relates to:
 - a. ☐ scientific theories.
 - b. ☐ mathematical theories.
 - c. ☐ plant varieties.
 - d. ☐ animal varieties.
 - e. ☒ essentially biological processes for the production of plants and animals, other than microbiological processes and the products of such processes.
 - f. ☐ schemes, rules or methods of doing business.
 - g. ☐ schemes, rules or methods of performing purely mental acts.
 - h. ☐ schemes, rules or methods of playing games.
 - i. ☐ methods for treatment of the human body by surgery or therapy.
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 - m. ☐ computer programs for which this International Searching Authority is not equipped to search prior art.
2. ☒ The failure of the following parts of the international application to comply with prescribed requirements prevents a meaningful search from being carried out:

☐ the description
 ☒ the claims
 ☐ the drawings
3. ☒ The failure of the nucleotide and/or amino acid sequence listing to comply with the standard provided for in Annex C of the Administrative Instructions prevents a meaningful search from being carried out.

☐ the written form has not been furnished or does not comply with the standard.
☒ the computer readable form has not been furnished or does not comply with the standard.
4. Further comments:

Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231	Authorized officer CHUNBURU SURYAPRABHA
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International application No.
PCT/US01/07771

The International Patent Classification (IPC) or National Classification and IPC are as listed below:

IPC(7): C07H 21/02; C12N 15/00; C07K 1/00 US CL: 536/23.1; 435/320.1; 530/350

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